

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 10, 2006, 06:41:45 ; Search time 4713.64 Seconds

(without alignments)
8942.712 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVPRVTRTPPLRGSR.....KDTLSLSGLSSDPTDMDPZ 2287

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlp
-Q=/abs/ABSSWEB_spool/US09611257/runat_10072006_064126_6972/app_query.fasta_1
-DB=Published Applications NA_Main -QMT=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -THR SCORE=pct -THR MAX=100
-MAXLEN=200000000 -HOST=abss06p
-USER=US09611257 @CGN_1_17492 @runat_10072006_064126_6972 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCH=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=0.5 -DELEXT=7

Database : Published Applications NA_Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	11980	99.6	6942	9	US-10-377-139-7 Sequence 7, Appli

2	11829	98.3	7285	3	US-09-383-894-3	Sequence 3, Appli
3	11673	97.0	7129	3	US-09-383-894-1	Sequence 1, Appli
4	10963.5	91.1	7825	10	US-10-756-149-31	Sequence 31, Appli
5	10963.5	91.1	7825	10	US-10-786-148-120	Sequence 120, App
6	10845.5	90.2	7648	9	US-10-377-139-10	Sequence 10, Appli
7	10845.5	90.2	7648	9	US-10-757-262-15	Sequence 15, Appli
8	10707	89.0	8116	7	US-10-062-674-2011	Sequence 2011, Ap
9	6242	89.0	8116	7	US-10-483-467-3	Sequence 3, Appli
10	6103	50.7	3993	9	US-10-930-301-51	Sequence 51, Appli
11	5432.5	45.2	6990	9	US-10-377-139-8	Sequence 8, Appli
12	5432.5	45.2	6990	15	US-11-000-688-609	Sequence 609, App
13	5420	45.1	6816	7	US-09-935-840-1	Sequence 1, Appli
14	5420	45.1	6816	7	US-10-425-801-1	Sequence 1, Appli
15	5420	45.1	6855	3	US-09-935-541-3	Sequence 3, Appli
16	5420	45.1	6855	7	US-10-425-800-3	Sequence 3, Appli
17	5407	45.0	6503	3	US-09-935-541-12	Sequence 12, Appli
18	5407	45.0	6503	7	US-10-425-800-12	Sequence 12, Appli
19	5361	44.6	5562	16	US-11-180-074-3	Sequence 3, Appli
20	3950	32.8	5562	3	US-09-030-482B-18	Sequence 18, Appli
21	3937.5	32.7	7969	13	US-11-097-143-8135	Sequence 8135, Ap
22	3861.5	32.1	6073	9	US-10-377-139-11	Sequence 11, Appli
23	3399.5	28.3	6933	10	US-10-450-763-10945	Sequence 10945, A
24	1745.5	14.5	7362	8	US-10-375-253-11	Sequence 11, Appli
25	1743.5	14.5	7376	6	US-10-033-026-3	Sequence 3, Appli
26	1739.5	14.5	7364	3	US-09-954-456-1179	Sequence 1179, Ap
27	1739.5	14.5	7364	6	US-10-033-026-5	Sequence 5, Appli
28	1739.5	14.5	7364	9	US-10-736-883-31	Sequence 31, Appli
29	1739.5	14.5	7364	10	US-10-843-641A-4206	Sequence 4206, Ap
30	1739.5	14.5	7364	10	US-10-483-467-5	Sequence 5, Appli
31	1739.5	14.5	7364	15	US-11-096-281-10	Sequence 10, Appli
32	1732.5	14.4	6984	9	US-10-736-883-37	Sequence 37, Appli
33	1727	14.4	7175	8	US-10-375-253-13	Sequence 13, Appli
34	1726.5	14.4	7121	9	US-10-736-883-43	Sequence 43, Appli
35	1725	14.3	7185	9	US-10-736-883-39	Sequence 39, Appli
36	1721	14.3	7177	6	US-10-033-026-7	Sequence 7, Appli
37	1721	14.3	7177	9	US-10-736-883-33	Sequence 33, Appli
38	1721	14.3	7177	10	US-10-483-467-7	Sequence 7, Appli
39	1720.5	14.3	6792	8	US-10-627-370-1	Sequence 1, Appli
40	1720	14.3	9695	9	US-10-736-883-27	Sequence 27, Appli
41	1720	14.3	9695	10	US-10-486-706-207	Sequence 207, App
42	1720	14.3	9695	15	US-11-096-281-12	Sequence 12, Appli
43	1717.5	14.3	6083	6	US-10-029-413A-21	Sequence 21, Appli
44	1717.5	14.3	6083	8	US-10-726-216-21	Sequence 21, Appli
45	1716.5	14.3	7713	9	US-10-736-883-41	Sequence 41, Appli

ALIGNMENTS

RESULT 1

US-10-377-139-7
; Sequence 7, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6942
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-377-139-7

Alignment Scores:	0	Length:	6942
Pred. No.:	11980.00	Matches:	2283
Score:			

Percent Similarity: 99.8%	Conservative: 0
Best Local Similarity: 99.8%	Mismatches: 3
Query Match: 99.6%	Indels: 2
DB: 9	Gaps: 0
US-09-611-257A-24 (1-2287) x US-10-377-139-7 (1-6942)	
Qy	1 MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20
Db	16 ATGCTCCCCACCGGGTCCCCCGTTGGTGAGGACACTCTCTCGAGGGCTCCGCTCG 75
Qy	21 ProSerSerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu 40
Db	76 CCTCTTTCCGACCCCGGGGCCCGCTGGCCAGAGGATGGACGAGGAGGATGGAG 135
Qy	41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
Db	136 CGGGCGCGAGAGTGGGACAGCCCCGTAGCTTCACGAGCTCAACGACTGTCGCGGG 195
Qy	61 ProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluA 80
Db	196 CCGGGGCGCGAGGGCCGGGTTCGACGGAAAGGACCCCGGGCAGCGCGGACTCCGAGG 255
Qy	80 laGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAsps 100
Db	256 CGGAGGGGCTCCGCTACCCGCGCTAGCCCGGTGGTTTCTTCTACTTTCAGCCAGGACA 315
Qy	100 erArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerM 120
Db	316 GCCGCCCGGAGCTGGGTCTCCGACGGTCTGTAAACCCGCTGGTTCGAGCGAGTCAGTA 375
Qy	120 etLeuValLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleA 140
Db	376 TGCTGGTCAATTCTTCTCACTGTGTGACTCTGGGTATGTTTCAGGCCGTGTGAGACATTG 435
Qy	140 laCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheP 160
Db	436 CCTGTGACTCCAGCGCTGCCGATCTCTGCAGCGCTTCGATGACTTCATCTTTGCCCTCT 495
Qy	160 heAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCysTyrL 180
Db	496 TTGCTGTGAAATGGTGGTGAAGATGGTGGCTTTGGGCATCTTTGGGAAGAAATGTTACC 555
Qy	180 euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS 200
Db	556 TGGGAGACACTTGGAAACGGGCTTGACTTTTTCATTTGTCATGTGCAGGATGCTGGAGTATT 615
Qy	200 erLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProL 220
Db	616 CGCTGGACCTCGAAGCTGACGTTCTCCGAGTCAGGACAGTCCGTGTGTGCGGACCGC 675
Qy	220 euArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrL 240
Db	676 TCAGGGCCATTAAACGGGTGCCAGCATGCGCATTTCTCGTCACATTAATGCTGGACACCT 735
Qy	240 euProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleV 260
Db	736 TGCCTATGCTGGGCAACGCTCTGCTGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCT 795
Qy	260 alGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheS 280
Db	796 TGGGCGTCCAGCTGTGGGCGAGACTGCTTCGCAACCGGTGCTTCTCTCCCGAGAACTTCA 855
Qy	280 erLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP 300
Db	856 GCCTCCCCCTGAGGCTGAGCTGGAGCCCTTATTACGACAGAGAAATGAGGACGAGAGCC 915
Qy	300 roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL 320
Db	916 CTTTCATCTGCTCTCAGCCTCGGAGAAATGCAATGAGATCTCTGAGGAGTGTGCCACAC 975
Qy	320 euArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS 340
Db	2056 GCATAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCTCGGGCCCGGACAGTTGTC 2115
Db	976 TCGTGGGGAAGCGGTGGTGGCCCACTTCGAGTCTGGAGCTATGAGACTATAACAGATT 1031
Qy	340 erSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH 360
Db	1036 CACGACACACCACTCTGTCTCACTGGAAACAGTACTATACCAACTGCTCTGCGGGCGAGC 1095
Qy	360 isAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIleP 380
Db	1096 ACAACCCCTTCAAAGCGGCATCAACTTTTGACAACTTGGCTATGCTGGATCGCATCT 1155
Qy	380 heGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHis 400
Db	1156 TCCAGGTCTATCACACTGGAGGGCTGGGTGCACATGATGACTTCGTAAATGGACGCTCACT 1215
Qy	400 erPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleA 420
Db	1216 CCTTCTACAACCTCATCTACTTCTTCTCATCATCATCGTGGGCTCTTCTTCTCATGATCA 1275
Qy	420 snLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL 440
Db	1276 ACCTGTGCTTGGTGGTGAITGCCACGAGTTCTCCGAGACAAACACGCGGAGAGTCCAGC 1335
Qy	440 euMetArgGluGlnArgValArgPheLeuSerSerAsnAlaSerThrLeuAlaSerPheSerG 460
Db	1336 TGATGGGGAGCAGCGTGTACGATTCCTGTCGAATGCTAGCACCCCTGGCAAGCTTCTCTG 1395
Qy	460 luProGlySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArgLysAlaAla 480
Db	1396 AGCCAGGCACTGCTATGAGGAGCTACTCNAGTACTCTGGTGTACATCTCTCCGAANAGCAG 1455
Qy	480 laArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP 500
Db	1456 CCCGAAGCTGGCCCGAGTCTCTAGGGCTATAGGCGTGGGGCTGGGCTCTCAGCAGCC 1515
Qy	500 roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA 520
Db	1516 CAGTGGCCCGTAGTGGGCGAGGAGCCCGAGCCAGTGGAGCTGCATCGCTCACACCGTC 1575
Qy	520 rgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyrHisLeuG 540
Db	1576 GTCTGTCTGTCCACCCTGGTCCACCACCATCACACCACCATCACCATTACCACTGG 1635
Qy	540 lyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG 560
Db	1636 GTAATGGACGCTCAGAGTTCCCGGCGCCAGCCAGAGATCCAGGACAGGATGCCAATG 1695
Qy	560 lySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGlyProProA 580
Db	1696 GGTCTCGCGGCTCATGTACACAGCTTCTACCATGCTGACTGCCACTTGGAGCCAGTCCGTT 1755
Qy	580 rgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC 600
Db	1756 GGGTGGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTGGAGCCAGTCCGTT 1815
Qy	600 ysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620
Db	1816 GCCAGGCACCCCTCCAGATGCCATCGAGGCACTCTGTAGGACTGTGGTAGTGGGA 1875
Qy	620 ysValTyrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuV 640
Db	1876 AGGTGTACCCCACTGTGCATACCAAGCCCTCCACGAGATACTCAAGAGATAAAGCAGCTAG 1935
Qy	640 alGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyP 660
Db	1936 TGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACAGCTTCAACATCCCACCTGGGC 1995
Qy	660 roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC 680
Db	1996 CCTTCAGCTCCATGCACAAGCTCTCTGGAGACACAGAGTACGGGAGCGCTGCCATGCTCCT 2055
Qy	680 yslYsIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP 700
Db	2056 GCATAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCTCGGGCCCGGACAGTTGTC 2115

QY 700 roTyrCysAlaA-gThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAsps 720
DB 2116 CCTACTGTGCGGACAGGAGGAGGAGCGAGAGTCCGCTGACCATGTTCATGCCGTGACT 2175
QY 720 erAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspp 740
DB 2176 CAGACAGCGAGGTGTGTATGAGTTTCACACGAGCGCTCAGACAGTGCATCCGGGATC 2235
QY 740 roHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA 760
DB 2236 CCACACGCGCGGCGACAGCGAGCTCGGCCAGATGCAGAGCCTAGTTCTGTGCTGG 2295
QY 760 laPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA 780
DB 2296 CTTTCTCGAGGCTGATCTGTGACACATTCGCGAAGATCGTAGATAGCAAAATACTTTGGCC 2355
QY 780 rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG 800
DB 2356 GGGGAATCATGATCGCCATCTCTGGTCAATACATCAGCATGGGCATCGAGTACACGAGC 2415
QY 800 lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA 820
DB 2416 AGCCCGAGGAGCTCACCAAGCCTCGGAATTCAGCAACATCGTCTTCACCAGGCTCTTCG 2475
QY 820 laLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProT 840
DB 2476 CCTTGGAGATGCTGTGAACACTGCTGTCTACGGTCCCTTTGGCTACATTAAGAAATCCCT 2535
QY 840 yrAsnIlePheAspGlyValIleValIleValIleSerValTrpGluIleValGlyGlnG 860
DB 2536 ACAACATCTTTGATGGTGTCAITTTGTGTCTATGAGTGTGGGAGATTTGGGGCCAGCAGG 2595
QY 860 lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgp 880
DB 2596 GAGGTGGCCTGTGGTGTCTGGGACCTTCCGCCGTGATCGGGTGTCTGAAGCTGGTGGCT 2655
QY 880 heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT 900
DB 2656 TCCTGCGGCGCTGCAGCGCCAGCTGCTGTGTCTCATGTAAGACCATGGACAACTGGGCCA 2715
QY 900 hrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuP 920
DB 2716 CCTTCTGCATGCTCTCATGCTGTTCATCTTTCATCTTTCAGCATCTCTGGGCATGCTCT 2775
QY 920 heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA 940
DB 2776 TTGGTTGCAAGTTTCGCATCTGAACGGGATGGGACACTTGGCCAGACCGGAAGAAATTTCC 2835
QY 940 spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL 960
DB 2836 ACTCCCTGCTCTGGGCCATCGTCACTGCTCTTTCAGATTCTGACTCAGGAAGACTTGAATA 2895
QY 960 ysValLeuTyrAsnGlyWeAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaL 980
DB 2896 AAGTCCCTCTCAACGGCATGGCCTCCACATCGTCTTGGGCTGCTCTTTACTTTCATCGCCC 2955
QY 980 euMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyP 1000
DB 2956 TCATGACTTTTGGCAACTATGTGCTCTTTAACTGCTGTGGGCCATTTCTTGTGAAGGAT 3015
QY 1000 heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV 1020
DB 3016 TCCAGGACAGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTTGGCCCAAGTG 3075
QY 1020 alAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG 1040
DB 3076 TGGATGTTGATGGGGACAGAAAGCGCTTTGGCCCTTGGTGGCTTTGGGAGAACACACGGG 3135
QY 1040 luLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH 1060
DB 3136 AACTACGAAAGAGCCTTTTGGCACCCCTTCATTCATCCATCGGCTGCAGACCAATGTAC 3195

QY 1060 isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrS 1080
DB 3196 ACCCAAGAGCTCCAGCACAGGTGTGGGGAGACACTGGGCTCTGGCTCTCGACGTACCA 3255
QY 1080 erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerA 1100
DB 3256 GTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCAACATGAGATGAAATGTCCGCCAAGTG 3315
QY 1100 laArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerS 1120
DB 3316 CCGCAGCTCCCGCAGACAGTCCCTGGAGTGGCGCAAGCAGCAGTGGACCGAGCGCTCCA 3375
QY 1120 erArgAsnSerLeuGlyArgAlaProSerSerLeuLysArgArgSerProSerGlyGluArgA 1140
DB 3376 GCAGGAACAGCTTGGGCGCGGCCCCAGACCTAAAGCGGAGGAGCCCGAGGGGAGCGGA 3435
QY 1140 rgSerLeuLeuSerGlyGluGlnGluSerGlnAspGluGluGluSerSerGluGluA 1160
DB 3436 GGTCCCTGCTGTCTGGAGAGGGCCAGAGAGTCAAGATGAGGAGGAAAGTTCAAGAGAGG 3495
QY 1160 spArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaL 1180
DB 3496 ACCGGCCAGCCAGCAGGCGAGTGACCATCGCCACAGGGGTTCCTTGAACGTGAGGCCA 3555
QY 1180 ysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG 1200
DB 3556 AGAGTTCTCTTTGACCTCGCTGACACTCTGCAGGTGCGGGGGCTGCACCGCACGCCAGCG 3615
QY 1200 lyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
DB 3616 GCCGGAGCTCTGCTCTTGAGCACAAGACTGTAAATGCAAGTGGCTTTAGGGCGTTTGG 3675
QY 1220 laArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyA 1240
DB 3676 CCGCACCTCTGAGSACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3735
QY 1240 snLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysA 1260
DB 3736 ATCTGAGCAAAAGGGAAACGATACAAAGCCTGGGTTCAGATCCCGGCTTCTCGCTGTGTC 3795
QY 1260 rgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeuC 1280
DB 3796 GAGAGCGAGATTCCTGGTGGCCCTATATCTTTCTCTCTCAGTCAAGGTTTCGTCCTCTGT 3855
QY 1280 yHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuA 1300
DB 3856 GTACACGGATCATCACCCACACAGATGTTTGACCATGTGTGGTCTCGTCATCATCTTCCTCA 3915
QY 1300 snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP 1320
DB 3916 ACTGTATACCATCGCTATGGAGCGCCCAAAATTGACCCCCACAGCGCTGAGCGCATCT 3975
QY 1320 heLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysV 1340
DB 3976 TCTGACCCCTCTCCAACTACATCTTACGGCAGTCTTTCTAGCTGAATGACAGTGAAGG 4035
QY 1340 alValAlaLeuGlyTyrCysPheGlyGlnAlaTyrLeuArgSerSerTrpAsnValL 1360
DB 4036 TGGTGCACCTGGGCTGGTGTCTTGGGAGCAGCGCTACCTCGCAGCAGCAGTGGAAATGTGC 4095
QY 1360 euAspGlyLeuLeuValLeuLeuSerValIleAspIleLeuValSerMetValSerAsps 1380
DB 4096 TGGACGGCTTGGCTGGTGTCTCATCTCGGTCAATCGACATCTCTGGTCTCCATGCTCTCCACA 4155
QY 1380 erGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProL 1400
DB 4156 CGGCGACCAAGATCTCTGGCATGCTGAGGCTGCTGGGCTGCTGGGACCCCTGCGCTCCAC 4215
QY 1400 euArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL 1420
DB 4216 TCAGGGTTCATCAGCGGGGCCGAGGACTGAAGCTGGTGGTAGAGACTCTGATGTATCCCC 4275
QY 1420 euLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleL 1440

4276	Db		TCAAACCAATTGGCAACATTGTGTGCTCAATTTGCTGTGCTTCTTCATCATTTTTCGAAATTC	4335
1440	Qy	euGlyValGlnLeuPheIysGlySLePheValCysGlnGlyGluAAspThrArgAsnI	1460	
4336	Db	TCGGGGTGCAGCTCTTCAAAGGGAAGTCTTCGTTGTCTCAGGTGAGGACACAGGAACA	4395	
1460	Qy	leThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnP	1480	
4396	Db	TCACTAACAAATCCGACTGGCTGAGCGCAGCTACCGATGGGTCCGGCACAAATCACACT	4455	
1480	Qy	heAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpV	1500	
4456	Db	TTGACAACCTGGGCGCAGGCTCTGATGTCCTGTTTGTGCTGGCCTCCAAGATGGTGTGG	4515	
1500	Qy	alAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH	1520	
4516	Db	TTGACATCATGATGATGGGCTGGATGCTGTGGGTGGGATCAGCAGCCCATCATGAACC	4575	
1520	Qy	isAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValI	1540	
4576	Db	ACAACCCCTGGATGCTGCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	4635	
1540	Qy	euAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluG	1560	
4636	Db	TGAACATGTTTGTGGCGTGTGTGGTGGAGAACTTCCATAAGTCAGACAGCACCGAGGAG	4695	
1560	Qy	luGluGluAlaArgArgGluCluLysArgLeuArgArgLeuGluLysLysArgArgS	1580	
4696	Db	AGSAGGAGGCGAGCGCGTGGAGAGAGCGACTACGGAGCGCTGGAGAAAAGAGAGGA	4755	
1580	Qy	erLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgP	1600	
4756	Db	GTAAGGAGAAGCAGATGGCCGAAGCCAGCTGTCAGACCCCTACTACTCTGACTCTCGAGAT	4815	
1600	Qy	heArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyV	1620	
4816	Db	TCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGGTG	4875	
1620	Qy	allIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA	1640	
4876	Db	TCATCGGGCTGAACGTGTCTACTATGCCCATGGAAACATTACCAAGCAGCCGCCATCCTCG	4935	
1640	Qy	spGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP	1660	
4936	Db	ACGAGGCTCTGAAGATCTGCAATTTACATCTTTACCGTCACTTTTGTCTTTGAGTCAGTTT	4995	
1660	Qy	heLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAspL	1680	
4996	Db	TCAAACCTTGTGGCTTTTGGCTTCGCGCTTCTTCCAGGACAGGTGGAAACAGCTGGACC	5055	
1680	Qy	euAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS	1700	
5056	Db	TGGCTATTGTGCTCTGTGCCATCATGGGCATCACACTGGAGGAGATTGAGGTCATCTGT	5115	
1700	Qy	erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValI	1720	
5116	Db	CGTGTCCCATCAACCCACCATCATCCGTATCATGAGGGTGCTCCGCATTTGCTCGAGTTC	5175	
1720	Qy	euLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaI	1740	
5176	Db	TGAAGCTGTTGAAGATGCTGTGGGCATCGGGGCACCTGTCACACACCGTGTATGCAGGCC	5235	
1740	Qy	euProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIal	1760	
5236	Db	TGCCCCAGGTGGGAACCTGGGACTCTCTTTCATGTTATTGTTTTCATCTTTGACGCTC	5295	
1760	Qy	euGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG	1780	
5296	Db	TGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTTGTGAGGGCTTGG	5355	
1780	Qy	lyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT	1800	

Db	5356	GTCCGATGCCACCTTTAGAACTTTGGTATGGCCCTTTCTGACCCCTCTTCGAGTCTCCA	5411
Qy	1800	hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT	1820
Db	5416	CTGGTGACACTGGAAATGGTATTATGAAGGACACCCCTCCGGGACTGTGACCAAGAGCTCCA	5475
Qy	1820	hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP	1840
Db	5476	CCTGCTACAAACCTGTCATCTCCCTCATCTACTTTGTGCTCTTCGTGCTGACGGCCAGT	5535
Qy	1840	heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysC	1860
Db	5536	TTGTGCTGGTCAACCTGGTCATAGCTGTGCTGATGAAGCACCTTGGAAAGAAAGCAACAAAG	5595
Qy	1860	luAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuSerP	1880
Db	5596	AGCCCAAGGAGGAGCCGAGCTCGAGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCC	5655
Qy	1880	roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS	1900
Db	5656	CGCAGCCCCACTCCCCGCTGGGCAGCCCTTCTCTGGCCCGGGGTGGAGGTGTCAACA	5715
Qy	1900	erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerC	1920
Db	5716	GTACTGACACCCCTAAAGCTGGGGCTCCACACCACTGCCACATTTGAGAGAGCTCGG	5775
Qy	1920	lyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG	1940
Db	5776	GCTTCTCCCTTGAGCACCCCAAGTGGTACCCACCCCGAGGAGGTGCCAGTCCCCCTAG	5835
Qy	1940	lyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA	1960
Db	5836	GACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTACGCGGACGCCACTCTCTGCCCAATG	5895
Qy	1960	spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpC	1980
Db	5896	ACAGCTACATGTGCGCAATGGGAGCAGCTGCTCAGAGATCCCTTAGGACACAGGGGTGGG	5955
Qy	1980	lyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS	2000
Db	5956	GGCTCCCAAGCCCAAGTCAAGGTCCATCTTGTCCGTTTCACTCCCAACCAGCAGACACCA	6015
Qy	2000	erCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProT	2020
Db	6016	GCTGCTCATCTACAGCTTCCCAAGATGTGCACATATCTGCTCCAGCCTCATGGGGCTCCCA	6075
Qy	2020	hrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProL	2040
Db	6076	CCTGGGGCGCCATCCCTTAACTACCCCAACCTGGCCGCTCCCTCTGGGTTCAGAGGCCCTC	6135
Qy	2040	euArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgG	2060
Db	6136	TCAGGCCCAAGCAGCAGCAATGAAGACTGACTTCCCTGGATGTGACAGGGCCTGGGTAGCCGGG	6195
Qy	2060	luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheT	2080
Db	6196	AAGACCTGTTGTGAGAGGTGAGTGGGCCCTCTCTGCCCTCTGACCCGCTCTCATCTCTTCT	6255
Qy	2080	rpGlyGlySerSerIleGlnValGlnArgSerGlyIleGlnSerLysValSerLysH	2100
Db	6256	GGGGCGGGTTCGAGCATCCAGGTGCAGCAGCGTTCCTGGCATTCAGAGCAAAAGTCTCAAGC	6315
Qy	2100	isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG	2120
Db	6316	ACATCCGCTTGCAGACCCCTTGGCCAGGCTTGNAACCCAGCTGGGCCAAGGACCTTCCAG	6375
Qy	2120	luThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeup	2140
Db	6376	AGACCAGAAGCAGCTTAGAGCTGAGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTCTTC	6435
Qy	2140	roSerSerGlnGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluT	2160
Db	6436	CCAGCAGCAGGAGAAACCCCTGTTCACCGGAGCCTGAAGAAGTCTCAGGTGTAGAGA	6495

QY 2160 hrGlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleA 2180
DB 6496 CCAGAGCTGACGGCGAGCGCTGGGTCTGGCTAGATGAACAGCGAGACATCCATATG 6555
QY 2180 laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG 2200
DB 6556 CTGTCACTGTCTGGACAGCGGTCCCAACCGCGCTATGTCCAAGCGCCCTCAAGCGCTCG 6615
QY 2200 lyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerI 2220
DB 6616 GGCGCCAACTCTTTGGGGGTCTGGAGCGCGCTTAAGAAAAAATCAGGCCCAACCCAGTA 6675
QY 2220 leSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysL 2240
DB 6676 TCCTATAGACCCCGCGAGAGCCAGGGCTCTCGGCCCCCATCGAGTCTGTGGTCTGTGCC 6735
QY 2240 euArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAsps 2260
DB 6736 TCAGGAGGAGGGCGCGCGCGAGTGAATCTTAAGGATCCCTCGGTCTCCAGCGCCCTTGACA 6795
QY 2260 erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerA 2280
DB 6796 GCAGGGCTGCTCACCTCTCCCAAGAAAGACAGCGTGAATCTCTGTGGTTGTCTTCTG 6855
QY 2280 spProThrAspMetAspPro 2286
DB 6856 ACCNACAGACATGGACCCC 6875

RESULT 2

US-09-383-894-3
; Sequence 3, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7285
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-3

Alignment Scores:
Pred. No.: 0 Length: 7285
Score: 11829.00 Matches: 2270
Percent Similarity: 97.7% Conservative: 1
Best Local Similarity: 97.7% Mismatches: 15
Query Match: 98.3% Indels: 38
DB: 3 Gaps: 2

US-09-611-257A-24 (1-2287) x US-09-383-894-3 (1-7285)

QY 1 MetLeuProHisArg-ValProArg-CysValArgThrProProLeuArgGlySerAlaA 20
DB 57 ATGCTCCCCACCGGGGTCCCCGGTGGTGAGGACACCTCTCTGAGGGGCTCCGCTC 116
QY 20 rgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetG 40
DB 117 GCCCTCTTCGACCCCCCGGGGCGCGGTGGCCAGAGGATGGACAGGAGGAGGATGG 176
QY 40 luArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProG 60
DB 177 AGCGGGCGCGAGGAGTCGGGACAGCCCGGTAGCTTACGACGCTCAACGACCTGTCCGG 236

QY 60 lyProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerG1 79
DB 237 GGCGGGGGCGCGCAGCGGGCGGGTCGACGGAAGAGCCCGGCGAGCGCGACTCCGA 296
QY 79 uAlaGluGlyLeuProTrpProAlaLeuAlaProValValPhePheTrpLeuSerGlnAs 99
DB 297 GGCGGAGGGCTGCGGTACCGCGGTAGCCCGGTGGTGTCTTCTTACTTGGAGCCAGGA 356
QY 99 pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe 119
DB 357 CAGCCGCCCGCGAGCTGGTGTCTCGCAGCGTCTGTAAACCCGTGGTTCGAGCGAGTCAG 416
QY 119 rMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspI1 139
DB 417 TATGCTGGTCACTTCTCAACTGTGTGACTCTGGGTATGTTTCAGGCGGTGTGAGGACAT 476
QY 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPh 159
DB 477 TGCTGTGACTCCAGCGCTGCCGATCTTCGAGGCTTCGATGACTTTCATCTTTGCCCTT 536
QY 159 ePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy 179
DB 537 CTTTGTGTGAAATGGTGTGAAGATGGTGGCTTTGGGCATCTTTGGGAAGAAATGTTA 596
QY 179 rLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTy 199
DB 597 CTTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTTGTCATTCAGGAGTGTGGAGTA 656
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr 219
DB 657 TTCGCTGGACCTCGAAGCTCAGCTTCCTCCGAGTCAGGACAGTCCGTGTGTCGACC 716
QY 219 oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh 239
DB 717 GCTCAGGGCCATTAAACGGGTGCCAGCATCTCTGTCACATTACTGCTGGACAC 776
QY 239 rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyI1 259
DB 777 CTTGCCCTATGCTGGCAACGTCCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 836
QY 259 eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh 279
DB 837 CGTGGGCGTCCAGCTGTGGGCGAGGCTGTCTCGCAACCGATGCTCTCTCCCGAGAACTT 896
QY 279 eSerLeuProLeuSerValAspLeuGluProTrpTrpGlnThrGluAsnGluAspGluSe 299
DB 897 CAGCCTCCCCCTGAGCGGTGACCTGGAGCTTATTACCACAGACAGAAATCAGGACGAG 956
QY 299 rProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh 319
DB 957 CCCCTTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGATCTCTGAGGAGTGTGCCAC 1016
QY 319 rLeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTrpClnThrTrpAsnSe 339
DB 1017 ACTGCGTGGGAAAGCGGTGGTGGCCACCCCTCGAGTCTGGACTATGAGACCTATAACAG 1076
QY 339 rSerSerAsnThrThrCysValAsnTrpAsnGlnTrpTrpThrAsnCysSerAlaGlyG1 359
DB 1077 TTCGACCAACACCCTCTGTGTCACTGGAAACAGTACTATACCACTGCTCTGCGGGCGA 1136
QY 359 uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTrpAlaTrpIleAlaI1 379
DB 1137 GCACAACCCCTTCAAGGGGCCATCAACTTTTGACAACATTTGGTATGCTGCTGAGTCCGCAT 1196
QY 379 ePheGlnValIleThrLeuGluGlyTrpValAspIleMetTrpPheValMetAspAlaHi 399
DB 1197 CTTTCCAGGTCATCACACTGGGGGTGGGTGGCATCATGATCTCTGTAATGAGCGCTCA 1256
QY 399 sSerPheTrpAsnPheIleTrpPheIleLeuLeuIleValIcLysSerPhePheMetI1 419
DB 1257 CTCTTCTACAACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1316
QY 419 eAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG1 439

Db ||||| 1317 CAACCTGTGCTGGTGGTGAATGGCCACGAGTCTTCCGAGACCAAAACGCGGAGAGTCA 1376
Qy nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe 459
Db ||||| 1377 GCTGATGCGGAGCAGCGGTGTACGATTCCTGTCCAATGCTAGCACCCCTGGCAAGCTTCTC 1436
Qy rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl 479
Db ||||| 1437 TGAGCCAGCAGCTGCTATGAGGAGCTACTCAAGTACCTGGTGTACATCTCCGAAAGC 1496
Qy aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe 499
Db ||||| 1497 AGCCCGAAGCTGGCCCAAGTCTCTAGGGCTATAGGCGTGGGGCTGGCTCAGCAG 1556
Qy rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr 519
Db ||||| 1557 CCCAGTGGCCGTGTAGTGGGCAGGAGCCCGCAGCCAGTGGCAGTGCATCTCGCTCACACCG 1616
Qy gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisLe 539
Db ||||| 1617 TCGTCTGTCTGCACCACTGGTCCACCATCACCACCATCACCACCTACCACCT 1676
Qy uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs 559
Db ||||| 1677 GGTTAATGGGAGCTCAGAGTTCCCGGGCCAGCCAGAGATCCAGGACGGGATGCCAA 1736
Qy nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr 579
Db ||||| 1737 TGGGTCTCGCGGCTCATGTACACCACTTACACCACTCCCTCTGGGGGCCCTTCC 1796
Qy oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr 599
Db ||||| 1797 GAGGGTCCGGAGTCTGTACACAGCTTCTCATGTCTGACTGACCTTGGAGCCAGTCCG 1856
Qy gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGl 619
Db ||||| 1857 TTGCCAGCACCCCTCCAGATGCCCATCGGAGCATCTGGTAGGACTGTGGGTAGTGG 1916
Qy yLysValTyrProThrValHisThrSerProProProProGluIleLeuLysAspLysAlaLe 639
Db ||||| 1917 GAAGGTGTACCCCACTGTGTACATACAGCCCTCCACAGAGATACTGAAAGGATAAAGCACT 1976
Qy uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGl 659
Db ||||| 1977 AGTGAGGTGGCCCCCAGCCCTGGGCCCCCCACCTCCACAGCTTCAACATCCCACTGG 2036
Qy yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe 679
Db ||||| 2037 GCCCTTCAGTCCATGCACAAGCTCTCGAGACACAGAGTACGGAGCCTGCCATAGCTC 2096
Qy rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy 699
Db ||||| 2097 CTGCAAAATCTCCAGCCCTGTCTCAAGCGCAGACAGTGGAGCCTGCGGGCCGGACAGTTG 2156
Qy sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs 719
Db ||||| 2157 TCCCTACTGTGCCCGCAGCAGGAGAGCCAGAGTCCGCTGACCATGTATCATGCCCTGA 2216
Qy pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs 739
Db ||||| 2217 CTCAGACGCGAGGCTGTGTATGAGTTCCACAGGAGCCTCAGCACAGTACCTCCGGGA 2276
Qy pProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLe 759
Db ||||| 2277 TCCCCACAGCGCGGCAGACGCGAGCCTGGGCCCCAGATCGAGAGCCTAGTCTGTGTCT 2336
Qy uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGl 779
Db ||||| 2337 GGCCTTCTGGAGGCTGATCTGTGACACATTCGGGAAGATCGTAGATAGCAATATCTTTGG 2396
Qy yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGl 799

Db ||||| 2397 CCGGGGAATCATGATGCCATCTCTGGTCAATACACTCAGCATGGGCATCGAGTACCACGA 2456
Qy uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh 819
Db ||||| 2457 GCACCCCGAGAGCTCACCAACGCCCTGGAAATCAGCAACATCGTCTTCCACAGCCTCTT 2516
Qy eAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnPr 839
Db ||||| 2517 CGCCTTGGAGATGTCTGAAACTGCTGTCTACGGTCCCTTGGCTACATTAAGAATCC 2576
Qy oTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGl 859
Db ||||| 2577 CTACAACATCTTTGATGGTGTCTTGGTTCATCAGTGTGTGGAGATGTGGGCGCAGCA 2636
Qy nGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr 879
Db ||||| 2637 GGGAGGTGGCCTGTGCGGTGTCGGACCTCCGCCCTGATCGGGTGTGGAAGCTGGTGGC 2696
Qy gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl 899
Db ||||| 2697 CTTCTCGCGGCCCTGCAGCGCCAGCTCGTGTGCTCATGAGACCATGGACACGTGGC 2756
Qy aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLe 919
Db ||||| 2757 CACCTTCTGCATGCTCCTCATGCTGTTCATCTTTCATCTTTCAGCATCTCTGGGCATGCT 2816
Qy uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh 939
Db ||||| 2817 CTTTGGTGTGAAGTTCGCATCTGAACGGGATGGGGACACGTTGCCAGACCCGGAAGAAATTT 2876
Qy eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs 959
Db ||||| 2877 CGACTCCTCTGCTGGGCCATCGTCACTGTCTTTCAGATCTGACTCAGGAAGACTGGAA 2936
Qy nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAl 979
Db ||||| 2937 TAAAGTCTCTACAAACGCATGGCTCCACATCTCTTGGGCTGCTCTTACTTTCATCGC 2996
Qy aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGl 999
Db ||||| 2997 CCTCATGACTTTTGGCAACTATGTGCTTTTAAACCTGCTGTGTGGCCATCTTGTGGAAGG 3056
Qy yPheGlnAlaGlu----- 1003
Db ||||| 3057 ATTCAGGCAGAGAAATCGGCAACCGGAGAGATGCGAGTGCAGTAAAGCTGTATTCA 3116
Qy -----GlyAspAlaThrLysSerGluSerGluProAspPhePh 1016
Db ||||| 3117 GCTGCTGTCAACTCTCAGGGGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTT 3176
Qy eSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGl 1036
Db ||||| 3177 TTCGCCAGTGTGATGGTGTATGGGACAGAAAGCGCTTGGCCCTTGGTGGCTTTGGG 3236
Qy yGluHiAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaTh 1056
Db ||||| 3237 AGAACCGCGAATACGAAAGAGCTTTTCCACCCCTCATCTCCATACGGCTGCAC 3296
Qy rProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySe 1076
Db ||||| 3297 ACCAATGTCAATACCAAGAGCTCCAGCACAGGTGTGGGGGAAGCAGCTTGGGCTC 3356
Qy rArgArgThrSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy 1096
Db ||||| 3357 TCGACGTACCAAGTAGAGTGGGTCCGCTGAGCCTGGAGCTGCCACCATGAGATGAATC 3416
Qy sProProSerAlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1116
Db ||||| 3417 TCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGGAGTGGCGCAAGCAGCTGGACAG 3476
Qy rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1136
Db ||||| 3477 CAGCGCTCCAGCAGGAACAGCCTGGGCCGGCCCCCAGCCCTAAAGCGGAGGAGCCCGAG 3536

Db 5697 GGTATAGTGTGCTGATGAAGCACCTTGGAGAAGCAACAAGAGCCAGGAGGAGGC 5756
Qy 1865 aGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerPr 1885
Db 5757 CGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCC 5816
Qy 1885 oLeuGlySerProPheLeuTrpProGlyValICluGlyValAsnSerThrAspSerProLy 1905
Db 5817 GCTGGGACGCCCTTCCTCTGGCCGGGGTGGAGGGTGTCAACAGTCTGTGACAGCCCTAA 5876
Qy 1905 sProGlyAlaProHisThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHi 1925
Db 5877 GCCTGGGGCTCCACACACCACTGCCACATTTGGAGCAGCCTCGGGCTTCTCCCTTGAGCA 5936
Qy 1925 sProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuTh 1945
Db 5937 CCCCACGATGTACCCACCCCGAGGAGTGCACGTCCCCCTAGGACCCAGACCTGTCTGAC 5996
Qy 1945 rValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyMetCysAr 1965
Db 5997 TGTGAGGAAGTCTGTGTGCACCGGACGCACTCTGTGCCCAATGACAGCTACATGTGCCG 6056
Qy 1965 gAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGl 1985
Db 6057 CAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGCTGGGGCTCCCCAAAGCCCA 6116
Qy 1985 nSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLe 2005
Db 6117 GTGAGGCTCCATCTGTTCGTTCATCTCCAAACCAGCAGACACAGCTGCATCTTACAGCT 6176
Qy 2005 uProLysAspValHisTyLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIlePr 2025
Db 6177 TCCCAAGATGTGACATATCTGCTCCAGCCTCATGGGGCCCCCACCCTGGGGCGGCATCCC 6236
Qy 2025 oLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAl 2045
Db 6237 TAACTACCCCACTGGCCGCTCCCTCTCGCTCAGAGGCTCTCTAGGCCCGCAGGCAGC 6296
Qy 2045 aIleArgThrAspSerLeuAspValGlnGlySerArgGluAspLeuLeuSerGl 2065
Db 6297 AATAAGGACTGACTCCCTCGATGTGCAGGGCTGGGTAGCCGGGAAGACCTGTGTGCAGA 6356
Qy 2065 uValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerIle 2085
Db 6357 GGTGAGTGGGGCTCTCTCCCTCTGACCCGGTCTCATCTCTCTGGGGCGGGTCCAGCAT 6416
Qy 2085 eGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAl 2105
Db 6417 CCAGGTGCAGCAGCGTTCCGGGCATCCAGCAAAAGTCTCCAAGCACATCCGCTGCCAGC 6476
Qy 2105 aProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLe 2125
Db 6477 CCTTGGCCAGCGCTGGAACCCAGCTGGGGCCCAAGACCCTCCAGAGACCAAGAAGCAGCTT 6536
Qy 2125 uGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGl 2145
Db 6537 AGAGCTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCTCTCCAGCACCCAGGAAGA 6596
Qy 2145 uProLeuPheProArgAspLeuLysCysTySerValGluThrGlnSerCysArgAr 2165
Db 6597 ACCCTGTCCCAACCGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCG 6656
Qy 2165 gArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAs 2185
Db 6657 CAGGCTGGGTCTCGGCTAGATGAACACGGAGACACTCCATTGCTGTGCTGCTGGA 6716
Qy 2185 pSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuGl 2205
Db 6717 CAGGGCTCCCAACCCCGCTATGTCCAAAGCCCTCAAGCCTCGGGGGCCCAACCTCTGG 6776
Qy 2205 yGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProPr 2225

Db 6777 GGGTCTCTGGAGCGCGCTTAAGAAAAAATCAGCCCAACCAGTAGTATCTCTATAGACCCCCC 6836
Qy 2225 oGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaPr 2245
Db 6837 GGAGAGCAGGGCTCTCGGCCCCCATCGAGTCTCTGGTGTCTGCTCAGGAGGAGGGCGCC 6896
Qy 2245 oAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerPr 2265
Db 6897 GSCCAGTAGACTCTTAAGATCCCTCGGTCTCAGGCCCTTGACAGCAGCGGTGCTCACC 6956
Qy 2265 oSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAs 2285
Db 6957 CTCCCCAAGAAAGACACGCTGAGTCTCTCTGGTTGTCTTCTGACCCACAGACATGGA 7016
Qy 2285 pPro 2286
Db 7017 CCCC 7020
RESULT 3
US-09-383-894-1
; Sequence 1, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 7129
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-1
Alignment Scores:
Pred. No.: 0 Length: 7129
Score: 11673.00 Matches: 2237
Percent Similarity: 97.8% Conservative: 1
Best Local Similarity: 97.7% Mismatches: 15
Query Match: 97.0% Indels: 36
DB: 3 Gaps: 2
US-09-611-257A-24 (1-2287) x US-09-383-894-1 (1-7129)
Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACAGAGGAGGATGGAGCGGCGCCGAGGAGTGGGACAGCCCCGTAGCTTCACGC 61
Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73
Db 62 AGCTCAACGACCTGTCCGGGCGCGGGCCGCGAGGGCGGTTCGAGCAAAAGGACC 121
Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProValP 93
Db 122 CGGCGAGCGCGAGCTCCGAGCGGAGGGGTGCCGTACCCCGCGCTAGCCCGGGTGT 181
Qy 93 hePheTyLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 113
Db 182 TCTTCTACTTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACGGTCTGTAACC 241
Qy 113 roTPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CGTGGTTTCGAGCGAGTCAGTATGTGTGTCATCTTCTCAACTGTGTGACTCTGGGTATGT 301
Qy 133 heArgProCysLeuAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCAGGCGGTGTGAGGACATTGCTGTGACTCCCGCGGTGCGGATCTCTGAGGCTTCG 361

Qy	153	spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI	173
Db	362	ATGACTTTCATCTTTGGCCCTCTTTGCTGTGAAATGGTGGTGAAGATGGTGCCCTTGGCGA	421
Qy	173	lePheGlyLysLysCysTyrlieuGlyAspThrTrpAsnArgLeuAspPhePheIleValI	193
Db	422	TCTTTGGGAAAGAAATGTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTTCATTGTGCA	481
Qy	193	leAlaGlyMetLeuGluTyS-SerLeuAspLeuGlnAsnValSerPheSerAlaValArgT	213
Db	482	TTGCAGGGATGCTGGAGTATTGCTGTGARCTGCAGAACGTCAGCTTCTCCGCAGTCAGGA	541
Qy	213	hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
Db	542	CAGTCCGTGTGTCGACCGCTCAGGCGCATTAACCGGGTGCCCGAGCATGCGCATTCCTCG	601
Qy	233	alThrLeuLeuLeuAspThrLeuPro-MetLeuGlyAsnValLeuLeuLeuCysPhePheV	253
Db	602	TCACATTACTGCTGGACACCTTGCTATGCTGGGCAACGTCCTGCTGCTCTGTGTTCTTC	661
Qy	253	alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
Db	662	TCITTTTCATCTTTGGCATGTGGGCGCTGCAGCTGTGGGAGGACTGCTTCGCCAACCCGAT	721
Qy	273	ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrrGlnT	293
Db	722	GCTTCCTCCCCAGAACTTCAGCCCTCCCCTGAGCGTGGACCTGGAGSCCTTATTACCAGA	781
Qy	293	hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
Db	782	CAGAGAAATGAGACGAGAGGCCCTTCATCTGCTCTCAGCCCTCGGGAGAAATGGCATGAGAT	841
Qy	313	erCysArgSerValproThrLeuArgGlyGluGlyGlyGlyGlyProproCysSerLeuA	333
Db	842	CCTGCAGAGGTGCCCACACTGCGTGGGGAAGCGGTGGTGGCCACCCTGCAGCTCGG	901
Qy	333	spTyrrGluThrTyrrAsnSer-SerSerAsnThrThrCysValAsnTrpAsnGlnTyrrTyrr	353
Db	902	ACTATGAGACCTATAACAGTTCACAGCAACACCACCTGTGTCACTGGAACCGACTACTATA	961
Qy	353	hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG	373
Db	962	CCAACCTGCTCTCGGGCGAGCACAAACCCCTTCAAAGGCGCCATCAACTTTGACAACATG	1021
Qy	373	lyTyrrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT	393
Db	1022	GCTATGCTTGATCGCCATCTTCAGGTGCATCACACTGGAGGGGTGGGTGGACATCATGT	1081
Qy	393	yrPheValMetAspAlaHisSerPheTyrrAsnPhelIeTyrrPheIleLeuIleIleV	413
Db	1082	ACTTCGTATGGAGCGCTCACTCTCTTACAACTTCATCTACTACTTCTCTCATCATCG	1141
Qy	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCTCTTCTCATGATCAACCTGTGCTGGTGGTGATTGGCCACGAGTTCTCCGAGA	1201
Qy	433	hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas	453
Db	1202	CCAACACGCGGAGAGTCAGCTGATGGGGAGCAGCGTGTACGATTCTGTCCAATGCTA	1261
Qy	453	erThrLeuAlaSer-PheSerGluProGlySerCysTyrrGluGluLeuIleTyrrLeuV	473
Db	1262	GCACCTTGGCAAGCTTCTCTGAGCCAGCAGCTGATAGAGGAGCTACTCAAGTAGTCTCG	1321
Qy	473	alTyrrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVala	493
Db	1322	TGTACATCTCTCGAAAAGCAGCCCGAGGCTGGCCCGAGGTCTCTAGGGCTATAGCGCTGC	1381
Qy	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCGAGAGCCCGCAGCCAGTGGCGA	1441

Qy	513	erCysThrArgSerHisArgArgLeuSerValHisHISleuValHisSHisHISleuHisHIS	533
Db	1442	GCTGCACCTCGCTCACACCCTGCTGTCTGTCCACACCTGGTGCACCACTATCACCACC	1501
Qy	533	iShiShiShiTyRHisLeuGlyVAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ACCATCACCACTACCACTCTGGGTAAATGGAGCGCTCAGATTTCCTCGGGCCAGCCCNAGA	1561
Qy	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT	573
Db	1562	TCCAGGACAGGATGCCAATGGTGCTCGCGGCTCATCTACCAACCCTCTACACCCA	1621
Qy	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyRHisAlaAspC	593
Db	1622	CTCCCTCTGGGGGCCCTCGAGGGGTGCGAGGTCTGTACACAGCTTCTACCATGCTGACT	1681
Qy	593	yShiLeuGluProValArqCysGlnAlaProProArgCysProSerGluAlaSerG	613
Db	1682	GCCACTGGAGCCAGTCCGTTGCCAGGACCCCTCCCAGATGCCCATCGGAGGCATCTG	1741
Qy	613	lyArgThrValGlySerGlyLysValTyRProThrValHisThrSerProProGluI	633
Db	1742	GTAGGACTGTGGTAGTGGGAAGGTATCCCCACATGTGCATACCAAGCCCTCCACCAGAGA	1801
Qy	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs	653
Db	1802	TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGAGCCCTGGGCCCCACCTCACCA	1861
Qy	653	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
Db	1862	GCTTCAACATCCCACTGTGGCCCTTCAGCTCCATGCACAAGCTCTGGAGACACAGATPA	1921
Qy	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CGGAGCGCTGCCATAGCTCTCGCAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAG	1981
Qy	693	laCysGlyProAspSerCysProTyRcysAlaArgThrGlyAlaGlyGluProGluSerA	713
Db	1982	CCTCGGGCGGACAGTTGTCCCTACTGTGCCGGACAGGAGCAGGAGCCAGAGTCGG	2041
Qy	713	laAspHisValMetProAspSerAspSerGluAlaValTyRGlutPheThrGlnAspAlag	733
Db	2042	CTACCATGTATGTCCTGACTACAGACAGCGAGCTGTATGAGTTTCACACAGGACGCTC	2101
Qy	733	lnhISerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyVProAspa	753
Db	2102	AGCACAGTGNACTCCGGGATCCCCACAGCGGGGGGCACAGCGGAGCCTGGGCCCNAGTG	2161
Qy	753	laGluProSerSerValLeuAlaPheTrpArgLeuilleCysAspThrPheArgLyelleiv	773
Db	2162	CAGAGCCTAGTTCTGTGTGGCTTTCTGGAGGCTGATCTGTACACATTCGGAAGATCG	2221
Qy	773	alaspSerLysTyRPhEGlyArgGlylleMetIleAlaIleLeuValAnthrLeuSerM	793
Db	2222	TAGATAGCAATAACTTTGGCGGGGAATCATGATGCCATCTCTGGTCAAATACACTCAGA	2281
Qy	793	etGlylleGluTyRHisGluGlnProGluGluLeuthrAsnAlaLeuGluIleIleSerAsni	813
Db	2282	TGGGCATCGAGTACCAACAGACAGCCCGAGAGCTCACCAACGCCCTGGAAAATCAGCAACA	2341
Qy	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyRGlyProp	833
Db	2342	TCGTCTTACCAGCCTCTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGTCTACCGTCCCT	2401
Qy	833	heGlyTyrlleLysAsnProTyRAsnIlePheAspGlyValIleValIleIleSerValIt	853
Db	2402	TTGGCTACATTAAGAATCCCTACAAATCTTTTGATGGTGTCTATTTGGTGCATCAGTGTGT	2461
Qy	853	rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2462	GGGAGATTGGGCCACAGAGGAGGTGGCTGTCTGGTGTCTGGGACCTTCCGCGCTGATGC	2521
Ov	873	rqValLeutyLysLeuValArqPheLeuProAlaLeuGlnArgGlnLeuValIleValMeL	893

Db 2522 GGGTGGCTGAAGCTGGTGGCTTCTCGCGGCCCTGCGAGCGCAGCTCGTGGTGCATGA 2581
Qy 893 ySThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheS 913
Db 2582 AGACCATGGACAAGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTCA 2641
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2642 GCATCCTGGGCATGCATCTCTTTGGTGCAGAGTTGCGCATCTGAAACGGGATGGGACACGT 2701
Qy 933 euProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleL 953
Db 2702 TGCCAGACCGGAAGATTTTCGACTCCCTGCTCTGGGCCATCGTCACGTCTTTCAGATTC 2761
Qy 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
Db 2762 TGACTCAGGAAGACTGGAAATAAGTCTCTCAACAGGCATGGCCTCCACATCGCTTTGGG 2821
Qy 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2822 CTGCTCTTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACTCTGTGG 2881
Qy 993 alAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2882 TGGCCATTCTTGTGGAAGGATTCAGGCAGAGGAAATCGGCAAAACGGGAAGATCGAGTG 2941
Qy 1004 -----GlyAspAlaThrLysSerG 1010
Db 2942 GACAGTTAAGCTGATTTCAGCTGCTGTCAACTCTCTCAGGGGGAGATGCCACCAAGTCTG 3001
Qy 1010 luSerGluProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgL 1030
Db 3002 AGTCAGAGCCCTGATTTCTTTTCGCCCATGTGGATGGTGGTGGGACAGAAAGAGCCCT 3061
Qy 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuI 1050
Db 3062 TGGCCCTGCTGGCTTTGGGAGAACACGCGAACTACGAAAGAGCCTTTTGGCCACCCCTCA 3121
Qy 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
Db 3122 TCATCCATACGGCTGCGACACCAATGTCTACTACCCAAAGAGTCCAGCACAGGTGTGGGG 3181
Qy 1070 luAlaLeuGlySerGlySerArgThrSerSerGlySerAlaGluProGlyAlaA 1090
Db 3182 AAGCACTGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCCTGAGGCTGGAGCTG 3241
Qy 1090 laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA 1110
Db 3242 CCCACCATGAGATGAAATCTCCGCCAAGTGGCCGAGCTCCCGCACAGTCCCTGGAGTG 3301
Qy 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130
Db 3302 CGGCAAGCAGTGGACCAAGAGCCCTCCAGCAGGAACAGCCTGGCCGGGCCCCCGACCC 3361
Qy 1130 euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluS 1150
Db 3362 TAAACGGAGAGGCCCGAGCGGGAGCGGAGGTCCCTGCTGTGGAGAGGGCCAGGAGA 3421
Qy 1150 erGlnAspGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3422 GTCAGGATGAGGAGGAAAGTTTCAGAAAGAGGACCGGGCCAGCCAGCAGCGCAGTGAACATC 3481
Qy 1170 rgHisArgLysSerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3482 GCCACAGGGGTTCCTTGGAAACGTGAGGCCAAGAGTTCTCTTTGACCTGCTGACACTCTGC 3541
Qy 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
Db 3542 AGGTCCCGGGGCTGCACCGCACAGCGGGCCGAGGTCTGCTCTGAGCACCCAGACT 3601
Qy 1210 ySAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230

Db 3602 GTAATGGCAAGTGGCTTTCAGGGCGTTTGGCCCCGCAACCTTGAGGACTGATGACCCCCAAC 3661
Qy 1230 euAspGlyAspAspAspAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT 1250
Db 3662 TGGATGGGGATGATGACAATGATGAGGAAATCTGAGCAAAAGGGAAACGCATACAAGCCT 3721
Qy 1250 rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
Db 3722 GGGTCAGATCCCGCTTCTGCTGCTGTTGCCAGAGCCAGATTCCTGGTCGCCTATATCT 3781
Qy 1270 heProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
Db 3782 TTCCTCCTCAGTCAAGGTTTCTGCTGCTGTCACCGATCATCACCACCAAGATGTTTG 3841
Qy 1290 spHisValValLeuValIleIlePheLeuLeuCysIleThrIleAlaMetGluArgProL 1310
Db 3842 ACCATGTGGTCTCGTCATCATCTTCTCAACTGTATCACCATCGCTATGAGGCGCCCA 3901
Qy 1310 ySileAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330
Db 3902 AAATTGACCCCAAGCGCTGAGCGCATCTTCTGACCTCTCCCACTACATCTTCACGG 3961
Qy 1330 laValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluG 1350
Db 3962 CAGTCTTTCTAGCTGAAATGACAGTGAAGGTGGTGACCTGGGCTGGTGTGGGGAGC 4021
Qy 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
Db 4022 AGGCTTACCTCGCAGCAGCTGGAAATGTCTGGACGGCTTCTGCTGCTCATCTCCGTCA 4081
Qy 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
Db 4082 TCGACATCTCTGCTCTCCATGCTCTCCGACAGCGGCACCAAGATCCTTTGGCATGCTGAGGG 4141
Qy 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
Db 4142 TGCTGCGCTCTCTCGGACCTCGCTCCACTCAGGGTTCATCAGCGGGCCCGGAGACTGA 4201
Qy 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
Db 4202 AGCTGGGTGAGAGACTCTGATGTCTCCCTCAAACCCATTTGGCAACATTTGGTGCATTT 4261
Qy 1430 ySysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
Db 4262 GCTGTGCTCTCTCATCATTTTGGAAATTCGCGGTGCAGCTCTTCAAAGGGAAGTTCT 4321
Qy 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
Db 4322 TCGTGTGTACGGGTGAGGACACCCAGGAACATCATTAAACAAATCCGACTGCGCTGAGGCCA 4381
Qy 1470 erTyrArgTrpValArgHisLysLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
Db 4382 GCTACCGATGGTTCGGCAACAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCC 4441
Qy 1490 eupheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaV 1510
Db 4442 TGTTTGTGCTGCTCCCAAGGATGTTGGGTGACATCATGTATGATGGCTGGATGCTG 4501
Qy 1510 alGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS 1530
Db 4502 TGGGTGTGGATCAGCAGCCCATCATGAACCAACACCCCTGGATGCTGTACTTCTCATCT 4561
Qy 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluA 1550
Db 4562 CTTTCTCTCATGCTGGCCCTTTTGTCTTGAACATGTTTGTGGGCGTGGTGGTGGAGA 4621
Qy 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysA 1570
Db 4622 ACTTCCATAAGTCAGACAGCACCGAGGAGGAGGAGCGGCGGCGCTGAGGAGAAC 4681
Qy 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 4682 GACTACGGAGCTGGAGAAAAAGAGAGGAATCTAAATCTTGACGATGTAAATGCTTCG 4741

Qy 1580 --SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
Db 4742 CGAGCTCAGCGCGCTGGCGTCAGAGCCAGCCAGTCAAGCCCTACTCTGACTACTCGA 4801
Qy 1599 rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG 1619
Db 4802 GATTCCGGCTCTTGTGTCCACCACCTGTGTACACAGCCACTACCTGGAGCTCTTCACTAC 4861
Qy 1619 lyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
Db 4862 GTGTATCTGGGCTGAAAGTGTGTACTATGGCCATGGAAACATTACACAGCCCCAGATCC 4921
Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
Db 4922 TGGACGAGGCTCTGAAGATCTGCAATTTACCGTCATCTTTGTCTTGTGAGTCAG 4981
Qy 1659 alPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuA 1679
Db 4982 TTTTCAAACCTTGTGGCCTTTGGCTTCCGCCGCTTTCTTCCAGGACAGGTGGAAACAGCTGG 5041
Qy 1679 spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
Db 5042 ACCTGGCTATTGTCTCTGTCTCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATG 5101
Qy 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
Db 5102 CTTGCGCTGCCCATCAACCCACCATCATCCGTATCATGAGGGTCTCCGCATTGCTCGAG 5161
Qy 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
Db 5162 TTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGCACCTGCTGCACACGCTGATGCAGG 5221
Qy 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA 1759
Db 5222 CCCTGGCCCCAGGTGGGAACTTGGACTTCTCTTCATGTTATTGTTTTCATCTTTGCAG 5281
Qy 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db 5282 CTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCT 5341
Qy 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals 1799
Db 5342 TGGGTGCGCATGCCACCTTTAGGAACTTTGATATGGCTTTCTGACCCCTCTTCCGAGTCT 5401
Qy 1799 erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
Db 5402 CCACTGTGTGACAACTGGAAATGGTATTATGAAGGACACCCCTCCGGGACTGTGACCGAGT 5461
Qy 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5462 CCACCTGCTACACACTGTCTCTCCCTATCTACTTTGTGCTCTTCTGCTGACGGGCC 5521
Qy 1839 lnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
Db 5522 AGTTTGTGCTGGTCAACGCTGGTCATAGCTGTGCTGATCAAGACACCTGGAAGAAAGCAACA 5581
Qy 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuS 1879
Db 5582 AAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGTGAAGACGCTCA 5641
Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
Db 5642 GCCCGCAGCCCACTCTCCCGCTGGGCAGCCCTTCTCTTGGCCCGGGGTGGAGGGTGTCA 5701
Qy 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlas 1919
Db 5702 ACAGTCTGACAGCCCTAAGCCTGGGCTCCACACACCACTGCCCCACATTGGAGAGCCT 5761
Qy 1919 erGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProL 1939
Db 5762 CGGCGCTTCTCCCTTGGACACCCCAACGATGGTATGATGATGATGATGATGATGATGATGAT 5821

Qy 1939 euGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA 1959
Db 5822 TAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGACGGCAGCACTCTCTGCCCCA 5881
Qy 1959 snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT 1979
Db 5882 ATGACAGCTACATGTGCGCAATGGGACACTGCTGAGAGATCCCTTAGGACACAGGGGCT 5941
Qy 1979 rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT 1999
Db 5942 GGGGGTCCCCAAAGCCAGCTCAGGCTCCATCTTGTCCGTTCACTCCCAACACAGACACA 6001
Qy 1999 hrSerCysIleLeuLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlap 2019
Db 6002 CCAGCTGCATCTTACAGCTTCCCAAGATGTGCACTATCTGCTCAGCCCTCATGGGGCCC 6061
Qy 2019 roThrTrpGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgP 2039
Db 6062 CCACCTGGGGCGGCATCCCTTAAACTATCCCCACCTGGCCGCTCCCTCTCGCTCAGAGGC 6121
Qy 2039 roLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerA 2059
Db 6122 CTCTCAGGCCCCAGGACGACCAATAGGACTGACTCCCTGGATGTGCAGGGCTGGGTAGCC 6181
Qy 2059 rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerP 2079
Db 6182 GGGNAGACCTGTTGTTCAGAGGTGAGTGGGCCCTCTGCTGCCCTCTGACCCGCTCATCTCT 6241
Qy 2079 heTrpGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL 2099
Db 6242 TCTGGGGCGGTTCAGCATCCAGGTGCAGAGCGTTTCCGGCATCCAGAGCAAACTCTCCA 6301
Qy 2099 yHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProp 2119
Db 6302 AGCACATCCGCTCCAGCCCTTGGCCAGCCCTGGNACCAGCTGGGCCAGAGACCTC 6361
Qy 2119 roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL 2139
Db 6362 CAGAGACCAGAACAGCTTAGAGCTGGACACGAGCTGAGCTGGATTTCAGGAGACCTCC 6421
Qy 2139 euProSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValG 2159
Db 6422 TTCCACAGACCCAGGAAGAACCCCTGTCCACCGGGACCTGAAAGAACTGTCTACAGTGTAG 6481
Qy 2159 luThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerI 2179
Db 6482 AGACCCAGAGCTCGAGCGCGAGCCCTGGGTCTCTGGCTAGATGAACACGCGAGACACTCCA 6541
Qy 2179 leAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerL 2199
Db 6542 TTGCTGTGAGCTGTCTGGACAGCGGCTCCCAACCCCGCTTATGTCCAAGCCCTCAAGCC 6601
Qy 2199 euGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProS 2219
Db 6602 TCGGGGGCCAACTCTTGGGGGTCTTGGGAGCGCGCTTAAAGAAAAAACTCAGGCCACCCA 6661
Qy 2219 erIleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValC 2239
Db 6662 GTATCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGAGTCTCTGGTGTCT 6721
Qy 2239 ysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuA 2259
Db 6722 GCCTCAGGAGAGGGCGCCCGCCAGTGACTTAAGGATCTCTGGTCTCTCCAGCCCCCTTG 6781
Qy 2259 spSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerS 2279
Db 6782 ACAGCAGGGTGTCTCACCTCCCAAGAAAGAACACGCTGAGTCTCTCTGGTGTCTCT 6841
Qy 2279 erAspProThrAspMetAspPro 2286
Db 6842 CTGACCCCAACAGACATGGACCCC 6864

Db 2021 ||||| CAGAGTGTGTGCACAGCTTCTTACCATGCCAGCTGCCACTTAGAGCCAGTCCGCTGCCAGG 2080
Qy 602 ||||| laProProArqCyseProSerGluAlaSerGlyArgThrValGlySerGlyLysValT 622
Db 2081 CGCCCCCTCCAGGTCCTCCCATCTGAGGCATCCGCGCAGACTGTGGGAGGAGGTGT 2140
Qy 622 YrProThrValHisThrSerProProProGluLeuLeuLysAspLysAlaLeuValGluV 642
Db 2141 ATCCACCGTGCACACAGCCCTCCACCGGAGAGCGCTGAAGGAGAGGCACACTAGTAGAGG 2200
Qy 642 alAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyProPheS 662
Db 2201 TGGCTGCCAGCTCTGGGCCCCCAACCTCCACAGCTTCAACATCCCAACCGGGGCCCTTACA 2260
Qy 662 erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI 682
Db 2261 GCTCCATGCACAAGCTCTGGAGACACAGAGTACAGGTGCTGCCAAGCTCTTTCAGAGA 2320
Qy 682 leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC 702
Db 2321 TCTCCAGCCCTTGTCTGAAGCAGACAGTGGAGCTGTGTCCAGACAGCTGCCCTACT 2380
Qy 702 ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps 722
Db 2381 GTGCCCGGGCCGGGCGAGGGAGGTGGAGCTCGCCGACCGTGAATGCCTGACTTCAGACA 2440
Qy 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHis 742
Db 2441 GCAGGAGGATTTATGAGTTACACAGGATGCCAGCAGCAGACCTCCGGGACCCCCACA 2500
Qy 742 erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db 2501 GC---CGCGGCAACGGAGCTGGGCCACAGATGCAGAGCCAGCTCTGTGCTGGCCTTCT 2557
Qy 762 rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db 2558 GGAGGCTTAATCTGTGACACCTTCCGAAAGATTTGGGACAGCAAGTACTTTGGCGGGGAA 2617
Qy 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
Db 2618 TCATGATCGGCATCCTCGTCAACACACTCAGCATGGGCATCGAATACACAGAGCAGCCCG 2677
Qy 802 luGluLeuThrAsnAlaLeuLysSerAsnIleValPheThrSerLeuPheAlaLeuG 822
Db 2678 AGGAGCTTACCAAGCCCTAGAAATCAGCAACATCGTCTTCACAGGCTCTTTGCCCTGG 2737
Qy 822 luMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
Db 2738 AGATGCTGTCTGAAGCTGCTGTGTATGCTGCCCTTTGGCTACATCAAGAAATCCCTTACAACA 2797
Qy 842 lePheAspGlyValIleValIleValIleSerValTTPGluIleValGlyGlnGlnGlyG 862
Db 2798 TCTTCGATGTGTCTATTGTGTGTCATCAGCTGTGGGAGATCGTGGGCGCAGCGGGGGCG 2857
Qy 862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
Db 2858 GCCTGTGGTGTGCGGACCTTCGCCCTGATGCGTGTGCTGAAGCTGGTGGCTTCTCTGC 2917
Qy 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db 2918 CGGCGCTGCACGGCGCAGCTGTGTGTGCTCATGAAGACCATGAGACCATGAGCAACGTCGCCACCTTCT 2977
Qy 902 ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db 2978 GCATGCTGTCTATGCTCTTCATCTTCATCTTCAGCATCCTGGGCGATGCATCTCTTCGGCT 3037
Qy 922 ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
Db 3038 GCAGTTTGTGCTCTGAGCGGGATGGGACACCCCTGCCAGACCCGGAAGAAATTTGACTCCT 3097
Qy 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962

Db 3098 TGCTCTGGGCCCATCGTCACCTGTCTTTTCAGATCTCTGACCCAGGAGGACTGGAAACAAAGTCC 3157
Qy 962 euTyrAsnGlyMetAlaSerThrSerSerTyrAlaLeuTyrPheIleAlaLeuMetT 982
Db 3158 TCTACAAATGGTATGGCTCCACGTCGTCTGGGGGGCCCTTTATTTCATTTGCCCTCATGA 3217
Qy 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db 3218 CTTTCGGCAACTACGTGCTCTTCAATTTGTGCTGCGCATTCCTGGTGGAGGCTTCCAGG 3277
Qy 1002 laGlu----- 1003
Db 3278 CGGAGGAATTCAGAAACGGGAAGATCGCGAGTGCAGAGTTAAGCTGTATTTCAGTGCCTG 3337
Qy 1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS 1019
Db 3338 TCAGACTCCCAAGGGGGAGATGCCAACAGTCCGAAATCAGAGCCCGATTTCTTCACCCA 3397
Qy 1019 erValAspGlyAspGlyAspArgLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039
Db 3398 GCCTGGATGGTATGGGACAGGAAGAGTGTGGCTTTGGTCTCCCTGGGAGAGCACC 3457
Qy 1039 laGluLeuArgLysSerLeuProProLeuIleIleHisThrAlaAlaThrProMetS 1059
Db 3458 CGAGAGCTGGGAAGAGCCTGCTGCCGCTCTCATTCACACGGCGCCGACACCCATGT 3517
Qy 1059 erHisProLysSerSerThrGlyValGlyAlaLeuLeuGlySerGlySerArgArgT 1079
Db 3518 CGCTGCCAAGACACACAGCGGCTGGGCGAGGCGCTGGGCCCTCGCTCGGCCCGCA 3577
Qy 1079 hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCyseProProS 1099
Db 3578 CCAGCAGCAGCGGCTCGGCAGAGCCTGGGGCGGCC---CACGAGATGAAGTCAACCGGCCA 3634
Qy 1099 erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1119
Db 3635 GCCTCCGCGAGCTCTCCGCGCAGCCCTCGAGCGCTGCAACAGCTGACACAGCAGCGGCT 3694
Qy 1119 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 1139
Db 3695 CCAGCCGGAACACGCTTCGGCCGTGCACCCAGCTGAAAGCGGAGNAGGCCAAGTGGAGNC 3754
Qy 1139 rgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluG 1159
Db 3755 GCGGCTCCCTGTTGTGGGAGAGGCGCAGGAGCAGGATGAAGAGGAGAGCTCAGAAG 3814
Qy 1159 luAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 1179
Db 3815 AGAGCGGGCGCAGCCCTCGCGGCGAGTGACCATGCCACAGGGGGTCCCTGGAGCGGGAGG 3874
Qy 1179 laLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaS 1199
Db 3875 CCAAGAGTTCTTTTGACCTGCCAGACACACTGCAGGTGCCAGGGCTGCATCGCACTGCCA 3934
Qy 1199 erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 1219
Db 3935 GTGGCGAGGGTCTGCTTCTGAGCACCGAGACTGCAATGGCAAGTCGGCTTCAGGGCGCC 3994
Qy 1219 euAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluG 1239
Db 3995 TGGCCCGGGCCCTCGCGGCTGTATGACCCCCCTCGATGGGATGGGATGACCGCGATGACGAGG 4054
Qy 1239 lyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysC 1259
Db 4055 GCAACTGAGCAAAAGGGGAACGGGTCCGCGCTGGATCCGAGCCCGACTCCCTGCCTGCT 4114
Qy 1259 ysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuL 1279
Db 4115 GCCTCGAGCGAGACTCTCTGTGTGAGCTTACATCTTCCCTCCTCAGTCCAGGTTCGCGCTCC 4174
Qy 1279 euCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheL 1299
Db 4175 TGTGTACCGGATCATCACCAAGATGTTTCACACAGTGTTCGACCGTGGTCTTGTTCATCATCTTCC 4234

Qy 1299 euAanCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgI 1319
Db 4235 TTAAGTGCATCACCATCGCCATGGAGCGGCCCAAAATGACCCCCACAGCGCTGAACGCA 4294
Qy 1319 lePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValL 1339
Db 4295 TCTTCTGACCTCTCCAAATTACATCTTCCCGCAGCTCTTCTGGCTGAATGACATGA 4354
Qy 1339 ysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnV 1359
Db 4355 AGGTGGTGGCCTGGGCTGTCTCGGGAGCAGCGGTACCTCGGAGCAGTGTGGAAACG 4414
Qy 1359 alLeuAspGlyLeuLeuValleuIleSerValIleAspIleLeuValSerMetValSerA 1379
Db 4415 TGCTGGAGCGGCTGTGTGTGCTCATCTCCGTCATCGACATTTCTGGTGTCCATGTCTCTG 4474
Qy 1379 spSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgp 1399
Db 4475 ACAGGGGACCAAGATCCTGGGCATGCTGAGGGTGTCTGGGCTGTGGGACCTGCGCC 4534
Qy 1399 roLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerS 1419
Db 4535 CGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTGGTGGTGGAGACGCTGATGTCT 4594
Qy 1419 erLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyI 1439
Db 4595 CACTGAAACCCATCGGCAACATGTAGTCATCTGCTGTGCGCTCTTTCATCATTTTCGGCA 4654
Qy 1439 leLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyLysAspThrArgA 1459
Db 4655 TCTTGGGGTGCAGCTCTTCAAAGGAAGTTTTTCGTGTGTCAGGGCGAGGATACCAGGA 4714
Qy 1459 snIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrA 1479
Db 4715 ACATCACCAATAAATCGGACTGTGCGAGGCGAGTTACCGTGGGTGTCGGCACAAGTACA 4774
Qy 1479 enPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyT 1499
Db 4775 ACTTTGACAACTTGGCCAGGCGCTGTATGTCCTTCTGTTTGGCTTCCAAAGATGTT 4834
Qy 1499 rpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIleMetA 1519
Db 4835 GGGTGGACATCATGTACCATGGCTGGATGCTGTGGGCGTGACAGCAGCCCATCA 4894
Qy 1519 snHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV 1539
Db 4895 ACCACACCCCTGGATGCTGTACTTCACTTCATCTCGTTCTCTGCTCATTTGGCCTTCTTTG 4954
Qy 1539 alLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnG 1559
Db 4955 TCCTGAAACATGTTTGGGGTGTGGTGTGGAGAACTTCCAAAGTGTGCGGAGCACCCAGG 5014
Qy 1559 luGluGluGluAlaArgArgGluGluLysArgLeuArgLeuGluLysLysArgA 1579
Db 5015 AGGAAGAGAGGCGCGCGGGAGGAGAGCGCTACGAAGACTGAGAGAAAAGAGAA 5074
Qy 1579 rg-----SerLysGluLysGlnMetAlaGluA 1588
Db 5075 GGAATCTAATGTGGACGATGTAATTGCTTCGGCAGCTCAGCCAGCGCTCGTCAGAA 5134
Qy 1588 laGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuC 1608
Db 5135 CCCAGTGAAACCTTACTCTCCGACTACTCCGCTTCCGGCTCTCGCTCCACCACTTGT 5194
Qy 1608 ysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrM 1628
Db 5195 GCACCAGCCACTACCTGGACCTCTTTCATCACAGGTGTTCATCGGGCTGAACGTGGTCA 5254
Qy 1628 etAlaMetGluHisTyrGlnProGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnT 1648
Db 5255 TGGCCATGGAGCACTACCAGCAGCGCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACT 5314

Qy 1648 yrIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheA 1668
Db 5315 ACATCTTCACTGTCATCTTTGTCTTGAGTTCAGTTTTCAAACTTGTGSCCTTTGGTTTC 5374
Qy 1668 rgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleM 1688
Db 5375 GTCGGTTCTTCCAGGACAGGTGGAACACAGCTGGACCTGGCCATTTGTCTGTCTCCATCA 5434
Qy 1688 etGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleI 1708
Db 5435 TGGGCATCAGCTGGAGAAATCGAGGTCAACGCTCGCTGCCCCATCAACCCCCACCATCA 5494
Qy 1708 leArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValG 1728
Db 5495 TCCGCATCATGAGGGTCTCGGCATTTGCCGAGTGTCTGAAGCTGCTGAAGATGCTGTGG 5554
Qy 1728 lyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyL 1748
Db 5555 GCATCGGGCGCTGCTGGACACAGGTGATGAGGCCCTGCCCCAGGTGGGAACTGGGAC 5614
Qy 1748 euLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspL 1768
Db 5615 TTCTCTTTCATGTTGTTTTCATCTTTGAGCTCTGGGCGTGGAGCTCTTTTGGAGACC 5674
Qy 1768 euGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnP 1788
Db 5675 TGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGGCGCTCATGCCACCTTTTCGGA 5734
Qy 1788 heGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleM 1808
Db 5735 TTGGCATGGGCTTCTTAACCTCTTCCGAGTCTCCACAGGTGACAATTGGGAATGGCATTA 5794
Qy 1808 etLysAspProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerP 1828
Db 5795 TGAAGGACACCTCCGGGACTGTACAGGAGTCCACCTGCTACACACGGTCACTCGC 5854
Qy 1828 rolIeTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleA 1848
Db 5855 CTATCTACTTTGTGCTCTCGTGTGACGGCCCCAGTTCTGTAGTCAACCGTGTGATCG 5914
Qy 1848 laValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuG 1868
Db 5915 CCGTGTCTGATGAACACCTTGGAGGAGAGCAACAAGAGGCGCAAGAGAGCGCCAGTAG 5974
Qy 1868 luAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlyS 1888
Db 5975 AGGCTGAGCTGGAGCTGGAGATGAAGACCTTCAGCCCCCAGCCCCACTCGCCACTGGGCA 6034
Qy 1888 erProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyA 1908
Db 6035 GCCCCCTTCTCTGGCTGGGTCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCTGGGG 6094
Qy 1908 laProHisThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThr- 1927
Db 6095 CTCTGCACCCAGCGCGCCACGCGAGATCAGCTCTCCACTTTTCCCTGGAGCACCCACGG 6154
Qy 1927 ----- 1927
Db 6155 ACAGGAGCTGTTTGACACCATATCCCTGTGTATCCAGGGCTCCCTGGAGTGGAGCTGA 6214
Qy 1927 ----- 1927
Db 6215 AGCTGATGGACGAGCTGGCAGGCCCGAGGGGCCAGCCCTCTGCTTCCCTTCTGCCCCCA 6274
Qy 1927 ----- 1927
Db 6275 GCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAGATGAGGCTCTGTCTCTGACGT 6334
Qy 1927 ----- 1927
Db 6335 CAGAGATTGTCTGAACCCGCTCCTCTCTAGCTCTGACGGATGACTCTTTGCTGCTGATG 6394
Qy 1928 -----MetValProHisProGluGluV 1935

```
Db 6395 ACATGCACACACTTACTTAGTCCCTGGAGAGCAATATGCAGCCCCACCCACGAGC 6454
Qy 1935 alProValProLeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrH 1955
Db 6455 TGCCA-----GGACACAGACTTACTGACTGCGGAAGTCTGGGGTCAGCGAAGC 6505
Qy 1955 isSerLeuProAsnAspSerTyrMetCysArgAenGlySerThrAlaGluArgSerLeuG 1975
Db 6506 ACTCTCTGCCAATGACAGCTTACATGTGTGGCATGGAGCAGCTCCGCGAGGGCCCTGG 6565
Qy 1975 lyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerG 1995
Db 6566 GACACAGGGGTGGGGCTCCCAAGAGCTCAGTCAGGCTCGGTCTTGTCCGTTCACCTCC 6625
Qy 1995 lnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnP 2015
Db 6626 AGCCAGCAGATACACAGCTACATCTGCAGCTTCCAAAGATGCACCTCATCTGCTCCAGC 6685
Qy 2015 roHisGlyAlaProThrTyrGlyAlaIleProLysLeuProProGlyArgSerProL 2035
Db 6686 CCCACAGCGCCCCAACCTGGGGCACCATCCCAACCTGCCCCACACAGGAGCTCCCTT 6745
Qy 2035 euAlaGlnArgProLeuArgGlnAlaIleArgThrAspSerLeuAspValGlnG 2055
Db 6746 TGGCTCAGAGGCCACTCAGGGCCAGGCGAGCAATAGGAGCTGACTCCTTGGACGTTCCAG 6805
Qy 2055 lyLeuGlySerArgGluAspLeuSerGlyValSerGlyProSerCysProLeuThrA 2075
Db 6806 GTCTGGGCGAGCGGGAAGACTGCTGCAGAGGTGAGTGGGCCCTCCCGGCCCTGGCCC 6865
Qy 2075 rgSerSerPheThrGlyGlySerSerIleGlnValGlnArgSerGlyIleGlns 2095
Db 6866 GGGCTACTCTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCACTCCCGCAGGCACA 6925
Qy 2095 erLysValSerLysIleArgLeuProAlaProCysProGlyLeuGluProSerTrpA 2115
Db 6926 GCAAGATCTCCAGACATGATCCCGCGAGCCCTTGCAGGCGCCAGAACCCCAACTGGG 6985
Qy 2115 laLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleS 2135
Db 6986 GCAAGGGCCCTCCAGAGACCAAGAGCAGCTAGAGTTGGACACCGAGCTGAGCTGGATT 7045
Qy 2135 erGlyAspLeuLeu---ProSerSerGlnGluGluProLeuPheProArgAspLeuLysL 2154
Db 7046 CAGAGACCTCTCTCCCTTGGCGCCAGGAGGAGCCCCCATCCACAGGACCTGAAGA 7105
Qy 2154 ysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluG 2174
Db 7106 AGTGCTACAGCGTGGAGGCCAGAGCTGCCAGCGCGGCTTACGCTCTGGCTGGATGAGC 7165
Qy 2174 lnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysP 2194
Db 7166 AGAGGAGACACTATCGCGCTGAGCTGCTGGACAGCGGCTCCCAACCCACCTGGGCA 7225
Qy 2194 roSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysL 2214
Db 7226 CAGACCCCTCTAACCTTGGGGGCCAGGCTCTTGGGGGGCTGGAGCGCGGCCCAAGAAA 7285
Qy 2214 ysLeuSerProProSerSerIleAspProProGluSerGlnGlySerArgProProC 2234
Db 7286 AACTCAGCCCGCTAGTATACCATACGACCCCGGAGGCAAGGCTCTCGGACCCCGC 7345
Qy 2234 ysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerV 2254
Db 7346 CCAGCCCTGGTATCTGCCCTCCGAGGAGGGCTCCGTCAGGAGCTCCAAGGATCCCTGG 7405
Qy 2254 alSerSerProLeuAspSerThrAlaLaSerProSerProLysLysAspThrLeuSerL 2274
Db 7406 CCTTGGCCCCCTTGACAGCATGCTGCTCGCCCTCCCAAGAGATGCTGTGAGTC 7465
Qy 2274 euSerGlyLeuSerSerAspProThrAspMetAspPro 2286
```

```
Db 7466 TCTCCGGTTTATCCTCTGACCCAGCAGACCTGGACCCC 7503
RESULT 5
US-10-786-148-120
; Sequence 120, Application US/10786148
; Publication No. US20050191634A1
; GENERAL INFORMATION:
; APPLICANT: LIN, SHIU-RU
; APPLICANT: WANG, JAW-YUAN
; TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER
; FILE REFERENCE: BHT/3230-85
; CURRENT APPLICATION NUMBER: US/10/786,148
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-148-120
Alignment Scores:
Pred. No.: 0 Length: 7825
Score: 10963.50 Matches: 2128
Percent Similarity: 89.6% Conservative: 34
Best Local Similarity: 88.2% Mismatches: 117
Query Match: 91.1% Indels: 135
Gaps: 7
DB:
US-09-611-257A-24 (1-2287) x US-10-786-148-120 (1-7825)
Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 281 CCGCGGGGCCCCCGGGTTCGCTGAGGACACCTCTCTGAGGGGCGCGCTTGCCTCT 340
Qy 23 SerAspProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGluArgAla 42
Db 341 CCGGATCGCCCGGGCCCCCGCTGGCCAGAGGATGGACGAGGAGGATGGAGCGGGCG 400
Qy 43 ProArgSerArgAspSerProValAlaSerArgSerThrThrCysProGlyProGly 62
Db 401 CCAGAGAGTCCGACACGCCCGGAGCTTCATGCGGCTCAACGACCTGTCCGGGGCCGGG 460
Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlu 82
Db 461 GCCGGCGGGGCGGGGTCAGCAGAGAAAGGACCCGGGCGAGCGGACTCCGAGCGGGAG 520
Qy 82 lyLeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgP 102
Db 521 GGCTGCGGTACCGCGGCTGCCCCCGGTGTTTTCTTTCTACTTGAGCCAGACAGCGGCC 580
Qy 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
Db 581 CGGGAGCTGGTGTCTCCGACCGGTCTGTAAACCCCTGGTTTGACCGCATCAGCATGTGG 640
Qy 122 alIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
Db 641 TCATCTCTTCAACTGCTGACCTCGGCATGTTCCGGCCATGCGAGGACATCGCTGTG 700
Qy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlav 162
Db 701 ACTCCACGCGCTGCGGATCCTGCAGGCCTTGTGATGACTTTCATCTTTCCTTTCCTCC 760
Qy 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyA 182
Db 761 TGGAGATGGTGGTGAAGATGTTGGCCCTTGGGCATCTTTGGGAAAAAGTTTACTCTGGAG 820
Qy 182 spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA 202
Db 821 AACTTGAACCGGCTTGACTTTTTCATCGTCATCGCAGGGATGCTGGAGTACTCGCTGG 880
Qy 202 spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
```


Qy 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962
Db 3098 TGCTCTGGGCGCATCGTCACTGTCTTTTCAGATCTCTGACCCAGGAGACTGGAAACAAGTCC 3157
Qy 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982
Db 3158 TCTACAATGGTATGGCTCTCACGTCGCTCGTGGGCGGCCCTTTATTTCAATTGGCCCTCATGA 3217
Qy 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db 3218 CCTTCGGCAACTAGTCTCTTCAATTTGTGTGGTCCGCAATCTGCTGGAGGGCTTCCAGG 3277
Qy 1002 laGlu----- 1003
Db 3278 CGAGGAAATCAGCAAAACGGGAAGATCGAGTGGACAGTTAAAGCTGTATTTCAGCTGCCTG 3337
Qy 1004 -----GlyAsAlaThrLysSerGluSerGluProAspPheSerProS 1019
Db 3338 TCGACTCCAGGGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTTCTTCTCACCCA 3397
Qy 1019 erValaspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039
Db 3398 GCCTGGATGGTATGGGACAGGAAGAAGTCTTTGGCTTGGTCTCCCTGGGAGAGACC 3457
Qy 1039 laGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetS 1059
Db 3458 CGGAGCTGCGGAAGAGCGCTGTCGCGCTCTCTCATCATCCACACGCGCGCCACACCCATGT 3517
Qy 1059 erHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT 1079
Db 3518 CGCTGCCCAAGAGACAGCAGCGGCTTGGCGAGGCGCTGGGCGCTCGCTGCGCGCGCA 3577
Qy 1079 hrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProS 1099
Db 3578 CCAGCAGCAGCGGTGCGCAGAGCGCTGGGCGGCC---CACGAGATGAAGTCAACCGCCCA 3634
Qy 1099 erAlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1119
Db 3635 GCGCCCGCAGCTCTCCGACAGCCCTGGAGCGCTGCAAGCAGCTGGACACGAGCGGCT 3694
Qy 1119 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 1139
Db 3695 CCAGCCGGAACAGCCTCGGCGCTGCACCCAGCTGGAAGCGGAGAACCCCAAGTGGAGAGC 3754
Qy 1139 rgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluG 1159
Db 3755 GCGGCTCCCTGTGTCGGGAGAGGCCAGAGAGCCAGGATGAAGAGAGAGCTCAGAAG 3814
Qy 1159 luAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 1179
Db 3815 AGGAGCGGGCCAGCCCTGCGGGCAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGGAGG 3874
Qy 1179 laLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlas 1199
Db 3875 CCAAGAGTTCTTTGACTGCCAGACACATGCAAGGTGCGAGGCTGCATCGCACTGCCA 3934
Qy 1199 erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 1219
Db 3935 GTGGCCGAGGGTCTGCTTCTGAGACACAGGACTGCATGCAAGTCCGCTTCAGGGCGCC 3994
Qy 1219 euAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluG 1239
Db 3995 TGGCCCGGGCCCTCGCGCTGATGACCCCGCTATGGATGGGATGACGCGCGATGACGAGG 4054
Qy 1239 lyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysC 1259
Db 4055 GCAACCTTGAGCAAAAGGGAACGGGTCCGCGCGTGGATCCGAGGCCGACTCCCTCGCTGCT 4114
Qy 1259 ysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuL 1279
Db 4115 GCCTCGAGCAGAGACTCTCTGTGTCAGCTACATCTTCCCTCTCTCAGTCCAGGTTCCGCCCTCC 4174
Qy 1279 euCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIlePheL 1299

Db 4175 TGGTGTCACCGGATCATCACCCACAAGATGTTCCACCACGCTGGTCTTGTCTATCATCTTCC 4234
Qy 1299 euAsnCysIleThrIleAlaMetGluArgProLysLysIleAspProHisSerAlaGluArgI 1319
Db 4235 TTAACGTGCATCACATCGCCATGGAGCGCCCAAAATTGACCCCAACAGCGCTGAACGCA 4294
Qy 1319 lePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValL 1339
Db 4295 TCTTCTGTGACCCCTCTCCAATTACATCTTACCCGAGCTCTTCTGGCTGAAATGACAGTGA 4354
Qy 1339 ysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnV 1359
Db 4355 AGGTGTGTGGCACTGGGCTGTGCTTCGGGAGCAGCGGTACCTGCGGAGCAGTTGGAAACG 4414
Qy 1359 alLeuAspGlyLeuLeuValIleSerValIleAspIleLeuValIleSerMetValSerA 1379
Db 4415 TGTGACGGGCTGTGGTGTCTCATCTCCGTATCGACATTCGTGTGTCATGTGTCTCTG 4474
Qy 1379 spSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgP 1399
Db 4475 ACAGCGCACCAAGATCCTCGGCATGCTGAGGTGCTGCGGCTGCTCGGACCCCTCGGCC 4534
Qy 1399 roLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerS 1419
Db 4535 CGCTCAGGTGTATCAGCCGCGCGCAGGGGTGAAGCTGGTGGTGGAGACGCTGATGTCT 4594
Qy 1419 erLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyI 1439
Db 4595 CACTGAAACCCATCGGCAACATTTAGTATCATCTGTGTGCTCTTCTCATCATTTTCGGCA 4654
Qy 1439 leLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgA 1459
Db 4655 TCTTGGGGTGCAGCTCTTCAAAGGAAAGTTTTTCTGTGTCAGGGCGAGGATACCAAGGA 4714
Qy 1459 snIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrA 1479
Db 4715 ACATCACCAATAAATCGGACTGTGCGAGGCCAGTTACCGGTGGGTCCGCGCACCAAGTACA 4774
Qy 1479 snPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyT 1499
Db 4775 ACTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTGTTTGGCTTCCAGGATGGTT 4834
Qy 1499 rpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetA 1519
Db 4835 GGGTGGACATCATGTACGATGGCTTGGATGCTGTGGGCGTGGACACGAGCCCATCATGA 4894
Qy 1519 snHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV 1539
Db 4895 ACCACAACCCCTGGATGCTGCTACTTCTATCTCTGTTCTCTGCTCATTTGGCCCTTCTTTG 4954
Qy 1539 alLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnG 1559
Db 4955 TCTGTAACATGTTTGTGGGTGGTGGTGGAGAACTTCCACAAGTGTGCGGAGCACCAGG 5014
Qy 1559 luGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgA 1579
Db 5015 AGGAAGAGGAGGCCCGCGCGGAGGAGAGAGCCCTACGAAGACTGAGAGAAAAGAGAA 5074
Qy 1579 rg-----SerLysGluLysGlnMetAlaGluA 1588
Db 5075 GGAATCTAATGCTGGACGATGTAATTGCTTCCGCGACGCTCAGCCAGCGCTCGCTCAGAAG 5134
Qy 1588 laGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuC 1608
Db 5135 CCAGGTGCAAAACCTTACTACTCGACTACTCCCGCTTCCGGCTCTCTGCTCCACCACTGT 5194
Qy 1608 ysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrM 1628
Db 5195 GCACGAGCAGCTACCTGGACCTCTTTCATCACAGGTGTGTCATCGGCTGAACGTTGGTACCA 5254
Qy 1628 etAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnT 1648

Db 5255 TGGCCATGGAGCACTACCAGCAGCCCCAGATTCTGTGATGAGGCTCTGAAGATCTGCAACT 5314
Qy 1648 YrIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheA 1668
Db 5315 ACATCTTCACCTGTCTCTGTGGAGTCAGTCTTCAAACTTGTGGCCCTTGGTTCC 5374
Qy 1668 rGArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleM 1688
Db 5375 GTCCGTTCTTCAGACAGAGTGGAAACCACTGGACCTGGCCATTGTGCTGCTGCCATCA 5434
Qy 1688 etGlyIleThrLeuGluIleGluValAsnLeuSerLeuProIleAsnProThrIleI 1708
Db 5435 TGGGCATCACCTGGAGAAATCGAGGTCAAGCTCGCTGCCCATCAACCCCACTCA 5494
Qy 1708 leArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValG 1728
Db 5495 TCCGCATCATGAGGCTGTGGCCATTGCCCGAGTGTGAAGCTGTGAAGATGGCTGTGG 5554
Qy 1728 lyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyL 1748
Db 5555 GCATCGGGCGCTGCTGGACACGGTGTATGCAGGCCCTGCCAGGTGGGGAACCTGGGAC 5614
Qy 1748 euLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValIleLeuPheGlyAspL 1768
Db 5615 TTCCTCTCATGTGTGTTTTTCATCTTTGCAGCTCTGGCGTGGAGCTCTTGGAGACC 5674
Qy 1768 euGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnP 1788
Db 5675 TGGAGTGTGAGAGACACACCCCTGTGAGGGCCCTGGGCCGTATGCCACCTTTCGGAACT 5734
Qy 1788 heGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleM 1808
Db 5735 TTGGCATGGCCCTTCTAAACCTCTCTCCAGTCTCCACAGGTGCACATTTGGAATGGCATT 5794
Qy 1808 etLysAspProSerArgAspCysAspGlnGluSerThrCysArgAsnThrValIleSerP 1828
Db 5795 TGAAGCACACCTCCGGGACTGTGACACAGGAGTCCACCTGTACAAACCGGTCTATCTCGC 5854
Qy 1828 roIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAla 1848
Db 5855 CTATCTACTTTGTGTCCTGTGCTGACGGGCCAGTTTCGTGTAGTCAACGTGTGTATCG 5914
Qy 1848 laValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuG 1868
Db 5915 CCGTCTCATGAAGCACTTGGAGGAGACCAACAGAGGCCCAAGAGAGGCCCGAGCTAG 5974
Qy 1868 luAlaGluLeuLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlys 1888
Db 5975 AGGCTGAGCTGGAGCTGGAGATGAAGACCTTCAGGCCCCAGCCCCACTCGCACCTGGGCA 6034
Qy 1888 erProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyA 1908
Db 6035 GCCCTTCTCTGGGCTGGGTCGAGGGCCCGACAGCCCCGACAGCCCCCAAGCCCTGGGG 6094
Qy 1908 laProHisThrThrAlaHisIleGlyAlaAsaSerGlyPheSerLeuGluHisProThr- 1927
Db 6095 CTCTGCACCCAGCGGCCACCGAGATCAGCTCCCACTTTTCCCTGGAGCACCCACCGG 6154
Qy 1927 ----- 1927
Db 6155 ACAGGCAGCTGTTTGACACCATTATCCCTGCTGATCCAGGGCTCCCTGGAGTGGGAGCTGA 6214
Qy 1927 ----- 1927
Db 6215 AGCTGATGACGAGCTGGAGGCCACAGGGGGCCAGCCCTCTGCTCCCTTCTGCCCCCA 6274
Qy 1927 ----- 1927
Db 6275 GCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAGATGGAGGCTCTGTCTCTGACGT 6334
Qy 1927 ----- 1927
Db 6335 CAGAGATTGTGCTGAACCGTCTCTGCTCTAGCTCTGACGGATGACTCTTTTGCCTGATG 6394

Qy 1928 -----MetValProHisProGluGluV 1935
Db 6395 ACATGCACACACTCTTACTTAGTCCCTGGAGAGCAATATGCAGCCCCACCCACGAGGAGC 6454
Qy 1935 alProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrH 1955
Db 6455 TGCCA-----GGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTACAGCGAAGCGC 6505
Qy 1955 isSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuG 1975
Db 6506 ACTCTCTGCCCAATGACAGCTACATGTGTCCGATGGAGAGCACTGCCAGAGGGGCCCTTGG 6565
Qy 1975 lyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerG 1995
Db 6566 GACACAGGGCTGGGGCTCCCCAAGCTCAGTCAGGCTCGTCTTGTCCGTTTCACTCCC 6625
Qy 1995 lnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnP 2015
Db 6626 AGCCAGCAGATACCAGCTACATCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGC 6685
Qy 2015 roHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProProGlyArgSerProL 2035
Db 6686 CCCACAGCGCCCAACCTGGGGCACCATGCCAAACTGCCCCACAGGACGCTCCCTT 6745
Qy 2035 euAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG 2055
Db 6746 TGGCTCAGAGCCCACTCAGGGCCCGAGGAGCAATAGGACTACTCTTGGACGTTTCAAG 6805
Qy 2055 lyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrA 2075
Db 6806 GTCTGGGCAGCGGGAAGACCTGTGCGAGAGGTGAGTGGGCCCTCCCGGCCCTGGGCC 6865
Qy 2075 rgSerSerSerPheTrpGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnS 2095
Db 6866 GGGCTACTCTTCTGGGGCCAGTCAAGTACCCAGGACACAGACACTCCCGCAGCCACA 6925
Qy 2095 erLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpA 2115
Db 6926 GCAAGATCTCCAGACATAGACCCCGCAGCCCTTGGCCAGGCCCAGAACCCAACTGGG 6985
Qy 2115 laLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleS 2135
Db 6986 GCAAAGGGCCCTCCAGAGACCAAGACAGCTTAGAGTTGGACACGAGCTGAGCTGATTT 7045
Qy 2135 erGlyAspLeuLeu---ProSerSerGlnGluProLeuPheProArgAspLeuLysL 2154
Db 7046 CAGGAGACCTCTGCCCTGGCGCCAGGAGGAGCCCCCATGCCACGGGACCTGAAGA 7105
Qy 2154 ysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluG 2174
Db 7106 AGTGTACAGCTGGAGGCCAGAGCTGCCAGCGCCGCTTACGTCTTGGTGGATGAGC 7165
Qy 2174 lnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysP 2194
Db 7166 AGAGGAGACACTCTATCGCCGTCAGCTGCCAGCGGGCTCCCAACCCCACTGGGCA 7225
Qy 2194 roSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysL 2214
Db 7226 CAGACCCCTCTAACTTGGGGGCCAGCCCTTGGGGGGCCCTGGGAGCGCGGCCCAAGAAA 7285
Qy 2214 ysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProProC 2234
Db 7286 AACTCAGCCCTTAGTATACCATAGACCCCGCCGAGAGGCAAGGTCTCTGGACCCCGC 7345
Qy 2234 ysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerV 2254
Db 7346 CCAGCCCTGGTATCTGCTCCGAGGAGGGCTCCGCTCCAGGACTCCCAAGGATCCCTTGG 7405
Qy 2254 alSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerL 2274
Db 7406 CCTTGGGCCCTTGACAGCATGGCTGCTTGCCTTCCCAAGAAAGATGTGCTGAGTC 7465

Db 1622 CCCTCTCGGGCCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACT 1681
Qy 593 ySHisLeuGluProValArgCysGlnAlaProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGACCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTCAGGCATCCG 1741
Qy 613 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
Db 1742 GCAGACTGTGGGAGCGGGAGGTGTATCCACCGTGCACACAGGCCCTCCACCGGAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
Db 1802 CGCTGAAGGAGAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGCCCCCAACCTCACCA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCGGGCCCTACAGCTCCATGCACCAAGCTCTGGGAGACAGAGTA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGTGCCCTGCCAAGACTCTTGCAGATCTCCAGCCCTTGTTCGNAAGCACACAGTGGAG 1981
Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGTCACAGACAGCTGCCCTTACTGTGCCCGCGGGCAGGGAGGTGCAGCTCG 2041
Qy 713 laAspHisValMetProAspSerSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAAATGCCTGACTCAGACAGCAGGAGGAGTTATGAGTTACACAGGATGCC 2101
Qy 733 lnHisSerAspLeuArgAspProHisSerArgAtgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGAGGACTCTCGGGACCCCCACAGC----CGGGCACAAGAGCTGGGCCAGATG 2158
Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCAGCTCTGTGTGGCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTTTGGCGGGGAATCATGATGCCCATCTGGTCAACACACTCAGCA 2278
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGATACACAGCAGCGCCGAGAGCTTACCAAGCCCTAGAAATCAGCAACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTCCACAGCCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTTGTGTATGCTCCCT 2398
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
Db 2399 TTGGCTACATCAAGAATCCCTACAACTCTTCGATGGTGTCAATTGTGTCTATCAGCGTGT 2458
Qy 853 rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCCAGCAGGGGGCGCGCTGCTGCTGCGGACCTTCCGCGCTGATGC 2518
Qy 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGTGGCTCTCTCGCGGGCTGTCAGCGGAGCTGGTGTGCTCATGA 2578
Qy 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2579 AGACCATGGACAACGTGGCCACCTTCTGCATGCTCTTATGCTCTTTCATCTTCATCTTCA 2638
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2639 GCATCTCTGGCATGCTATCTCTCGGCTGCAAGTTTGGCTCTGAGCGGATGGGACACCC 2698
Qy 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGAAATTTTGACTCTTGTCTTGGGCCATCGTCACTGTCTTTCAGATCC 2758

Qy 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpDA 973
Db 2759 TGACCCAGGAGGACTGGAAACAAGTCTCTACAAATGTATGGCTTCACAGTCTGCTCTGGG 2818
Qy 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2819 CGGCCCTTTATTTCAATGCTCTCATGACCTTCGGCAACTAGTGTCTCTTCAATTTGCTGG 2878
Qy 993 alAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2879 TCGCCATTCTGTGGAGGGCTTCCAGCGGAGGAAATCAGCAAAACGGGAAGATCGAGTG 2938
Qy 1004 -----GlyAspAlaThrLysSerG 1010
Db 2939 GACAGTAAGCTGTATTACGTGCTGCTGCTGCCAGGGGGAGATGCCAACAGTCCG 2998
Qy 1010 luSerGluProAspPheSerProSerValAspGlyAspGlyAspArgLysArgL 1030
Db 2999 AATCAGAGCCCGATTCTTCTCACCCAGCTGGATGGTATGGGACAGGAAGAAGTGCT 3058
Qy 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuI 1050
Db 3059 TGGCTTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCTGCTGCCGCTCTCA 3118
Qy 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyV 1070
Db 3119 TCATCCACAGCGCCGCCACACCCATGTCTGCTGCCAAGAGCACCCAGCAGCGGCTGGCG 3178
Qy 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGGCGCTGGGCCCTGCTGCGCGCGCACCCAGCAGCAGCGGCTCGGCAGAGCTGGGGCG 3238
Qy 1090 laHisHisGluMetLysCysProSerAlaArgSerSerProHisSerProTrpSerA 1110
Db 3239 CC---CACGAGATGAAGTCAACCGCCAGCGCCGACGCTCTCCGACAGCCCTGGAGCG 3295
Qy 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130
Db 3296 CTGCACAGCTGAGCAGCAGAGGCGCTCCAGCCGGACAGCCTCGGCGCTGCACCCAGCC 3355
Qy 1130 euLysArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluS 1150
Db 3356 TGAAGCGGAGAAGCCCAAGTGGAGAGCGCGCTCCCTGTTCTCGGGAGAGAGCCAGGAGA 3415
Qy 1150 erGlnAspGluGluLysSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3416 GCCAGGATGAAGAGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTCGGGCGAGTGACCATC 3475
Qy 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGTCTCTGGAGCGGAGGCCAAGAGTTCCTTTGACTGCTGCACACACACTGC 3535
Qy 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
Db 3536 AGGTGCCAGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAGGACT 3595
Qy 1210 ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
Db 3596 GCAATGGCAAGTGGCTTCAGGGCGCTTGGCCCGGGCCCTCGCGCTGATGACCCCCAC 3655
Qy 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaI 1250
Db 3656 TGGATGGGATGACGCCGATCAGCAGGCAACCTTGAGCAAAAGGGAACGGGTCCGCGCT 3715
Qy 1250 rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
Db 3716 GGATCCGAGCCGAGTCTCCCTGCTGCTCGAGCGAGACTCTCTGGTCAGCTACATCT 3775
Qy 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
Db 3776 TCCCTCTCAGTCCAGGTTCCGCCCTCTCTGTGTACCGGATCATCACCCACCAAGATGTCG 3835

Db 5996 CTCTGACGGATGACTTTTGGCTGATGACATGCACACACTCTTACTTAGTCCCTGGAGA 6055
Qy 1928 -----MetValProHisProGluValProValProLeuGlyProAspLeuThrV 1946
Db 6056 GCAATATGACGCCACCCACGGAGCTGCCA-----GGACCCAGACTTACTGACTG 6106
Qy 1946 alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
Db 6107 TGGCGAAGCTGGGGGTGACCGAAGCACTCTCTGCCCAATGACAGCTACATGTGTGGC 6166
Qy 1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlns 1986
Db 6167 ATGGGAGCACTGCCGAGGGGCCCCCTGGGACACAGGGGCTGGGGCTCCCCAAAGCTCAGT 6226
Qy 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
Db 6227 CAGGCTCCGTCTTGTCCCTTCACTCCACGACGAGATACCAGCTTACATCTCGCAGCTTC 6286
Qy 2006 roLysAspValHisTyrIleLeuGlnProHisGlyAlaProThrTyrGlyAlaIleProL 2026
Db 6287 CCAAGATGCACCTCATCTGCTCAGCCCCACAGCGCCCCCACTGGGGCAACCTCCCCA 6346
Qy 2026 ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIaI 2046
Db 6347 AACTGCCCCACAGGAGCTCCCCCTTTGGCTCAGAGGCCAATCAGGCGCCAGGACGAA 6406
Qy 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGluV 2066
Db 6407 TAAGGACTGACTCTTGGACGTTGAGGCTTGGGACGCGGGAAGACCTGTGCGAGAGG 6466
Qy 2066 alSerGlyProSerCysProLeuThrArgSerSerPheTyrGlyGlySerSerIleG 2086
Db 6467 TGAGTGGGCCCTTCCCGCCCTTGGCCCGGCTACTCTTTCTGGGGCAGTCAGTATCCC 6526
Qy 2086 InValGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaP 2106
Db 6527 AGGCACACGACGACTCCCGCAGCCACACGAAGATCTCCAAGCACATGACCCCGCAGGCC 6586
Qy 2106 roCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSerLeuG 2126
Db 6587 CTTGCCACGAGCCCAAGCCCACTGGGCAAGGGCCCTCCAGAGACCAAGACGACTTAG 6646
Qy 2126 luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu--ProSerSerGlnGluG 2145
Db 6647 AGTTGGACAGGAGCTGAGCTGGATTTCCAGAGACTCTCTGCCCTGGCGCCAGGAGG 6706
Qy 2145 luProLeuPheProArgAspLeuLysCysTyrSerValGluThrGlnSerCysArgA 2165
Db 6707 AGCCCCCATCCCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGCCCAGAGCTGCCAGC 6766
Qy 2165 rgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuA 2185
Db 6767 GCCGCGCTACGTCCTGGCTGGATGACGAGAGAGACACTCTATCGCCCTCAGCTGCCTGG 6826
Qy 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuG 2205
Db 6827 ACAGCGGCTCCCAACCCACCTGGGCACAGACCCCTCTAACCTTGGGGCCAGCCTCTTG 6886
Qy 2205 lyGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProp 2225
Db 6887 GGGGCGCTGGGAGCGCGGCCCAAGAAAAAATCAGCGCCGCTAGTATCACCATAGACCCCC 6946
Qy 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaP 2245
Db 6947 CCGAGAGCAAGGTCTCTCGAGCCCCCGCCAGCCCTGGTATCTGCTCCGAGGAGGGCTC 7006
Qy 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265
Db 7007 CGTCAGGCACTCCCAAGATCCCTTGGCCCTCTGGCCCCCTTGACAGCATGGCTGCTCGC 7066
Qy 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetA 2285
Db 7067 CTTCCCCCAAGAAAGATGCTGCTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGG 7126

Qy 2285 spPro 2286
Db 7127 ACCCC 7131

RESULT 7

US-10-757-262-15
; Sequence 15, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21185, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7134)
US-10-757-262-15
Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.7% Conservative: 33
Best Local Similarity: 89.3% Mismatches: 110
Query Match: 90.2% Indels: 135
DB: 9 Gaps: 7
US-09-611-257A-24 (1-2287) x US-10-757-262-15 (1-7648)

Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValalaSerArg 53
Db 2 TGGACGAGGAGGAGATGGAGCGGCGCCGAGGAGTCGGACAGCCCCGGAGCTTCATGC 61
Qy 54 SerSerThrThrCysProGlyAla-AlaGlyAla-GlySerThrGluLysApp 73

Db 62 GGCTCAACGACTGTTCGGGGGCGGGGGCGGGGGCGGGGGTCTACAGAGAAAGGACC 121
Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValp 93
Db 122 CGGGCAGCGGGACTCCGAGCGGAGGGGGTGCCTACCGGGCGCTGGCCCGGGTGGTTT 181
Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 113
Db 182 TCTTCTACTTGAGCCAGGACAGCGCGCGGAGCTGGTGTCTCCGACGAGTCTGTAACC 241
Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetp 133
Db 242 CCTGGTTTGAGCGCATCAGCATGTGTGTCTCTCAACTGCGTGAACCTGGGCAATG 301
Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATCGGAGGACATCGCTGTGACTCCAGCGCTGCGGATCTCTGACGGCTTTG 361
Qy 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTTGCGCTGGAGATGGTGTGAAGATGGTGGCTTGGGCA 421
Qy 173 lePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGGAAAAAGTTACTCTGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGAGGGATGCTGGAGTACTCGCTGGACCTGCGAAGACGTACGCTTCTCAGCTGTCA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 233
Db 542 CAGTCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTGGCCAGCATCGCATCTTG 601
Qy 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 253
Db 602 TCACGTTGCTGCTGGATACGCTGCCCATGTGGGCAACGCTGCTGCTCTGCTTCTTCG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCGAGGGCTGCTTCGNAACGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTrpGln 293
Db 722 GCTTCTCTACCTGAGAAATTCAGCGCTCCCTCGAGCTGGACCTGGAGCGCTATTACCA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 313
Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCCGACCGCAGAACCGCATGCGGT 841
Qy 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGACGGTGCCTGCGCGGGAGCGGGGGCGGTGGCCCACTTGGGCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTrp 353
Db 902 ACTATGAGGCTCAACAGCTCCAGCAACACCACTGTGTCACTGGAACAGTACTACA 961
Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 373
Db 962 CCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGGCATCAACTTTGACAACTG 1021
Qy 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 393
Db 1022 GCTATGCTGATCGCCATCTTCAGGTATCAGCTGGAGGGCTGGGTGCACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 413
Db 1082 ACTTTGTGATGATGCTCATCTTCTTACAAATTTCTACTTCTCATCTCTCATCATCG 1141
Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1201

Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 453
Db 1202 CCAAGCAGCGGAAAGCCAGCTATCGGGAGCAGCGTGTGCGTCTCTGCTCCAACGCCA 1261
Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 473
Db 1262 GCACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATAGGAGCTGCTCAAGTACCTGG 1321
Qy 473 alTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTCTGTAGGACCGCCGAGGCTGAGTCTCTGGGCGAGGAGTGTGC 1381
Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGly 513
Db 1382 GGGTGGCTGCTCAGCAGCCAGCACCCCTCGGGGCGCAGGAGACCAGCCAGCAGCA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCACCGCGCTATCCGTCCACCACTGGTGCACCCACCCACCC 1501
Qy 533 ishHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGlu 553
Db 1502 ATCACCACCACTACCACTGGCAATGGAGCGCTCAGGGCCCCCGGGCGCAGCCGAG 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 573
Db 1562 TCCAGGACAGGATGCAATGGTCCCGCAGGCTCATGTGTCACCACTCGACGCGCTG 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAsp 593
Db 1622 CCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCACT 1681
Qy 593 yshHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSer 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCAGGGCCCCCTCCAGGTCCCATCTGAGGCATCCG 1741
Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 633
Db 1742 GCAGGACTGTGGCAGCGGGAAGGTGTATCCACCGTGCACACCCAGCCCTCCACCGG 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThr 653
Db 1802 CGCTTAGAGAGAGGACACTAGTAGAGGTGGCTGCCAGCTCTGGGGCCCCCAACCTCA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSer 673
Db 1862 GCCTCAACATCCACCGGGCCCTCAGCTCCATGCACAAGCTGCTGGAGACACAGATA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGly 693
Db 1922 CAGGTGCTGCCAAAGCTCTTCAAGATCTCCAGCCCTTCTTGAAGAGCAGACAGTGGAG 1981
Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSer 713
Db 1982 CTTGTGTCCAGACAGTGCCTTACTGTGCCGGCGGGCGGAGGGAGGTGGAGTGC 2041
Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 733
Db 2042 CCACCGTGAATATGCTTGACTCAGACAGCGGAGGAGTTTATGAGTTCACACAGATGCC 2101
Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAsp 753
Db 2102 AGCACAGCGACCTCCGGGACCCCCACAGC--CGGGGCAACAGGAGCTGGGCCAGATG 2158
Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 773
Db 2159 CAGAGCCCACTGTGCTGCGCTTCTGGAGGCTAATCTGTGACACCTTCGAAAGATTG 2218
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 793
Db 2219 TGGACAGCAAGTACTTTGGCGGGGGAATCATGATCGGCATCTCTGGTCAACACACTCAG 2278

Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACACAGAGAGCCGAGGAGCTTACCAGCCCTAGAAATACGACACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTACCAGCGCTCTTTGCGCTGGAGATGCTGCTGAAGCTGTTGTGTATGTCCT 2398
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
Db 2399 TTGGCTACATCAAGATCCCTACACATCTTCGATGGTGTCAATTGTGTGTCATCAGCGTGT 2458
Qy 853 rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCAGCAGGGGGCGGCGCTGTGCTGCTCGGACCTTCCGCTGATGC 2518
Qy 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGGTGGCTTCTGCGCGCGCTGCAGCGCGAGCTGGTGTGTCTATGA 2578
Qy 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2579 AGACCATGGACAACGTTGGCCACTTCTGCATGCTGCTTATGCTCTTCACTTCACTTCA 2638
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2639 GCATCCTGGGCATGCAATCTTTCGGCTGCAAGTTTGGCTCTGAGCGGGATGGGACACCC 2698
Qy 933 euProAspArgLysAsnPheAspSerLeuLeuThrAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGAAATTTGACTCTTGTCTGGGCCATCGTCACTGCTTTTTCAGATCC 2758
Qy 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
Db 2759 TGACCCAGAGGACTGGAAACAAAGTCTCTCAATGGTATGGCCTCCACGTCGTCCTGGG 2818
Qy 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2819 CGGCCCTTTATTTTCAATGCCCTCATGACTTTCGGCACTACGTGCTCTTCAATTTGCTGG 2878
Qy 993 alAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2879 TCGCCATCTTGTGGAGGGCTTCAGCGGAGGAAATCAGCAAAACCGGAAGATCGAGTG 2938
Qy 1004 -----GlyAspAlaThrLysSerg 1010
Db 2939 GACAGTTAAGCTGTATTGAGTGCCTGTGCAGTCCAGGGGGAGATGCCAACAGTCCG 2998
Qy 1010 luSerGluProAspPhePheSerProSerValAspGlyAspArgLysLysArgL 1030
Db 2999 AATCAGAGCCCGATTTCTTCTCACCCAGCCTGGATGGTGTATGGGACAGGAAGTGTCT 3058
Qy 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuI 1050
Db 3059 TGGCCTTGGTGTCCCTGGGAGAGCACCCCGAGCTCGGGAAGAGCTGTGCTGCCCTCTCA 3118
Qy 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
Db 3119 TCATCCACAGCGCCGCCACACCATGTGCTGCCCAAGAGCAGCAGCGGCTGGGGCG 3178
Qy 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGGCCCTGGGCCCTGGCTCGGCCCGCACAGCAGCAGCGGGTCCGCAGAGCTGGGGCGG 3238
Qy 1090 laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA 1110
Db 3239 CC---CAGAGATGAAGTACCGCCAGCGCCGAGCTCTCCGCACAGCCCTGGAGCG 3295
Qy 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130
Db 3296 CTCGAAGCAGCTGGACACAGCGCGCTCCAGCGGAACAGCTCTCGGCCGTGACCCAGCC 3355
Qy 1130 euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluS 1150

Db 3356 TGAAGCGGAGAGCCCAAGTGGAGAGCGCGGTCCTGTTGTCGGGAGAGCGCCAGGAGA 3415
Qy 1150 erGlnAspGluGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3416 GCCAGGATGAAGAGGAGAGCTCAGAAGAGGAGGGCGGCGCCCTCGCGGCGAGTACCATC 3475
Qy 1170 xgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGTCCCTGGAGCGGAGGCCAAGATTCTTTGACCTGCCAGACACACTGC 3535
Qy 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
Db 3536 AGGTGCCAGGGCTGCATCGCACGTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCGACT 3595
Qy 1210 ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
Db 3596 GCAATGGCAAGTCCGGCTTCAGGGCGCTGCGCGGCCCTGCGGCCCTGATGACCCGCCAC 3655
Qy 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT 1250
Db 3656 TGGATGGGGATGACCCCGATGACGAGGGGCAACCTTGAGCAAGGGGAACGGGTCCGCGGT 3715
Qy 1250 rpValArgSerArgLeuProAlaCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
Db 3716 GGATCCGAGCCGACTCCCTGCTGCTCGCTCGAGCGAGACTCCTGTGTCAGCTACATCT 3775
Qy 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
Db 3776 TCCCTCTCTCAGTCAGGTTCGCGCTCTGTGTACCCGGATCATCACCACAAAGATGTTCG 3835
Qy 1290 spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
Db 3836 ACCACGTGTCCTTGTCTCATCTCTTCTTAACATCACCATCGCCATGAGCGGCCCA 3895
Qy 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330
Db 3896 AAATTGACCCCAACAGCGCTGAACGCATCTCTCTGAGCCCTCCAAATACATCTTCACCG 3955
Qy 1330 laValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluG 1350
Db 3956 CAGTCTTCTGCTGGAATGACAGTGAAGTGGTGGCACCTGGGCTGGTGTCTCGGGAGC 4015
Qy 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
Db 4016 AGGCGTACCTCGCGAGCAGTTGGAACTGTCTGGACGGGCTGTGTGTCTCATCTCCGTC 4075
Qy 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
Db 4076 TCGACATTTCTGCTCCATGCTCTGACAGCGGCACCAAGATCCTGGGCAATGCTGAGGG 4135
Qy 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
Db 4136 TGCTGCGGCTGCTCGGACCTTCCGCGCTGAGGTGATCAGCGGGCGGAGGGGCTGA 4195
Qy 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
Db 4196 AGCTGGTGGTGGAGCGCTGATGTCCTCCTCACTGAAACCCATCGGCAACATTTGTAGTCACT 4255
Qy 1430 ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
Db 4256 GCTGTGCTTCTTCTCATCATTTTTCGGCATCTTTGGGGGTGCGACTCTTCAAAAGGAAGTTT 4315
Qy 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
Db 4316 TCGGTGTCAGGGCGGAGGATACAGGAACATCACCATAAATTCGAGACTGTGCCGAGGCCA 4375
Qy 1470 erTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
Db 4376 GTTACCGTGGTCCGGCACAAAGTACAACTTTGACAACTTTGGCCAGGCCCTGTATGCC 4435
Qy 1490 euPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaV 1510

Db 4436 TGTTGTTTTGGCCCTCCAAAGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTG 4495
Qy 1510 alGlyValAspGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIleS 1530
Db 4496 TGGCGTGGACAGCCCATCATGAACCAACCCCTGGATGCTGCTACTTCACT 4555
Qy 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
Db 4556 CGTTCTCTGCTCATTTGTCGCTCTTTCTCTGAAACATGTTTGTGGGTGTGGTGGAGA 4615
Qy 1550 snPheHisLeuLeuGlnHisGlnGluGluGluAlaAArgArgArgGluGluysA 1570
Db 4616 ACTTCCACAAGTGTGGCAGCACCAGAGGAAGAGGAGGCCCGCGCGGAGAGAAGC 4675
Qy 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 4676 GCCTACGAAGACTGGAGAAAAGAGAAGGAATCTAATGCTGGACGATGTAATTGCTTCCG 4735
Qy 1580 --SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
Db 4736 CGAGCTCAGCCAGCGCTGCGTGCAGAGCCAGTGCACAAACCTTACTACTCCGACTACTCCC 4795
Qy 1599 rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG 1619
Db 4796 GCTTCCGGCTCTCGTCCACCACTTGTGCACCAAGCCACTACCTGGACCTTCTTCATCACAG 4855
Qy 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnProGlnIleL 1639
Db 4856 GTGTCATCGGCTGNAACGTGGTCAACCATGGCCATGGAGCACTACCAGACAGCCCGAGATTTC 4915
Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
Db 4916 TGGATGAGGCTCTGAAGATCTGAACATCTCAACTACATCTTCACTGTCATCTTTGTCTGGAGTCAG 4975
Qy 1659 alPheLysLeuValAlaPheAlaPheArgPheGlnAspArgTyrAsnGlnIleuA 1679
Db 4976 TTTTCAAACTTGTGGCCCTTTGGTTTCGTCGGTTCTTTCCAGGACAGTGAACAGCTGG 5035
Qy 1679 spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
Db 5036 ACCTGGCCATTTGCTGCTGCTCCATCATGGGCATCAGCTGGAGGAATCGAGGTCAACG 5095
Qy 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
Db 5096 CCTCGCTGCCCATCAACCCACCATCATCCGCATCATGAGGTGCTCGCGATTGCCCGAG 5155
Qy 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
Db 5156 TGTGAAGCTGCTGAAGATGGCTGTGGGCATGGCGGCGCTGCTGGACACGGTGAATGCAGG 5215
Qy 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA 1759
Db 5216 CCTGCCCCAGTGGGGAACTGGGACTTCTCTCATGTTGTTGTTTTCATCTTTGTCAG 5275
Qy 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db 5276 CTCTGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCC 5335
Qy 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
Db 5336 TGGGCCGTATGCCACCTTTTCGGAACCTTTGGCATGGCCCTTCTTAACCCCTTTCGAGTCT 5395
Qy 1799 erThrGlyAspAsnTyrAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
Db 5396 CCACAGTGAACATTTGAATGGCAATTATGAAGNACCCCTCCGGACTGTGACCAGAGT 5455
Qy 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5456 CCACCTGTCAACACAGGTCTATCTCGCTATCTACTTTGTGTCCTTGTGTCGTCAGCGGCC 5515
Qy 1839 lnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
Db 5516 AGTTGCTGCTAGTCAACGTGGTGTATCGCCGTGCTGATGAAGCACCTGGAGAGAGCAACA 5575

Qy 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuS 1879
Db 5576 AGAGGCGCAAGAGGAGGCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTCA 5635
Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyValA 1899
Db 5636 GCGCCACAGCCCACTCGCCACTGGGCAAGCCCTTCTCTGGCTGGGGTTCAGGGGCCCCG 5695
Qy 1899 snSerThrAspSerProLysProGlyValaProHisThrThrAlaHisIleGlyAlaAlaS 1919
Db 5696 ACAGCCCCAGACAGCCCAAGCCCTGGGGCTCTGCACCCAGCGGCCCCACCGAGATCAGCCT 5755
Qy 1919 erGlyPheSerLeuGluHisProThr----- 1927
Db 5756 CCCACTTTTCCCTGGAGACCCCCACCGACAGGCGAGCTGTTGACACCATATCCCTCTGTGA 5815
Qy 1927 ----- 1927
Db 5816 TCCAGGCTCCTCTGGAGTGGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCGAGGGGCC 5875
Qy 1927 ----- 1927
Db 5876 AGCCCTCTGCTTCCCTTCTGCCCCAGCCCTGGAGGCTCCGACCCACAGATCCCTCTAG 5935
Qy 1927 ----- 1927
Db 5936 CTGAGATGGAGGCTCTGCTCTGACGTCAGAGATTGTGCTGAACCCGCTCTGCTCTAG 5995
Qy 1927 ----- 1927
Db 5996 CTCTGACGGATGACTCTTTTGCCTGATGACATGCACACACTCTTACTTAGTGCCTGGAGA 6055
Qy 1928 -----MetValProHisProGluValProValProLeuGlyProAspLeuLeuThrV 1946
Db 6056 GCAATATGACAGCCCAACCCACCGAGCTGCCA-----GGACACAGACTTACTGACTG 6106
Qy 1946 alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
Db 6107 TGGGAAGTCTGGGGTCAGCCGAACGCACCTCTGCCCCATGACAGCTACATGTGTGCGC 6166
Qy 1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnS 1986
Db 6167 ATGGGACACTGCGAGGGGCCCCCTGGGACACAGGGCTGGGGCTCCCCAAAGCTCAGT 6226
Qy 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeup 2006
Db 6227 CAGGCTCCGCTTGTTCGTTTCACTCCCGACGACAGATACAGCTACATCTCTGAGCTTC 6286
Qy 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTyrGlyAlaIleProL 2026
Db 6287 CCAAGATGCACCTCATCTGCTCCAGCCCCACAGCGCCCCCAACCTGGGGCACCATCCCCA 6346
Qy 2026 ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046
Db 6347 AACTGCCCCCACCAGGACGCTCCCTTTTGGCTCAGAGGCCACTCAGGCGCCAGGACGAA 6406
Qy 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV 2066
Db 6407 TAAGGACTGACTCTTGGAGCTTCAGGCTTGGGACCCGGGAAGACCTCTGTCAGCAGG 6466
Qy 2066 alSerGlyProSerCysProLeuThrArgSerSerPheTyrPheGlySerIleG 2086
Db 6467 TGAGTGGGCCCTCCCCGCCCTTGGCCGGGCTTACTCTTTCTGGGGCCAGTCAAGTACCC 6526
Qy 2086 lnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaP 2106
Db 6527 AGGCACAGCAGCACTCCCGCAGGCCACAGCAAGATCTCCAAGCACATGACCCCGCAGCCC 6586
Qy 2106 roCysProGlyLeuGluProSerTyrAlaLysAspProProGluThrArgSerSerLeuG 2126
Db 6587 CTTGCCCCAGGCCCAACCACTGGGGCAAGGGCCCTTCCAGAGACCAGAAGCAGCTTAG 6646


```
Qy 2126 luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu- --ProSerSerGlnGluG 2145
Db 6647 AGTTGGACACGGAGCTGAGCTGGATTTTCAGGAGACCTCTCTCCCTCGGGCCAGGAGG 6706
Qy 2145 luProLeuPheProArgAspLeuLysCysTyrSerValGluThrGlnSerCysArgA 2165
Db 6707 AGCCCCCATCCACCGGACCTGAAGAAGTCTACAGCGTGGAGGCCAGAGCTGCCAGC 6766
Qy 2165 rgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuA 2185
Db 6767 GCCGGCTTACCTCCCTGGCTGGATGAGCAGAGAGAGACACTCTATCCCGCTCAGCTGCCTGG 6826
Qy 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG 2205
Db 6827 ACAGCGGCTCCCAACCCACCTGGGCACAGACCCTCTAACCTTGGGGGCCAGGCTCTTG 6886
Qy 2205 lyGlyProGlySerArgProLysLysLeuSerProProSerIleSerIleAspProp 2225
Db 6887 GGGGCTGGGAGCGCGGCCAAGAAAAAACAACCTACGCCCTAGTATCACCATAGACCCCC 6946
Qy 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaP 2245
Db 6947 CCGAGAGCAAGGTCTCCGACCCCGCCAGCCCTGGTATCTGCTCCGGAGGAGGCTC 7006
Qy 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265
Db 7007 GGTCCAGCGACTCCAGAGATCCCTTTGGCTCTGGCCCCCTGACAGCATGCTGCTCGC 7066
Qy 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetA 2285
Db 7067 CTTCCCAAGAAAGATGCTGAGTCTCTCCGGTTTATCTCTCTGACCCAGCAGCCTGG 7126
Qy 2285 spPro 2286
Db 7127 ACCCC 7131
```

RESULT 8

```
US-10-062-674-2011
; Sequence 2011, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2011
; LENGTH: 8116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 404183.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (8116)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-2011
```

Alignment Scores:

Pred. No.:	0	Length:	8116
Score:	10707.00	Matches:	2098
Percent Similarity:	89.9%	Conservative:	52
Best Local Similarity:	87.7%	Mismatches:	130
Query Match:	89.0%	Indels:	112
DB:	7	Gaps:	6

US-09-611-257A-24 (1-2287) x US-10-062-674-2011 (1-8116)

```
Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 321 CCGCCGGGGCCCCCGGTTTGGGTGAGGACACCTCTCTCTGAGGGGGCGGCTTGGCCCTCT 380
Qy 23 SerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAla 42
Db 381 CCGGATCGCCCGGGCCCCCGCTGGCCAGAGGATGGACGAGGAGGAGATGAGAGCGGCG 440
Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
Db 441 CCGAGGAGTCCGGACACCCCGGAGCTTCATGGGGCTCAACGACCTCTCGGGGGCCGGGG 500
Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82
Db 501 GCCGGCCGGGGCCGGGGTCCAGCAGAAAAAGACCCGGGCGAGCGGACTCCGAGGCGGAG 560
Qy 82 lyLeuProTrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
Db 561 GGCTGCCGTACCCCGCGCTGGCCCGGTGGTTTTCTTCTACTTGAGCGACGACAGCCGCC 620
Qy 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
Db 621 CGCGAGCTGGTGTCTCCGACCGGTCTGTAAACCCCTGGTTTGAGCGCATCAGCATGTGG 680
Qy 122 alIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
Db 681 TCATCTTCTCAACTGCTGACCTGGGCATGTTCCGGCCATGCGAGGACATCGCTGTG 740
Qy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaV 162
Db 741 ACTCCAGCGCTGCCGATCTCTGCAGGCTTTGTATGACTTTCATCTTTGCCCTCTTTGCCG 800
Qy 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA 182
Db 801 TGGAGTGGTGGTGAAGATGGTGGCCCTTGGGCATCTTTGGAAAAAGTTTACTCTGGAG 860
Qy 182 spThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuA 202
Db 861 ACCTTGGAAACCGGCTTGACTTTTTTCATCGTCAATCGCAGGAGATGCTGGAGTACTCGCTGG 920
Qy 202 spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
Db 921 ACCTGCGAAGCGTCAGCTTCTCAGCTGTTCAGGACAGTCCGTGTCTGCGACCGCTCAGGG 980
Qy 222 laIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM 242
Db 981 CCATTAAACCGGGTCCCGAGCATGCGCATCTTGTCACGTTGTCGCTGCTGGATAGCTGCCCA 1040
Qy 242 etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyV 262
Db 1041 TGCTGGGCAACGTCCTGCTGCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1100
Qy 262 alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP 282
Db 1101 TCCAGCTGTGGGCGAGGCTGCTTCGGAACCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1160
Qy 282 roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI 302
Db 1161 CCTGAGCGTGGACTGGAGCGCTATTACACAGACAGAAACAGAGATGAGAGCCCTTCA 1220
Qy 302 leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG 322
Db 1221 TCTGCTCCCGACCGCAGAAACGGCATGCGGTCTCTGAGAAGCGGTGCGCCACGCTGCGCG 1280
Qy 322 lyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerA 342
Db 1281 GGGACGGGGGGGGTGGCCACCTTGGCTCTGGACTATGAGCGCTTACAAACAGCTCCAGCA 1340
Qy 342 snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP 362
Db 1341 ACACCACCTGTGTCACTGGAAACCACTACTACCACTGTCTACGCGGGGAGCACAACC 1400
Qy 362 roPheLysGlyAlaIleAsnPheAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV 382
```

Db 1401 CCTTCAAGGGCGCCATCAACTTTGACAACTATGGCTATGCTGATCGCCATCTTCCAGG 1460
Qy 382 alileThrLeuGluGlyTyrValAspileMetTyrPheValMetAspAlaHisSerPheT 402
Db 1461 TCATCAGCTGGAGGGCTGGGTGCACATCATGTACTTTGTGATGGATGCTCATTTCTTCT 1520
Qy 402 YrAsnPheileTyrPheileLeuLeuilelleValGlySerPhePheMetileAsnLeuC 422
Db 1521 ACRAATTTCACTACTCTCATCTCTCATCTCATCTGTTGGCTCTCTTCTTATGATCAACCTGT 1580
Qy 422 YsLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA 442
Db 1581 GCCTGGTGGTATTCGCCAGCTTCTCAGAGACCAAGCAGCGGAAAGCAGCTGATGC 1640
Qy 442 rGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG 462
Db 1641 GGGAGCAGCTGTGCGGTCTCTGTCTCAACGCCAGCACCTTGGCTAGCTTCTTCTGAGCCCG 1700
Qy 462 YsSerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgGlyAlaAlaArgA 482
Db 1701 GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGTGTGTATCATCTTCTGTAAGCAGCCCGCA 1760
Qy 482 rGluAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA 502
Db 1761 GGCTGGCTCAGGTCTCTCGGCGCAGCAGGTGTGCGGGTGGGCTGCTCAGCAGCCAGCAC 1820
Qy 502 laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS 522
Db 1821 CCCTCGGGGGCCAGGAGCCAGCCAGCCAGCAGCTGCTCTCGCTCCACCGCCGCTAT 1880
Qy 522 erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis 542
Db 1881 CCGTCCACCACTTGGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTA 1940
Qy 542 lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA 562
Db 1941 GGACGCTCAGGGCCCCCGGCGCAGCCGCGAGATCCAGGACAGGATGCCAATGGGTCCC 2000
Qy 562 rArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProArgGlyA 582
Db 2001 GCGGGCTCATGCTGCCACACCTTCGACGCTGCGCTCTCGGGGGCCCCCTGGTGGCG 2060
Qy 582 laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA 602
Db 2061 CAGAGTCTGTGCAGCTTCTACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGG 2120
Qy 602 laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT 622
Db 2121 CGCCCCCTCCAGGTCCCTCATCTGAGGCATCCGGCAGGACTGTGGGCGAGCGGAAGGTGT 2180
Qy 622 YrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV 642
Db 2181 ATCCCAACCGTGACACACAGCCCTCCACGGAGACGCTGAAGGAGAACGCACTAGTAGAGG 2240
Qy 642 alaLaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS 662
Db 2241 TGGCTGCCAGCTCTGGGCCCCCAACCTCCACCAGCTCAACATCCACCCCGGGCCCTACA 2300
Qy 662 erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisHisSerSerCysLysI 682
Db 2301 GCTCCATGCACAAGTCTGTGAGACACAGACTACAGGTGCTGCAAAAGCTCTTTGCAAGA 2360
Qy 682 leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC 702
Db 2361 TCTCAGCCCTTGTGTAAGACACAGACTGAGGCTGTGGTCCAGACAGCTGCCCCCTACT 2420
Qy 702 YsAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps 722
Db 2421 GTGCCCGGGCGGGCAGGGAGGTGGAGCTCGCCGACCGTGAATGCCTGACTCAGACA 2480
Qy 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS 742

Db 2481 GCGAGGCGAGTTTATGATTTACACAGGATCCCGCAGCACAGCAACTTTCGGGAAACCCCAAA 2540
Qy 742 exArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db 2541 AGCGGG--GGGCAACGGAGCTGGGCCAGATGCAGAGCCAGCTCTGTGCTGCGCTTCT 2598
Qy 762 rPArgLeuileCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db 2599 GGAGGCTAATCTGTGACACCTTCGMAAAGATGTGGAGCAGCAAGTACTTTGGCCGGGAA 2658
Qy 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
Db 2659 TCATGATCGCCATCTCTGGTCAACACACTCAGCATGGGCATCGAATACACAGAGCAGCCCG 2718
Qy 802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
Db 2719 AGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTCCACAGGCTCTTTGCCCTGG 2778
Qy 822 luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
Db 2779 AGATGCTGCTGAAGCTGCTTGTGTATGGTCCCTTTGGCTACATCAAGAATTTCTTACAACA 2838
Qy 842 lePheAspGlyValIleValIleValIleSerValTrpGluIleValGlyGlnGlnGlyG 862
Db 2839 TCTTCGATGGTGTCTTGTGGTTCATCAGCGTGTGGGAGATCGTGGGCCAGCAGGGGGCG 2898
Qy 862 lyLeuSerValLeuArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
Db 2899 GCCTGTGGTGTCTGGGACCTTCCGGCTGATGGGTGCTGAGAGCTGGTGGCTTCTTCCG 2958
Qy 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db 2959 CGGCGCTGCAGCGCAGCTGGTGTGTCTCATGAAGACCATGGACAACGTCGCCACCTTCT 3018
Qy 902 YsMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db 3019 GCATGTGCTATGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3078
Qy 922 YsLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
Db 3079 GCAAGTTTGGCTCTGAGCGGGATGGGACACCTTCCAGACCCGGAAGAAATTTTACCTCT 3138
Qy 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 962
Db 3139 TGCTCTGGGCGCATCGTCACTGTCTTTTTCAGATCTCTTCCAGAGGAGCTTGGAAACAAGTCC 3198
Qy 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaLeuLeuTyrPheIleAlaLeuMetT 982
Db 3199 TCTACAATGGTATGGGCTCCACGTCGTCTTGGGCGGCCCTTTATTTTCTTCTTCTTCTTCT 3258
Qy 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db 3259 CTTTCGGCAACTAGTGTCTTCTTCAATTTGCTGGTCCGCTTCTTGGTGGAGGGCTTCCAGG 3318
Qy 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
Db 3319 CGGAGGGAGATGCCAACAGTCCGAAATCAGAGCCGATTTCTTCTTCTTCTTCTTCTTCTTCT 3378
Qy 1022 lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
Db 3379 GTATGGGACAGAAAGTGTGTGGCTTGGCTTGGTGTCTTGGGAGAGACCCCGAGGTGC 3438
Qy 1042 rGlySerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL 1062
Db 3439 GGAAGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3498
Qy 1062 YsSerSerThrThrGlyValGlyAlaLeuGlySerGlySerArgArgThrSerSerS 1082
Db 3499 AGAGCACCAAGCGGCTGGGCGAGCGCTGGGCCCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 3558
Qy 1082 erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102
Db 3559 GCGGGTGGCAGAGCTTGGGGCGGCC---CACGAGATGAAGTCAACCCCGCAGCCCGCGCA 3615

Qy 1102 erSerProHisSerProTrpSerAlaIaSerSerTrpThrSerArgArgSerSerArgA 1122
Db 3616 GCTCTCCGCACAGCCCTGGAGCGCTCAAGACGCTGGACCGAGCGCTCCAGCCGGA 3675
Qy 1122 enSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL 1142
Db 3676 ACAGCCTCGGCGGTGCACCCAGCCTGAAGCGGAGAGGCCAAGTGGAGAGCGGCTCCC 3735
Qy 1142 euSerSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAspArgA 1162
Db 3736 TGTGTTCGGGAGAAAGCCAGGAGCCAGGATGAAGAGGAGAGCTCAAGAGAGAGCGGG 3795
Qy 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerS 1182
Db 3796 CCAGCCTTCGGGCGAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGAGGCCAAGAGTT 3855
Qy 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202
Db 3856 CTTTGTGACCTGCCAGACACATCGAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAG 3915
Qy 1202 erSerAlaSerGluHisGlnAspCysAenGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
Db 3916 GGTCTGCTTCTGAGCACCGAGACTGCAATGCAAGTCGGCTTCAGGGCGCTGCCCGGG 3975
Qy 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuS 1242
Db 3976 CCCTGCGGCCCTGATGACCCCCCATCTGGATGGGATGACCGCGATGACGAGGGCAACCTGA 4035
Qy 1242 erLysGlyGluArgGlnAlaTrpValArgSerArgLeuProAlaCysCysArgGluA 1262
Db 4036 CCAAGGGGAACGGGTCCGCGGTGGATCCAGGCCGACTCCCTGCTGCTCGCCTCGAGC 4095
Qy 1262 rgAspSerTrpSerAlaTrpIlePheProProGlnSerArgPheArgLeuLeuCysHisA 1282
Db 4096 GAGACTCTGCTGAGCCTACATCTTCCCTCCTCAGTCCAGGTTCGGCTCCGCTCTGTGTACC 4155
Qy 1282 rgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI 1302
Db 4156 GGATCATCACCACACAAAGATGTCGACACCGTGGTCTTGTTCATCATCTTCTTAACGTGA 4215
Qy 1302 leThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuT 1322
Db 4216 TCACCATCGCCATGGAGCGCCCAAAATGACCCCAAGCGCTGAACGCATCTTCTCTGA 4275
Qy 1322 hrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLysValValA 1342
Db 4276 CCCTCTCCAATTACATCTTACCGCAGTCTTCTGGCTGAAATGACAGTGAAGGTGGTGG 4335
Qy 1342 laLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuArgSerSerTrpAsnValLeuAspG 1362
Db 4336 CACTGGGCTGGTCTTCGGGAGCAGGCGTACCTCGGAGCAGATTGGAACTGCTGGAGC 4395
Qy 1362 lyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyT 1382
Db 4396 GGCCTGTGGTCTCATCTCCGTTCATCGACATCTCTGGTTCATGCTCTTCGACAGCGCA 4455
Qy 1382 hrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgV 1402
Db 4456 CCAAGATCTTGGGCATGTGAGGGTGTCTGGGCTCTCGGACCTCGGACCTGCGCGCTCAGGG 4515
Qy 1402 alIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysP 1422
Db 4516 TGATCAGCCGGCGCAGGGGCTGAAGCTGGTGGTGAGACGCTGAATGCTCTCACTGAAAC 4575
Qy 1422 roIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyV 1442
Db 4576 CCATCGGCAACATTGATGATCATCTGCTGCGCTTCTTCATCATTTTCGGCATCTTGGGG 4635
Qy 1442 alGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrA 1462
Db 4636 TGCAGCTCTTCAAGGGAAGTTTTTCTGTGTGTCAGGGCGAGGATACCAAGAACATCACCA 4695

Qy 1462 snLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspA 1482
Db 4696 ATAAATCGGACTGTGCCAGGCCAGTTACCGTGGGTCCGGCACAAGTACAACTTTGACA 4755
Qy 1482 snLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspI 1502
Db 4756 ACCTTGGCCAGGCGCTCATGTCTGTTTGGCTTCCAGGATGGTTGGGTGGACA 4815
Qy 1502 leMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnP 1522
Db 4816 TCATGTACGATGGCTGCATGCTGTGGCGTGGACAGCAGCCCATCATGAACCAACACC 4875
Qy 1522 roTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnM 1542
Db 4876 CTTGATGTCTGCTACTTCTCATCTGTTCTGCTCATTTGTGGCCTTCTTTGCTCTGAACA 4935
Qy 1542 etPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG 1562
Db 4936 TGTTGTGGGTGTGGTGGAGAACTTCCACAAAGTGTCCGACGACACCCAGGAGGAAGAG 4995
Qy 1562 luAlaArgArgArgGlu-GluLysArgLeuArgArgLeuGluLysLysArgArgSerLys 1581
Db 4996 AGGCCCGCGCGGAGCCAGAGCGCTACGAAGACTGGCGAAAAGAGACGACGCTAG 5055
Qy 1582 GluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArg 1601
Db 5056 GAGAGCAGATGGCTGAAGCCCATGTCANACCTTACTACTCCGACTACTCCCGCTTCGG 5115
Qy 1602 LeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIle 1621
Db 5116 CTCTCTGCCACCACTTGTGCACCAGCCACTTACCTGGACCTTCTTCATCACAGGTGTCTATC 5175
Qy 1622 GlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGlu 1641
Db 5176 GGGCTGAACGGTGCACCATGGCCATGGAGCATTACAGAGACCCCGAATCTCGATGAG 5235
Qy 1642 AlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLys 1661
Db 5236 GCTCTGAAGATCTGCACTACATCTTCATCTCATCTTGTCTTGGAGTCAGTTTTCAAA 5295
Qy 1662 LeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAla 1681
Db 5296 CTTCTGGCCTTGGTTCCTGGTGGTTCCTTCAGGACAGGTGGAAACCACTGGACCTGGCC 5355
Qy 1682 IleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeu 1701
Db 5356 ATTGTGCTGCTGCATCATCGGCATCAGCTGGAGAAATCGAGGTCAACGCCCTCGCTG 5415
Qy 1702 ProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLys 1721
Db 5416 CCCATCAACCCCACTATCCGCATCATGAGGGTGTCTGCATTTGCCGAGTGTCTGAAG 5475
Qy 1722 LeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuPro 1741
Db 5476 CTGTGTAAGATGGCTGTGGGATCGGGCGCTGTCTGGACACGGTGTATCGAGCCCTGGCC 5535
Qy 1742 GlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGly 1761
Db 5536 CAGGTGGGAACCTTGGGACTTCTCTTCAITGTGTGTGTTCATCTTTCAGCTCTGGGC 5595
Qy 1762 ValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg 1781
Db 5596 GTGGAGCTCTTGGAGACCTGAGTGTGCAGAGACACACCCCTGTGTGGGCGCTGGCCGT 5655
Qy 1782 HisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGly 1801
Db 5656 CATGCCACTTTCGGAACCTTGGCATGGCTTCTTAACTTCTTCCAGCTCTCCACAGGT 5715
Qy 1802 AspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--AspGlnGluSerThr 1820
Db 5716 GACAAATGGAAATGGCATTTATGAGGACACCTCCGGGACTGCACCCACGACGAGCGCAGC 5775
Qy 1821 CysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheValLeuThrAla 1838

Score: 6242.00 Matches: 1387
Percent Similarity: 65.0% Conservative: 208
Best Local Similarity: 56.5% Mismatches: 536
Query Match: 51.9% Indels: 325
DB: 10 Gaps: 64

US-09-611-257A-24 (1-2287) x US-10-483-467-3 (1-7898)

Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaAraProSer 22
Db 188 CCGGGGCGATCCCGCGGGAGACCGCGCGGCGAGAGCGAGGTGTGC-CGGCGC--- 243
Qy 23 SerAspProProGlyProArgLeuAlaArgGly-----Trrp 34
Db 244 -----CCACCATGACCGAGG---GCGACGCGGCGCGGACGAGTTCGGGTGCCCTCTGG 294
Qy 35 ThrArgArg-----ArgMetGluArgAlaProArgSer 45
Db 295 GCGCGCGCGCCCTGGCGCTGCGCGGTGGTGGGGCGTCCCGGAGAGCCCCGGGGCGC 354
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 355 CGGGACGCGGCGGAGCGGGGGTCCGAGCTCGCGGTGTACACCTCCCGAGAGCGCG-CGC 413
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 414 GCC-----GAGCGCGCGGAGCTGGGTGCCGAGGAGAGCGCGCTCCCGTAC 464
Qy 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrrp 105
Db 465 CCGGCTTGGCGGCCACCGGTCTTCTTCGCTCGTCCGTCAGACCCAGCGCGCGCGAGCTGG 524
Qy 106 CysLeuArgThrValCysAsnProTrrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 525 TGCCTCCGGCTGGTCTGCAACCCATGGTTCGAGCACGTGACATGCTGGTAAATCATGCTC 584
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 585 AACTTCGTGACCCCTGGGGATGTTTCGGCCCTGTGAGGACGTGTAGTGGCGTCCGAGCGC 644
Qy 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaValGluMetVal 165
Db 645 TGCAACATCTCGGAGCCCTTTGACGCTTACCTTTTCGCTTTTTCGCTGGAGATGGTC 704
Qy 166 ValIysMetValAlaLeuGlyIlePhePheClyIysIysCysTyrLeuGlyAspThrTrpAsn 185
Db 705 ATCAAGATGGTGGCTTGGGCTGTTCGGGCGAGAAGTGTACCTGGGTGACACGTGGAAC 764
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 765 AGGCTGGATTCTTCATCGTCTGGCGGCGCATGATGGAGTACTCGTTGGACGGACACAC 824
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 825 GTGAGCTCTCGGCTATCAGGACCGTGGGGTGTTCGGGCGAGAGTGTACCTGGGTGACAC 884
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 885 GTGCTTAGCATGCGGATCTGGTCACTCTGCTGTGGATACGCTGCCCATGCTCGGGAAAC 944
Qy 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrrp 265
Db 945 GTCTCTTCGTGCTGCTTCCTTCCTTCATTTTCGGCATCGTTGGGTCCAGCTCTGG 1004
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 1005 GCTGCTCTCTCGGAAACCGCTGCTTCCTGGACAGTGCCTTTGTGAGAAACAACACCTG 1064
Qy 286 Asp---LeuGluProTrrpTrrpGlnAsnGluAspGluSerProPheIleCysSer 304
Db 1065 ACCTTCTTCGGCGCGTACTACAGACGGAGGCGGAGGAGAACCCGTTTCATCTGCTCC 1124
Qy 305 GlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 324

Db 1125 TCACGCGGACACAAACGCGATGTCAGAACTGCTGCACATCCCC-----GGCGCGCGC 1175
Qy 325 GlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsn----- 338
Db 1176 GAGCTGGCGCATGCCCTGCACCCCTGGGCTGGAGGCGCTACACGACGCGCGAGCGGAGGG 1235
Qy 339 ---SerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1236 GTGGCGCTGCACGCAACGCGCTGCATCACTTGGAAACAGTACTACAACAGTGTGCGGCTCG 1295
Qy 358 GlyGluHisAsnProPheLysGlyValAlaIleAsnPheAspAsnIleGlyTyrAlaTrrpIle 377
Db 1296 GGTGACTCCAAACCCCAACGCGTGCATCACTTCGACAAACATCGGTACGCGCTGGATT 1355
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrrpValAspIleMetTyrPheValMetAsp 397
Db 1356 GCCATCTTCAGGTGATCAGCTGGAAGGCTGGGTGGACATCATGTACTACGTTCATGGAC 1415
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1416 GCCCACCATCTTACAACTTCATCTATTTCATCTGCTCATCATCTGGGGCTCTTCTTTC 1475
Qy 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1476 ATGATCAACCTGTGCTGGTGGTATGCCACGCGAGTTCGAGAGACGAGCAGCGGGAG 1535
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1536 AGTCAGCTGATGCGGGAGCAGCGGCGCACCGCACCTGTGCCAACGACGACGCTGGCGAGC 1595
Qy 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTrrpIleLeuArg 477
Db 1596 TTCTCCGAGCTGGCAGCTGCTACGAAGAGCTGCTGAAGTACGTGGGGCCACATATTCCGC 1655
Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1656 AAGGTCAAGCGCGCGCAGCTTTCGCGCTCTAGCGCGCTGGCAGAGCGCTGGCGCAAGAAG 1715
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1716 GTGACCCCATGTGTGTGCAAGCGCAGGCTCC-----GGG 1751
Qy 518 HisArgArg-----LeuSerValHisHisLeuVal---HisHis 529
Db 1752 CACCGCCAGCGCGCGGCGAGCGACACACGCTCGGTGGTGACACCTGGTCTACCCACAC 1811
Qy 530 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAla 549
Db 1812 CATCACCAACCAACCACTTACCACTTTCAGCCATGGCAGCCCGCGAGCGCGCGCGCC 1871
Qy 550 SerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu-----Pro 567
Db 1872 GAGCAGCGCGCTCGGAC-----ACCAGCTGGTCCGAGCTGGCGCGC 1913
Qy 568 ProProSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSer 587
Db 1914 CCCCCCTTCGCACCTTCCCGAGCGCGGAGCCCCC---GACGCGAGAGTGTGTGCACAGC 1970
Qy 588 PheTrrpHisAlaAspCysHisLeuGlu-----ProValArgCysGlnAlaProProPro 605
Db 1971 ATCTACCATGCGGACTGCCACATAGAGGGGCGCGAGAGAGGGCGCGCGGTGGCACATGCC 2030
Qy 606 ArgCysProSerGluAlaSerGlyArg---ThrValGlySerGlyLysVal---TrrpPro 623
Db 2031 GCAGCCACTGCGCTCGGCGGCGGCGGCAAGAGCAGCAGCAGCGCGGACCACTTACCC 2090
Qy 624 ThrVal-----HisThrSerProProProGluIle 633
Db 2091 ACATCTGCGCTCAGGGGTGGCGGCGGCAAGAGCAGCAGCAGCGCGGACCAAG--- 2147
Qy 634 LeuLysAspLysAlaLeuValGluValAlaProSerPro-----Gly 647

Qy 1320 PheLeuThrLeuSerAsnTyrIlePheThrAlaValaPheLeuAlaGluMetThrValiys 1339
Db 4227 TTCTCAGCGTCTCCAATTACATCTTCAGGCCATCTTCGGGGAGATATGTTGAAG 4286
Qy 1340 ValValAlaLeuGlyTyrCysPheGlyGlnAlaTyrLeuArgSerSerTyrAsnVal 1359
Db 4287 GTGGTGGCCCTGGGGCTGCTCTCCGGGAGCACGCCCTACCTGCAGAGCAGCTGGAACCTG 4346
Qy 1360 LeuAspGlyLeuValLeuValLeuSerValIleAspIleLeuValSerMetValSerAsp 1379
Db 4347 CTGGATGGCTGCTGGTGTCTGGTGTCTGGTGTGGACATTCGTGGCCATGGCCCTCGGCT 4406
Qy 1380 SerGlyThrIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPro 1399
Db 4407 GGTGGCCCAAGATCTGGGGTTCCTGGCGGTCTGGTCTGGTCTGGGACCTCGGGCT 4466
Qy 1400 LeuArgValIleSerArgAlaGlnGlyLeuIysLeuValValGluThrLeuMetSerSer 1419
Db 4467 CTAAGGGTCAACAGCGGGCCCGGGCTCAAGCTGGTGGTGGAGACGCTGATATCGTCG 4526
Qy 1420 LeuIysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIle 1439
Db 4527 CTCAGGCCATTTGGAAACATGCTCTCATCTGCTCGCCCTTCTTCATCATTTTTGGCATC 4586
Qy 1440 LeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsn 1459
Db 4587 TTGGGTGTCAGCTCTTCAAGGAAGTTCTACTCTGCGAGGGCCCGCACCCAGGAAC 4646
Qy 1460 IleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsn 1479
Db 4647 ATCTCCCAAGGCACAGTCGCGGGCCGCCACTACCGCTGGTGGCAGCAAGTACAAAC 4706
Qy 1480 PheAspLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrp 1499
Db 4707 TTCGACAACTTGGCCAGGCCCTGATGCTGCTGTCTGCTCATCAAGATATGGATGG 4766
Qy 1500 ValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsn 1519
Db 4767 GTGAACATCATGTACGACGGCTGGATGCCGTGGGTGTCGACGAGCCCTGTGCAGAAC 4826
Qy 1520 HisAsnProIleMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPheVal 1539
Db 4827 CACAACCCCTGGATGCTGCTACTTCACTCCCTTCTGCTCATCGTCAGCTTCTTCTGTG 4886
Qy 1540 LeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGlu 1559
Db 4887 CTCAACATGTTCTGGGGCTGCTGTCGAGAACTTCACAAAGTCCGGCAGCACACAGGAG 4946
Qy 1560 GluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysArgArg 1579
Db 4947 CGGAGGAGGCGCGGCGGAGAGAGAGAGCGGCTGCGGCCCTAGAGAGAGGCGCAGG 5006
Qy 1580 SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArg 1599
Db 5007 AGCATTTTCCCCAGC-CCAGAGGCCCGAGCGCGGCCCTACTATGCGCACTACTCGGCC 5063
Qy 1600 PheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThrGly 1619
Db 5064 ACGCGCGCTCCATTCATCTGCTGTGCACAGCACTATCTCGACCTTTCATCACCTTC 5123
Qy 1620 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu 1639
Db 5124 ATCATCTGTGTCACGTCATCACCATGTCCATGGAGCACTATAACCAACCCCAAGTCGCTG 5183
Qy 1640 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerVal 1659
Db 5184 GACGAGGCCCTCAAGTACTGCAACTACGCTTCCACCATCGTGTGTCTTCGAGGCTGCA 5243
Qy 1660 PheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTyrAsnGlnLeuAsp 1679
Db 5244 CTGAAGCTGGTAGCATTTGGGTTCGTCGTTCTTCAAGGACAGGTGGAACAGCTGGAC 5303
Qy 1680 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu 1699

Db 5304 CTGGCCATCTGCTGCTGCTCACTCATGGGCATCAGCTGGAGGAGATAGAGATGAGGCC 5363
Qy 1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719
Db 5364 GCGTGGCCCATCAACCCACCATCATCCGATCATGCGCGCTGCTTCGCATTTGCCGTGTG 5423
Qy 1720 LeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739
Db 5424 CTGAAGCTGCTGAAGATGGCTACGGGCATGCGGCCCTCTGTGGACATGTGGTGCAGCT 5483
Qy 1740 LeuProGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPhePheIlePheAlaAla 1759
Db 5484 CTCCTCCAGGTGGGGAACTTGGGCTTCTTTCATGCTCTGCTGTTTATCTATGCTGCG 5543
Qy 1760 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1779
Db 5544 CTGGAGTGGAGCTGTTTCGGAGGCTGGAGTGCAGTGAAGACAACCCCTTCGAGGGCCTG 5603
Qy 1780 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1799
Db 5604 AGCAGGCACGCCACCTTCAGCACTTCGGCATGGCCTTCTCAGCTGTTCCGGGTGTCC 5663
Qy 1800 ThrGlyAspAsnTyrAsnGlyIleMetLysAspProSerArgAspCys-Asp 1816
Db 5664 ACGGGGACAACTGGAACGGGATCATGAAGACACGCTGCGCGAGTGTCCCGTGAGGAC 5723
Qy 1817 GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu 1836
Db 5724 AAGCACTGCCTGAGTACCTGCGCGCCCTGTGCGCCGTACTTCTGACCTTCGTGCTG 5783
Qy 1837 ThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGlu 1856
Db 5784 GTGGCCAGTTCTGCTGTGTAACCTGTTGGTGGCCGTGCTCATGAAGACCTCGAGGAG 5843
Qy 1857 SerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLys 1876
Db 5844 AGCAACAAGGAGGACACGGGAGGATCGGAGCTGCAGCCGAGATCGAGTGGAGTGGCG 5903
Qy 1877 ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpGlyValGlu 1896
Db 5904 -----CAGGGCCCCGGG 5915
Qy 1897 GlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly 1916
Db 5916 AGTCACCGCGGTGGAGCGGCAGACAGCCT----- 5945
Qy 1917 AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValPro 1936
Db 5946 -----CCTTGTCCCGCAGAGAGTCCG 5966
Qy 1937 ValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer 1956
Db 5967 GCGGCCAGGATGCCCAACCTGTTGCAGCAGAGGTGTCGCTCGGCGCCCCACCCCGC 6026
Qy 1957 LeuProAsnAspSerTyrMetCysArgAsnGlySerThrAla----- 1970
Db 6027 CTGCCCAACGACACTACATGTTTTCAGGCCCTGTTGCTGCTGCTCGGCGCCCCACCCCGC 6086
Qy 1971 -----GluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGly 1987
Db 6087 CCGCTGCGAGGAGTGGAGATGGAGACCTATGGGCGCGCACCCCT-----TTGGGC 6137
Qy 1988 SerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuLeuLeuProLys 2007
Db 6138 TCCGTGCTGCTGTGCACCTCTCCGCGCGCAGAGTCTGTGCTGCTCCCTCCAGATCCCATG 6197
Qy 2008 AspValHis-----TyrLeuLeuGlnProHisGlyAla 2018
Db 6198 GCTGTGCTCCCGACGAGGCGGCGAGCCCTCCACGCGCTGTCCTCCCTCGGGGCACA 6257
Qy 2019 ProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2038


```
Db 6258 -----GCCCGCTCCCCAGTCTCAGCCGG 6281
Qy 2039 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2058
Db 6282 CTGCTCTGCAGACAGGAGCTGTGCACACCATTCCTTGGNAGGAAG---ATTGACAGC 6338
Qy 2059 ArgGluAspLeuLeuSerGluVal-----SerGlyProSerCysProLeuThr 2074
Db 6339 CCTAGGCACACCTCGATCTCTGCAGAGCCTGGTGAGAAAAACCCCGGTGAGCCCGTGCACC 6398
Qy 2075 ArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnAlaArgSerGlyIleGln 2094
Db 6399 CAG-----GGGGGCTCCCTGCAGTCCCCACACACCGCTCCCCACGCGCC 6440
Qy 2095 SerLysVal-----SerLysHis-----IleArgLeuProAlaPro 2106
Db 6441 GCCAGCTCCGCACTCTGATACATACCTTGGACAGCACTGCGTCTCAGCCGCGCGCG 6500
Qy 2107 CysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuGlu 2126
Db 6501 GCGCCAGCGGAGAGGCGCGAGCGCTCGGACCCA-----6536
Qy 2127 LeuAspThrGluLeuSerTrpIleSerGlyAspLeuPro-----SerSerGlnGluGlu 2145
Db 6537 GCCAGCAGGAGGTGACCCACATCACCAGCTCCCGCTCGCCCTGGCAGCCACACAGCGAG 6596
Qy 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyr 2156
Db 6597 CCQATGCGCCGGAAGCTCTCCGCTGGCGCGCGGAGCGGAGCTCGCAGAGCTCTAC 6656
Qy 2157 SerValGluThrGlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArg 2176
Db 6657 AGCGTGACGCTCAGGGCTCTCTGACAAAGCGGCG---CGGGCAGACGAGCAGTGGCGG 6713
Qy 2177 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerPro 2196
Db 6714 CCCTCGCGGAG-----CTGGCAGCGGGGAG-----CCTGGGGAG 6749
Qy 2197 SerSerLeuGlyGlnProLeuGlyGlyPro-----GlySerArgProLysLys 2214
Db 6750 GCGAAGCGCTGGGC---CCTGAGCGGAGCCCGCTCTGGGTGCGCGCAGAAAGAAAG 6806
Qy 2215 LeuSerProProSerIleSerIleAspProPro---GluSerGlnGlySer---ArgPro 2232
Db 6807 ATGAGCCCCCTGCATCTCGTGTGAACCCCTCTCGGAGGAGCGAGGCTCTGCGCGGCC 6866
Qy 2233 ProCysSerProGly-----ValCysLeuArgArgAlaProAla-----2246
Db 6867 TCCGCGCAGGCGCGGCGCAGCACCACACTGAGGCGCAGGACCCCGCTCTGTGAGGCCACG 6926
Qy 2247 -----SerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSer 2264
Db 6927 CCTCAGAGGACTCCTGAGGCCACACAGAGGCTCAGGCGCGGGGGGAGCCCTGCGAGCC 6986
Qy 2265 -----ProSerProLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6987 AAGGGGAGCGCTGGGCGCAGCGCTCTCGCGGCTGAGCAGCCTGACCGTCCCGACGCTT 7046
Qy 2278 SerSerAspProThrAspMet-----AspPro 2286
Db 7047 GCCTTTGAGCGCTGGACCTCGGGGTCCCGAGTGGAGACCT 7088
```

RESULT 10

```
US-10-930-301-51
; Sequence 51, Application US/10930301
; Publication No. US20050026207A1
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CAGNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/10/930.301
; CURRENT FILING DATE: 2004-08-30
```

```
; PRIOR APPLICATION NUMBER: US/09/398,522
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CAGNA1G - a gene encoding a T-type calcium channel
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (373)...(3993)
US-10-930-301-51
```

Alignment Scores:

```
Pred. No.: 0 Length: 3993
Score: 6103.00 Matches: 1173
Percent Similarity: 95.5% Conservative: 12
Best Local Similarity: 94.5% Mismatches: 52
Query Match: 50.7% Indels: 4
Gaps: 2
```

US-09-611-257A-24 (1-2287) x US-10-930-301-51 (1-3993)

```
Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 281 CCGCGCGGGCCCCCGGGTTCGTGTGAGGACACCTCTCTGAGGGCGCGCTTGCCTCT 340
Qy 23 SerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAla 42
Db 341 CCGGATCCCGCGGGCCCCCGCTGGCCAGAGGATGGACGAGGAGGAGGATGAGCGGCG 400
Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGly 62
Db 401 CCAGAGGAGTGGGACACGCCCGGAGCTTCATGCGGCTCAACGACCTGTGCGGGGCCGGG 460
Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlu 82
Db 461 GCCCGCGGGCGCGGGTTCAGAGAAAGAGCCCGGCGAGCGGAGTCCGAGCGCGAGG 520
Qy 82 LysLeuProTrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
Db 521 GGCTGCGGTACCGCGGCTGCGCGCTGGCTGCTTCTTCTACTTGTGAGCAGGACGCGCC 580
Qy 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
Db 581 CCGGAGCTGGTGTCTCCGACGCTGTAAACCCCTGGTTGAGCGCATCAGCATGTGG 640
Qy 122 alIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
Db 641 TCATCTTCTCACTGGTGCACCTTGGCATGTTCCGCGCATGCGAGGACATCGCTGTG 700
Qy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaV 162
Db 701 ACTCCAGCGCTGCGGATCTTCAGGCGCTTGTATGACTTTCATCTTGTGCTTCTTTCGCG 760
Qy 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA 182
Db 761 TGGAGATGGGTGAAGATGGTGGCCTTGGGCATCTTTGGGAAAAGTGTACTTGGGAG 820
Qy 182 spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA 202
Db 821 ACATTGGACCGGCTTGACTTTTTCATCGTCGCGGAGATCGTGAGTACTCGCTGG 880
Qy 202 spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
Db 881 ACCTGCAAAACGTGAGCTTCTCAGCTGTCAGGACAGTCCGCTGTGCTGCGACCGCTCAGG 940
Qy 222 laIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeuProM 242
Db 941 CCATTAAACCGGGTGCCCGAGCATGCGCATCTTGTGCTGTGCTGCTGATACGCTGCCA 1000
```

Qy	242	etLeuGlyAsnValLeuLeuLeuCysPheValPhePheIlePheGlyIleValGlyV	262
Db	1001	TGCTGGGCAACGTCCTGCTGCTCTTCTTGGTCTTCTTCATCTTCGGCATCGTCGGCG	1060
Qy	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPhSerLeuP	282
Db	1061	TCCAGCTGTGGCGAGGCGTCGTCGGAACCGATGCTTCTTCTACCTCGAGATTTCAGCCTCC	1120
Qy	282	roLeuSerValAspLeuGluProTyrTyrrGlnThrGluAsnGluAspGluSerProPheI	302
Db	1121	CCCTGAGCGTGGACCTGGAGCGCTATTACACAGACAGAGAAGAGATGAGAGCCCTTCA	1180
Qy	302	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
Db	1181	TCTGCTCCAGCCACGCGAGAACGGCATCGGTCTCGAGAACGGTCCCCACGCTGGCG	1240
Qy	322	lyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrrAsnSerSerSerA	342
Db	1241	GGGACGGGGCGGTGGCCCACTTGGCGGTCTGGAGCTATGAGGCCTACAACAGCTCCAGCA	1300
Qy	342	snThrThrCysValAsnTrpAsnGlnTyrTyrrThrAsnCysSerAlaGlyGluHisAsnP	362
Db	1301	ACACCACTGTGTCACTGGNACCGACTATACCAACTGCTCAGCGGGGAGCACAACC	1360
Qy	362	roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrrAlaTrpIleAlaIlePheGlnV	382
Db	1361	CCTTCAAGGGCGCCATCAACTTTGACAACATTGGCTATGCTGGATCGCCATCTTCCAGG	1420
Qy	382	alIleThrLeuGluGlyTrpValAspIleMetTyrrPheValMetAspAlaHisSerPheT	402
Db	1421	TCATCAGCTGTGAGGGCTGGGTGCACATCATGTACTTGTGTGATGATGTCTCATTTCT	1480
Qy	402	yrAsnPheIleTyrrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuC	422
Db	1481	ACAATTTCATCTACTTCACTCTCTCATCATCATCTGGGGCTCTCTTTCATGATCAACCTGT	1540
Qy	422	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
Db	1541	GCCTGGTGGTATTGCCACGCAGTCTTCAGAGACCAAGACGCGGGAAGCCAGCTGATGC	1600
Qy	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPhSerGluProG	462
Db	1601	GGGAGCAGCGTGTGGGTTCGTGTCCAACGCCACGACGCTGGCTGAGCTTCTCTGAGCGCG	1660
Qy	462	lySerCysTyrrGluGluLeuLeuLysTyrrLeuValTyrrIleLeuArgGlyAlaAlaArgA	482
Db	1661	GCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTATCTTCTGTAAGCAGCCCGCA	1720
Qy	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1721	GGCTGGCTCAGTCTCTCGGGCAGCAGGTGTGGGGTGGGTGCTCTCAGCAGCCCGCAC	1780
Qy	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1781	CCCTCGGGGGCCAGGAGACCCAGCCCGCAGCAGCTGCTCTCTCGCTCCACCGCGCGCTAT	1840
Qy	522	erValHisHisLeuValHisHisHisHisHisHisHisHisTyrrHisLeuGlyVAsnG	542
Db	1841	CCGTCCACCACTGGTGACCACCAACCAACCACTACCACTACCACTACCACTGGGCAATG	1900
Qy	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA	562
Db	1901	GGACGCTCAGGGCCCCCGGGCCAGCCGGAGATCCAGGACAGGGATGCCAATGGGTCCC	1960
Qy	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1961	GCCGGCTCATGTGCCACACCCCTCGACGCTGCGCTCTCCGGGGGGCCCCCTGGTGGCG	2020
Qy	582	laGluSerValHisSerPheTyrrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTCTGTGCACAGCTTCTTACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGG	2080
Qy	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622

2081	Db	 CGCCCCCTCCAGGTCCTCCATCTAGAGCATCCGGCAGGACTGTGGGCACGCCGAAGTGTT
622	Qy	yrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuValGluV
2141	Db	ATCCCACCGTGCACACAGCCCTCCACCGGAGCGCTGAAGAAGGACCTAGTAGAGG
642	Qy	alaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS
2201	Db	TGGCTGCCAGCTCTGGGCCCCCAACCCTCACGAGCCTAACATCCCACCGGCCCTACA
662	Qy	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI
2261	Db	GCTCCATGCACAAGCTGCTGGAGACACAGAGTACAGTGCTGCCAAAGCTCTTGAAGA
682	Qy	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTrVC
2321	Db	TCGCCAGCCCTGCTTGAAGAAGACAGAGTGGAGCCCTGTGTCCAGACAGCTGCCCTACT
702	Qy	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps
2381	Db	GTCCCCGGCCGGGCGAGGGAGTGGAGCTGCCGACCGTGAATGCGCTGACTCAGACA
722	Qy	erGluAlaValTyrgluPheThrGlnAspAlaGlnHissSeraspLeuArgaspProHisS
2441	Db	GCAGGCGAGTTTATGAGTTTACACAGAGATGCCAGACAGCGACCTCCGGGACCCCCACA
742	Qy	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaphet
2501	Db	GC---CGCGGGCAACGGAGGCTGGGCCAGATGCAGAGCCAGCTGTGTGGCCCTTCT
762	Qy	rpaArgLeuileCysAspThrPheArgLysileValAspSerLysrPheGlyArgGlyI
2558	Db	GGAGGCTAATCTGTGACACCTCCGHAAGATTGTGGACAGCAAGTACTTTGGCCGGGAA
782	Qy	leMettIeAlalieLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG
2618	Db	TCATGATCGCATCTCTGGTCAACACACTCAGCATGGGCATCGAATAACACGAGACGCCCG
802	Qy	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaleuG
2678	Db	AGAGGCTTACCAAGCCCTAGAAATCAGCAACATCGTCTTCCACAGCCTCTTTGCCCTGG
822	Qy	luMetLeuLysLeuLeuValTyrglyProPheGlyTyrlieLysAsnProTyraSnI
2738	Db	AGATGCTGCTGAAGCTGTTGTGTATGGTCCCTTTGGCTACATCAAGAATCCCTCAACA
842	Qy	lePheaspGlyValIlevalValIleservalTrpGluIleValGlyGlnGlnGlyGlyG
2798	Db	TCITTGATGGTGCATTGTGGTCATCAGCGTGTGGAGATCTGTGGGCCAGCAGGGGGCG
862	Qy	lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAtqPheLeuP
2858	Db	GCCTGTCCGGTGTCCGAGACCTCCCGCTGATGCGTGTGTGAAGCTGGTGGCTTCTGCG
882	Qy	roAlaLeuGlnArgGlnLeuValLeuMetLysThrMetAspAsnValAlaThrPheC
2918	Db	CGGCGCTGCAGCGGACGCTGGTGTCTCATGAAGACCATGGACAACAGTGGCCACCTTCT
902	Qy	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC
2978	Db	GCATGCTGCTTAATGCTCTTTCATCTTACATCTCCAGCATCTCTGGGCATGCATCTCTCGGCT
922	Qy	ysLysPheAlaSerGluAtcAspGlyAspThrLeuProaspArgLysAsnPhAspSerL
3038	Db	GCAAGTTTGGCTCTGAGCGGGAATGGGACACCTGCCAGACCCGGAAGAAATTTTGACTCTCT
942	Qy	euleuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValI
3098	Db	TGCTCTGGGCCATCGTCACTGCTTTTCAGATCCTGACCCAGGAGGAGTGGAAACAAAGTCC
962	Qy	eutyraenGlyMetAlaSerThrSerSerTrpAlaIleuTyrrPheIleAlaLeuMetf

Qy 306 ProArgGluAenGlyMetArgSerCysArgSerValProThrLeuAraGlyGluGlyGly 325
Db 814 TCGGGGACATGGGTAATGGGTGCATGAGATCCCCCGCTCAAGGACGAG----- 867
Qy 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 868 --GGCGGTGAGTGTGCTCTCCAAAGGACGACGCTACGACTTTGGGGCGGGCGCCAG 924
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrThrAsnCysSerAla 357
Db 925 GACCTCAATCCAGCGCGCTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCGGCACG 984
Qy 358 GlyGluHisAsnProPheLeuGlyAlaAlaAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 985 GGCAGGCCAACCCCAAGGGTGCCTCAACTTTGACACATCGGTATGCTTGGATT 1044
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1045 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTGATGGAT 1104
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIleValGlySerPhePhe 417
Db 1105 GCTCACTCTTCTCAAACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTCTTC 1164
Qy 418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1165 ATGATCAACCTGTGCTGCTGTATAGCGACCCAGTTCTCGGAGACCAAGCAAGGGAG 1224
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1225 CACCGGTGATGCTGGAGCAGCGCGCTACCTGTCC--TCCAGCACGGTGGCCAGC 1281
Qy 458 PheSerGluProGlySerCysTyrGluLeuLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1282 TACCCGAGCTGGCGACTGTCTACGAGGAGATCTCCAGTATGTCTGCCACATCTCTCGC 1341
Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1342 AAGGCCAAGCGCGCGCTGGGCTCTTACAGGCCCTCGAGAGCGCGCGCCAGCCCTG 1401
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1402 --GGCCCGGAGCGCGCGCGCGCCAAACCTGGGCGC----- 1437
Qy 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHis----- 533
Db 1438 -----CACGCCAAGGAGCGCGCGCACTACCTACCTGGAAGACTAAG 1476
Qy 534 -----HisHisHisTyrHisLeuGlyAsn-----GlyThrLeuArgValPro 547
Db 1477 GGTCAAGGAGATGAAGGAGACATCTCGAAGCGCGCATTCGCACACTTGCATGGGCT 1536
Qy 548 ArgAlaSerPro-GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPr 567
Db 1537 --GCTCCCTCGGAAATGATCACTCGGGAAGAGAGCTGTGCGCCCAACATA---GCCCC 1590
Qy 567 oProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVa 585
Db 1591 CTGGATCGCAGCGCCCAACACCTGTGTGAGCCCATCCCGCCGACGC----- 1636
Qy 585 lHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605
Db 1637 -----TGCTTCCGATCCC 1650
Qy 605 oArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVa 625
Db 1651 GCCAGCTGCCCTTGTGCGCAGCATGAGACGCGCGCGCGCTCGCGGCTG- 1702
Qy 625 lHisThrSerProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSe 645
Db 1703 -----GCAGCACCGACTCGGGCCAGGAGGCTCGGCT----- 1735
Qy 645 rProGlyProThrThrLeuThrSerPheAsnIleProProGlyProPheSerSerMethi 665

Db 1736 -CCGGGAGCTCCGCTGCTGGCG----- 1756
Qy 665 sLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr 685
Db 1757 -----AGGACGAGCGGATGGGG----- 1774
Qy 685 oCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgTh 705
Db 1775 -----AC 1776
Qy 705 rGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaVa 725
Db 1777 GGGGCCCGGAGCAGCGAGG----- 1795
Qy 725 lTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgAr 745
Db 1796 -----ACGGAGCTCTCTCAGAACTGGGGAAGAGG-----AGGAGGAGAG 1836
Qy 745 gGlnArgSerLeuGluProAspAlaGluProSerSerValLeuAlaPheTyrArgLeuI 765
Db 1837 GAGCAGCGGATGGGCGGTCTGGCTG-TGGCGGGATGTG-----TGGCGGGAGAC 1886
Qy 765 eCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAl 785
Db 1887 GCGAGCCAAAGTGGCGGCATCTGGGACAGCAAGTACTTCAACCGGGGCATCATGTGCG 1946
Qy 785 alleLeuValAsnThrLeuSerMetGlyIleGlyTyrHisGluGlnProGluGluLeuTh 805
Db 1947 CATCTCTGTCAACACCTGAGCATGGGCATCGAGCACCAGCAGCAGCGGAGGAGCTGAC 2006
Qy 805 rAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLe 825
Db 2007 CAACATCTGGAGATCTGCAATGTGGTCTTCCACGACATGTTTCCCTCGGAGATGATCT 2066
Qy 825 uLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGl 845
Db 2067 GAAGCTGGCTCATTTGGGCTCTTCGACTACTCTGCTAAACCCCTACAACTCTTCGACAG 2126
Qy 845 yValIleValValIleSerValTyrGluIleValGlyGlnGlnGlyGlyGlySerVa 865
Db 2127 CATCATTTGCATCATCAGCATCTGGGAGATCTGGGAGCGCGGAGCGGCTGCTCGGT 2186
Qy 865 lLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGl 885
Db 2187 GCTCGGACCTTCCGGCTGCTGCGGTGCTGAAACTGCTGCGCTTCATGCTGCCCTCG 2246
Qy 885 nArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLe 905
Db 2247 GCGCCAGCTCTGTTGCTCATGAAGACCATGGACAACCGTGGCCACCTTCTGCATGCTCT 2306
Qy 905 uMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAl 925
Db 2307 CATGCTCTTCATCTTCATCTTCAGCATCTTGGGATGTCATATTTTGGCTGCAAGTTCAG 2366
Qy 925 aserGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr 944
Db 2367 CCTCGCAGCAGACACTGGAGACACGGTCCCGCCGACAGGAAGAACTTCGACTCCCTGCTGT 2426
Qy 944 pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAs 964
Db 2427 GGCCATCGTCACTGTGTTCAGATCCTCACCCAGGAGGACTGGAAACGTCGTCTCTACAA 2486
Qy 964 nGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl 984
Db 2487 TGGATGGCTTCCACTTCTCCCTGGGCTCCCTTACTTTGTGGCCCTCATGACCTCGG 2546
Qy 984 yAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnAlaGluGl 1004
Db 2547 CAACATGTGCTCTTCAACCTGTGTGGCCATCTCTGTGGAGGCTTCCAGGCGGAGGG 2606
Qy 1004 yAspAlaThrLysSerGluSerGluProAspPheSerProSerVal----- 1020
Db 1004 yAspAlaThrLysSerGluSerGluProAspPheSerProSerVal----- 1020

Db 2607 TGACGCCAATCGCTCTACTCGGACGAGGACGAGCTCATCAACATAGAAAGTTTGA 2666
Qy 1021 -----AspGlyAspGlyAspArgGlySerGlyLeuAlaLeuValAl 1034
Db 2667 TAAGTCCAGGAAGGCTGACAGCAGCGAGATCCCAAG-----CTCTGCCAATCCC 2720
Qy 1034 aLeuGlyGluHiAlaGluLeuArgGlySerLeuLeuProProLeuIleIleHisThr-- 1053
Db 2721 CATGACCCCAATGGGCACCTGGACCCCACTCTC-----CCACTGGGTGGGCACCTAGG 2774
Qy 1054 -----AlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
Db 2775 TCCTGTGGGGCTGCGGGACCTGCC-----CCCCGACTCTCATGCGAGCGGACCCCAT 2828
Qy 1070 uAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAl 1090
Db 2829 GCTGGTGGCCCTGGCTCCCGAAGAGACAGTGTCTCTCTA-----GGGAGGAT 2879
Qy 1090 aHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAl 1110
Db 2880 GAGCTATGACAGCGCTCCCTGCTCCAGCTCCGAGCTCTACTACGGGCATGGGGCCG 2939
Qy 1110 aAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLe 1130
Db 2940 CAGCGGGCTGGGCCAGCGCTCGCTCCAGCTGGAAC-----AGCCT 2981
Qy 1130 uLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnG 1149
Db 2982 CAAGCACAAAGCCGCTGCGCGGAGCATGATCCCTGCTCTCTCGGAGCGCGGGCGG 3041
Qy 1149 uSerGlnAspGluGluSerSerGluGlu-----AspArgAlaSerProAlaGlySe 1167
Db 3042 CGCCCGGCTGCGAGGTTGCGCGGACGAGGGCGCGCGCGCGCACCCCTGCGACAC 3101
Qy 1167 rAspHis-----ArgHisAr 1172
Db 3102 CCACACGCCCCACACATTCATCGGGGCCCATCTGCGCGACCGCCCGCACCCACCG 3161
Qy 1172 gGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValPr 1192
Db 3162 CCGGACGCTCTCCTCGACAAAGGACTCGGTGGACTCGGCGAGCTGGTGGCCGGT 3221
Qy 1192 oGlyLeuHisArgThrAlaSerGlyArgSerSer-----AlaSerGluHisGlnAspCy 1210
Db 3222 GGGCGCCACCCCGGGCCCTGAGGGCGGCGAGCGCGCGCGCGCGCATGAGGACTG 3281
Qy 1210 sAnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAsp---AspProG 1229
Db 3282 CAATGGCAGGATGCCAGC-----ATCGCCAAAGACGTCTTCACCAAGATGGCGGACCG 3335
Qy 1229 nLeuAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAl 1249
Db 3336 CCGGGATCGGGGAGATGAGGAGGAATCGACTACACCTGTGCTTCCGCTCGCCAA 3395
Qy 1249 aTrpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTrpI 1269
Db 3396 GATGATCGAGCTCTATAAGCCCGACTGTCGAGGTCGCGAAGACTGGTCTGTACTCT 3455
Qy 1269 ePheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPh 1289
Db 3456 CTCTCTCCCGAGAACAGGTTCGGGTCCTGTGTGACAGCATTTATGCCCAACAATCTT 3515
Qy 1289 eAspHisValValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPr 1309
Db 3516 CGACTAGCTGTCTGGCCCTTCATCTTCTCACTGATCACCATCGCCCTGGAGCGGCC 3575
Qy 1309 oLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheTh 1329
Db 3576 TCAGATCGAGCGCGGACGACCGAACGCATCTTCTCACCGTGTCCCAACTACATCTTCA 3635
Qy 1329 rAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyG 1349
Db 3636 GGCCATCTCGTGGCGGAGATGATGATTGAAGGTAGTCTCGCTGGGCCCTGTACTTCGGCGA 3695

Qy 1349 uGlnAlaTrpLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLeuSerVa 1369
Db 3696 GCAGGCGTACTACGACGAGCTGGAACGCTGGATGGCTTCTTGTCTTCTGTGTCAT 3755
Qy 1369 lIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuAr 1389
Db 3756 CATCGACATCGTGGTGTCTCCCTGGCCCTCAGCGGGGAGCGCAAGATCTTGGGGTCTCCG 3815
Qy 1389 gValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLe 1409
Db 3816 AGTCTTGGGCTCTCTGGGACCTCATCGCCCTCGCTGCTCATCAGCGGGCGCGGCGCT 3875
Qy 1409 uLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValI 1429
Db 3876 GAAGCTGGTGGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCAT 3935
Qy 1429 eCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPh 1449
Db 3936 CTGCTGTGCTCTTCTCATCTTCTGGCATCTCTGGGAGTGCAGCTCTTCAAGGCAAGTT 3995
Qy 1449 ePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAl 1469
Db 3996 CTACCACTGTCTGGGCTGGACACCGCAACATCACCAACCGCTCGGACTGCGTGGCGC 4055
Qy 1469 aSerTrpArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSe 1489
Db 4056 CAACTACCGCTGGGTCCATCACAATAACAACTTTCGACAACCTGGCGCAGGCTCTGTATGTC 4115
Qy 1489 rLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAl 1509
Db 4116 CTTCTTTGCTCGGCATCCAAAGATGGTGGGTGGAACATCATGTACAAATGGACTGGAATGC 4175
Qy 1509 aValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIl 1529
Db 4176 TGTGTGTGGACAGCAGCGCTGTGACCAACACCAACCCCTGGATGCTGTGTACTTCAT 4235
Qy 1529 eSerPheLeuLeuIleValAlaPhePheValLeuLeuAsnMetPheValGlyValValValG 1549
Db 4236 CTCCTTCTCTCATCGTCAGCTCTTGTGCTCAACATGTTTGTGGTGTCTGTGTGGGA 4295
Qy 1549 uAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLy 1569
Db 4296 GAACTTCCAAAGTGGCGGACAGCAGAGGCTGAAGAGGACGCGCGCGTGAAGAGAA 4355
Qy 1569 sArgLeuArgGluGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaG 1589
Db 4356 GCGGCTGGCGCGCTGGAGAAAGCGCCG-----AAGGCCCA 4394
Qy 1589 nCysLysProTrpTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysTh 1609
Db 4395 GCGGCTGCCCTACTATGCCACCTATTGTACACCGGCTCTCATCCACTCCATGTGCAC 4454
Qy 1609 rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1629
Db 4455 CAGCCACTACTCGGACATTTCTATCCTTCACTCATCTGCTCAACGCTGCTCAACATGTC 4514
Qy 1629 aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl 1649
Db 4515 CTTGGAGCACTACAATCAGCCACGCTCCCTGGAGACGCGCTCAAGTACTGCAACTATAT 4574
Qy 1649 ePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgAr 1669
Db 4575 GTTCACCACTGTCTTGTGTGTGGAGGTGTGCTGAAAGCTGGTGGCATTTGTCTGAGGCG 4634
Qy 1669 gPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG 1689
Db 4635 CTTCTTCAAGGACCGATGGAAACAGCTGGACCTGGCCATTTGTCTACTGTCAAGTCAAGG 4694
Qy 1689 yIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleAr 1709
Db 4695 CATCACCTGGAGAGATCGAGATCAATGCGCGGCTGCCCATCATATCCGACCATCATCCG 4754

FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(6990)
 ; OTHER INFORMATION: calcium channel, voltage-dependent, alpha 1i
 ; OTHER INFORMATION: subunit (CACNA1I) gene.
 US-11-000-688-609

Alignment Scores:

Pred. No.: 0 Length: 6990
 Score: 5432.50 Matches: 1234
 Percent Similarity: 62.2% Conservative: 241
 Best Local Similarity: 52.0% Mismatches: 514
 Query Match: 45.2% Indels: 387
 DB: 15 Gaps: 62

US-09-611-257A-24 (1-2287) x US-11-000-688-609 (1-6990)

Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
 Db 16 TCCCGCCCTCTCATCTGCAGCAGCCCGCAGCCGCTGAGCCAGGAGTCAACACGAGCAG 75
 Qy 26 ProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGluAlaProArgSer 45
 Db 76 CCGGACCCCG----- 87
 Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
 Db 88 -----AGCCCCCATCTCCCGCCAGCGCTGGAGGAGCTCTGGATGGAGCT----- 135
 Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
 Db 136 -----GATCCT-----CATGTCCACAC 153
 Qy 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
 Db 154 CCAGACTGGCGCTATGTCCTTCTGCTGCGCAGACACACCGCCCGGAACTGG 213
 Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValLeuLeu 125
 Db 214 TGCAATCAAGATGGTGTGCAACCGTGTGTTGAATGTGTGACATGCTGGTATCTCTGT 273
 Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
 Db 274 AACTGCGTGACATGGCATGTGTACGACCGTGCAGCAGCATGGACTGCCTGTCCGACCGC 333
 Qy 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValGluMetVal 165
 Db 334 TGCAGATCTTGCAGGTCTTTGATGACTTCATCTTTATCTTCTTGTCCATGGATGGTG 393
 Qy 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
 Db 394 CTCAAGATGGTGGCCCTGGGATTTTGGCAAGAAGTGTACCTCGGGGACACATGGAAC 453
 Qy 186 ArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
 Db 454 CGCTGTGATTTCTTTCATCGTATGCGCAGGATGGTGCAGTACTCCCTGGACCTTCAGAAC 513
 Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
 Db 514 ATCAACCTGTGAGCCATCCGCGCTGCGGTCTGTAGGGCCCTCAAGGCCATCAACCGC 573
 Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
 Db 574 GTGCCAGATGCGGATCTTGTGAACCTGCTCTCTGGACACACTGCCCATGCTGGGGAAT 633
 Qy 246 ValLeuLeuLeuCysPheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
 Db 634 GTCTGTGCTGCTCTTGTCTTGTCTTTCATCTTTTGGCATCATAGTGTGCAGCTCTGG 693
 Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluLeuPheSerLeuProLeuSerVal 285
 Db 694 GCGGGCTGTGTCGTACCCGCTGCTTCTGAGGAGGAACTTCAACATACAAAGGGGATGTG 753

Qy 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
 Db 754 GCCTTGCCCCCATACTACCAAGCGGAGGAGATGATGAGATGCCCTTTCATCTGCTCCCTG 813
 Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly 325
 Db 814 TCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCGCGCTCAAGAGCAG----- 867
 Qy 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
 Db 868 ---GGCGTCTAGTCTGCTCTCAAGGACGACGCTCTACGACTTTGGGGGGGGCGCCAG 924
 Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
 Db 925 GACCTCAATGCCAGCGGCTCTGTGTCACTGGAAACGTTACTACAATGTGTGCGCAGC 984
 Qy 358 GlyGluHisAsnProPheTyrGlyAlaIleAsnPheAspIleGlyTyrAlaTrpIle 377
 Db 985 GGACGCGCCCAACCCCAAGGGTGCCATCACTTTGACAACTCGGTATTGCTTGGATT 1044
 Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397
 Db 1045 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTATGGAT 1104
 Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
 Db 1105 GCTCACTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTCTTC 1164
 Qy 418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGluArgGlu 437
 Db 1165 ATGATCAACTGTGCTCTGTTGTCATAGCAGCCAGTCTCGGAGACAAGCAACGGGAG 1224
 Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
 Db 1225 CACGGCTGATGTGGAGCAGCGCAGCTACTCTGCTCC---TCCACACGGTGGCCAGC 1281
 Qy 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
 Db 1282 TAGCCGAGGCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCTGCG 1341
 Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
 Db 1342 AAGGCCAAGCGCGCCCTGCGGCTCTACAGGCCCTGCGAGCCGCGCCGCGCCAGCCCTG 1401
 Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
 Db 1402 ---GGCCGAGGCGCGCGCCCGCCCAACCTGGGCCC----- 1437
 Qy 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHis 533
 Db 1438 -----CACGCCAAGGAGCGCCCGGCACTACCATGGGAGACTAAG 1476
 Qy 534 -----HisHisTyrHisLeuGlyAsn-----GlyThrLeuArgValPro 547
 Db 1477 GGTGAGGAGATGAAGGAGACATCTCGAAGCGCGGCAATTGCCAGACTTTCATGTTGGGCT 1536
 Qy 548 ArgAlaSerPro-GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPr 567
 Db 1537 ---GCCTCCCTGGAAATGATCACTCGGGAAGAGAGAGCTGTGCCGCGCAACATA---GCCCC 1590
 Qy 567 OProProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVa 585
 Db 1591 CTGGATGCGAGCGCCACACACCTGTTGTCAGCCCATCCCGCCAGC----- 1636
 Qy 585 HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605
 Db 1637 -----TGCTTCCGATCC 1650
 Qy 605 OArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVa 625
 Db 1651 GCACAGTCCCTTGTCTGCCAGCATGAGACGGCGGGCGGCTCGGCGCTGG----- 1702
 Qy 625 HisThrSerProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSe 645

Db	1703GCACCGACTCGGCGCAGAGGGCTCGGGCT-----	1735	Db	2547	CAACTATGTGCTCTTCAACCTGTGTGGCGCATCTCTGGTGGAGGGCTTCCAGCGGAGGG	2606
Qy	645	rProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHi	665	Qy	1004	yAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal-----	1020
Db	1736	-CCGGAGCTCCGCTGGTGGG-----	1756	Db	2607	TGACGCCAATCGCTCTACTCGGACGAGGACGAGCTCATCAACATAGAAGAGTTTGA	2666
Qy	665	sLysLeuLeuThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr	685	Qy	1021	-----AspGlyAspGlyAspArgLysLysArgLysLeuAlaLeuAla	1034
Db	1757	-----AGGACGAGCGGATGGGG-----	1774	Db	2667	TAAGCTCCAGAAAGGCTGGACAGCAGCGAGATCCCAAG-----CTCTGCCCAATCCC	2720
Qy	685	oCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgTh	705	Qy	1034	aLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleHisThr--	1053
Db	1775	-----AC	1776	Db	2721	CATGACCCCAATGGGCACCTGGACCCCACTCTC-----CCACTGGGTGGCACCCTAGG	2774
Qy	705	rGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaVa	725	Qy	1054	-----AlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG	1070
Db	1777	GGGCGCGGAGCAGCGAGG-----	1795	Db	2775	TCCTGTGGGGCTCGGGGACCTGCC-----CCCCGACTCTCACTGACGCGGACCCCAT	2828
Qy	725	lTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgAr	745	Qy	1070	uAlaLeuGlySerGlySerArgThrSerSerSerGlySerAlaGluProGlyAlaAl	1090
Db	1796	-----ACGAGCGCTCTCAAACTGGGGAAGGAG-----AGGAGGAGGAG	1836	Db	2829	GCTGTGGCTGGCTCCCGAAGACGAGTGTCTCTCTA-----GGGAGGAT	2879
Qy	745	gGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuI	765	Qy	1090	aHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAl	1110
Db	1837	GAGCAGCGCGATGGGCGGTCTGGCTG-TGGCGGGATGTG-----TGGCGGGAGAC	1886	Db	2880	GAGCTATGACAGCGCTCCCTGTCCAGCTCCGAGCTCTCTACTACGGGCCATGGGCGC	2939
Qy	765	eCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAl	785	Qy	1110	aAlaSerSerTrpThrSerArgSerArgSerArgAsnSerLeuGlyArgAlaProSerLe	1130
Db	1887	CGCAGCCAAGCTGGCGGCATCGTGGACAGCAAGTACTTCAACCGGGGCATCATGTGC	1946	Db	2940	CAGCGCGCTGGGCCAGCGCTGCTCCAGCTGGAAC-----AGCCT	2981
Qy	785	aIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuTh	805	Qy	1130	uLysArgArgSerProSerGlyGluArgSerLeuLeuSerGlyGlu---GlyGlnG	1149
Db	1947	CATCTGTGTCAACACCGTCAGCATGGGCATCGAGCACCAGCAGCGGAGGAGCTGAC	2006	Db	2982	CAAGCACAAGCCCGCTGGCGGAGCATGACTCCCTGCTCTCTCGGAGCGCGCGCGG	3041
Qy	805	rAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLe	825	Qy	1149	uSerGlnAspGluGluSerSerGluGlu-----AspArgAlaSerProAlaGlySe	1167
Db	2007	CAACATCTGGAGATCTCATATGGTCTTCCACGACATGTTTGGCTGGAGATGATCCT	2066	Db	3042	CGCGGGGTCTCGAGGTTCGCGGACGAGGGCGCGCGGCGCACCCCTGCACAC	3101
Qy	825	uLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGl	845	Qy	1167	rAspHis-----ArgHisAr	1172
Db	2067	GAAGCTGGCTGATTTGGGCTCTTCGACTACCTGCTAAACCCCTACAACTCTTCGACAG	2126	Db	3102	CCCACACGCCCCACCATTTCAATCATCGGGCCCATCTGGCGGACCGCACCCGCCACCCG	3161
Qy	845	yValIleValIleSerValTrpGluIleValGlnGlnGlnGlyGlyLeuSerVa	865	Qy	1172	gGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValPr	1192
Db	2127	CATCATTTGCATCATCAGCATCTGGAGATCGTGGGCGAGCGGACGCTGGGCTGTCTGGT	2186	Db	3162	CCGACGCTGTCTCCCTCGACAAACAGGAGCTCGTGACCTCGCGAGCTGGTGGCGCGGT	3221
Qy	865	lLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGl	885	Qy	1192	oGlyLeuHisArgThrAlaSerGlyArgSerSer-----AlaSerGluHisGlnAspCy	1210
Db	2187	GCTGGGACCTTCGGCTGCTCGCGGTGCTGAAACTGGTGGCTTCATGCTGCCCTGCG	2246	Db	3222	GGGCGCCACCCCGCGCGCTGGAGGGCGGAGCGCGCGCGCGGCGCATGAGGACTG	3281
Qy	885	nArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLe	905	Qy	1210	eAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAsp---AspProGl	1229
Db	2247	CGCGCAGCTCGTGTGCTCATGAAGACCATGGACAACTGGCGCACCTTCTGCATGCTGCT	2306	Db	3282	CAATGGCAGGATGCCAGC-----ATCGCCAAAGACGTCTTCAACAGATGGGCGCACCG	3335
Qy	905	uMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAl	925	Qy	1229	nLeuAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAl	1249
Db	2307	CATGCTCTTCATCTTTCATCTTCAGCATCTTGGGATGATATTTTGGCTGCAAGTTGAG	2366	Db	3336	CGGGATCGCGGGGAGGATGAGGAGAAATCGACTACACCTGTGCTTCCGCGTCCGCAA	3395
Qy	925	aserGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr	944	Qy	1249	aTrpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrI	1269
Db	2367	CCTCGCAGGACACTGGAGACACCGTGGCCGACAGGAAGAACTTCGACTCCCTGCTGTG	2426	Db	3396	GATGATCGACGCTATTAAGCCCGACTGCTGGTGGAGTCCGCGAAGACTGGTCTGTACTCT	3455
Qy	944	pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAs	964	Qy	1269	ePheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPh	1289
Db	2427	GGCCATCTGCTACTGTGTTCAGATCTCTCACCAGGAGGACTGGAACTGCTCTCTACAA	2486	Db	3456	CTTCTCTCCGAGAACAGGTTCCGGGCTCTGTGTGACAGCACTATTATGCCCAAACTCTT	3515
Qy	964	nGlyMetAlaSerThrSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl	984	Qy	1289	eAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPr	1309
Db	2487	TGGCATGCCCTCACTTCTCCCTGGGCTCCCTCTACTTTGCGCCCTCATGACCTTCGG	2546	Db	3516	CGACTACGCTGCTCTGGCTTCTCACTTCTCAACTGCATCATCCTCGCCCTGGAGCGGC	3575
Qy	984	yAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGl	1004	Qy	1309	oLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheTh	1329
				Db	3576	TCAGATCGAGCGCGCAGCACCGAACGCACTTTCTTCCCGTGTCCAACTACATCTTAC	3635

1329 rAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyG1 1349
1349 uGlnAlaTyLeuArgSerTrpAsnValLeuAspGlyLeuValLeuLeuSerVa 1369
3636 GGCCATCTTGTGGCGAGATGACATTGAAGGTAGTCTCGTGGCCCTGTACTTCGGCGA 3695
1349 uGlnAlaTyLeuArgSerTrpAsnValLeuAspGlyLeuValLeuLeuSerVa 1369
3696 GCAGCGGTACTACGACAGCAGCTGGAACGTGCTGGATGGCTTTCTTGTCTTCGTGCTCAT 3755
1369 lIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuAr 1389
3756 CATCGACATCGTGTGTCTTGGCTCAGCGGGGAGCCCAAGATCTTGGGGGTCTCCG 3815
1389 gValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLe 1409
3816 AGTCTTGGCGCTCTCGCGACCTACGCCCTTGGGTGTGCATCAGCGCGGGCGCGGSCCT 3875
1409 uLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValI1 1429
3876 GAAGCTGTGTGGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCAT 3935
1429 eCysCysAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPh 1449
3936 CTGCTGTGCTCTTTCATCATCTTTGGCATCTTGGGAGTGGAGCTCTTCAAGGGCAAGTT 3995
1449 ePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluA1 1469
3996 CTACCATGTCTGGCGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCGCG 4055
1469 aSerTyArgTrpValArgHisLysTyAsnPheAspAsnLeuGlyGlnAlaLeuMetSe 1489
4056 CAACCTACCGTGGGTCCATCACAAATACAACTTCGACAACTCGGCCGAGGCTCTGTATGTC 4115
1489 rLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyArgPheLeuAspAl 1509
4116 CTTCTTTGTCTGGATCCAAAGGATGTTGGTGGTGAACATCATGTACAAATGATGATGATGC 4175
1509 aValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyPheI1 1529
4176 TGTGTCTGTGGACGAGCTGTGACCAACCAACCAACCCCTGGATGTCTGTACTTTCAT 4235
1529 eSerPheLeuLeuValAlaPhePheValLeuAsnMetPheValGlyValValValG1 1549
4236 CTCCTTCTGTCTATCTGCTACTTCTTTGTGTCTCAACATGTTTGTGGGTGTCTGTGTGA 4295
1549 uAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLy 1569
4296 GAACCTTCCAAAGTGCCTGGCAGCACCCAGGAGGTGAAGAGGCACGGCGGTGAGGAGAA 4355
1569 sArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaG1 1589
4356 GCGGCTCGGCGCTGTGAGAAAGCCCGG-----AAGGCCCA 4394
1589 nCysLysProTyTrpSerAspTyTrpSerArgPheArgLeuLeuValHisLeuCysTh 1609
4395 GCGGCTCGCTTACTATGCCACCTATTGTCAACCCGCGTGTCTATCCACTCCATGTGCAC 4454
1609 rSerHisTyLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1629
4455 CAGCCATCTACTGTGACATCTTCACTCATCTTCACTCATCTGCTCAACGTGGTCAACATGTC 4514
1629 aMetGluHisTyTrpGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyTr1 1649
4515 CTTGGAGCATACATCAGCCACCGTCCCTGGAGACAGCCCTCAAGTACTGCACTATAT 4574
1649 ePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgAr 1669
4575 GTTCACCACTCTCTTTGTCTGGAGGTGTCTGTAAGCTGTGGCAITTTGCTCTGAGGCG 4634
1669 gPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG1 1689
4635 CTTCTTCAAGGACCGTGAACCAAGCTGGACCTGGCCATGTGTACTGTCTGAGTCATGGG 4694

1689 yIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleAr 1709
4695 CATCACCTTGGAGGATCGAGATCAATGCGGCGCTGCCCATCAATCCACCATCATCCG 4754
1709 gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMe 1729
4755 CATCATGAGGGTTCTCGCATTCGCCAGTGTCTGAAGCTGTTGAAGATGGCCACAGGAAT 4814
1729 tArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe 1749
4815 GCGGGCCCTCTGGACACGGTGTGCAAGCTTTCGCCCAGTGGCAACCTTGGSCCTCT 4874
1749 uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG1 1769
4875 CTTTCATGCTCTCTTCTTCTATCTATGCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGT 4934
1769 uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG1 1789
4935 CTGCAACGAGAGAACCCGTGCGAGGCATGAGCGGCATGCCACCTTCAGAACTTCGG 4994
1789 yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy 1809
4995 CATGGCTCTCTCACACTCTTCCAGGTCTCCACGGGTGACAACTGGAAACGGATCATGAA 5054
1809 sAspProSerArgAspCys---AspGlnGluSerThrCysTyAsnThrVal-----I1 1826
5055 GGACACGCTCGGAGCTGACCCACACGACGAGCGAGCTGCTGAGCAGCCTGCAAGTTGT 5114
1826 eSerProIleTyPheValSerPheValLeuThrAlaGlnPheValLeuValLeuValVa 1846
5115 GTCGCGCTGTACTTGTGAGCTTGTGCTCACCGCAGTTCGTGCTCATCAACGTGGT 5174
1846 lIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaG1 1866
5175 GGTGGCTGTCTCATGAGCACCTGGACGACAGCAACAGAGGCGCAGGAGGACGCGA 5234
1866 uLeuGluAlaGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr 1885
5235 GATGGATCGGAGCTCGAGTGGAGATGGCCATGGCTTGGCCCTGCGCCGAGGCTGCC 5294
1885 oLeuGlySerProPheLeuTrpPro-----GlyValGluGlyValAsnSe 1900
5295 TACCGCTCCCGGGCGCC---CTGGCCGAGGCGCGGAGGCGCGCGGGGGCGGA 5351
1900 rThrAsp-----SerProLysProGlyAlaPro----- 1909
5352 CACGAGGCGGCTTGTGCGCGCTGTACTCTCGCTGC-CCAGAGAACCTGTGGCTGG 5410
1910 ----HisThrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMe 1928
5411 ACAGCGTCTCTTTAATCATCAAGGACTCTCTTGGAGGG---GGAGCTGACCAT----- 5459
1928 tValProHisProGluValProValProLeuGlyProAspLeuLeuThrValArgLy 1948
5460 -----CATCGAACCTGTGCGGCTCCATCTTCCACCATCTCTCTCGCTCGCGCT 5512
1948 sSerGlyValSerArgThrHisSerLeuProAsnAspSerTyMetCysArgAsnGlySe 1968
5513 GCAAGAAGTGTCA-----CCACGACAA----- 5534
1968 rThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySe 1988
5535 ----GCAAGAGGTGCAGCTGGCTGAGCGGAGGCTTCTCCCTGAACCTCAGCAGGCTCT 5590
1988 rIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAs 2008
5591 CGTCCATCTCTGGGTGAGCAGCTGAGTCTCGAGGA----- 5627
2008 pValHisTyTrpLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuPr 2028
5628 -----CCCCACACCTGCCACCTGG-----CCGCAAGACA 5659
2028 oPro-----ProGlyArgSerProLe 2035

```
Db 5660 GCAAGGTGACCTGGACCCACCTGAGCCCTGCGTGGGAGACTGGGCGAATGCTTCT 5719
Qy ualaGlnArgProLeuArgArgGlnAlaAilaileArgThrAspSerLeuAspValGlnG 2055
Db TCCCTTGT-CCTCTAGCGCGTCTCGCGGATCCAGAGAACTTCTGT---GTGAGATG 5775
Qy yLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrAr 2075
Db GAGGAGATCCCAT-----TCAACCTGTCCGGTCTCTGGCTGAACATGACAA-- 5821
Qy gserSerPheThrGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSe 2095
Db ----- 5821
Qy rLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAl 2115
Db -----GCAGTCAAGCACCCCAAGTCCCTTCTCCC----- 5851
Qy aLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe 2135
Db -CGATGCTCCAGCC-----CTCTC 5871
Qy rGlyAspLeuLeuProSerSerGlnGluProLeuPhePro-----ArgAspLeuLy 2153
Db CTGCCCCATGCCAGCGAGTCTTCCACCTCGAGTGTCTGCAGCCAGCAAGGCCAGAA 5931
Qy sLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheThrLeuAspGl 2173
Db AAGGCACTGGCACTGGAAACCTCCCCAAGATTGCGCTG-CAGGGCTCTCGGCATCT-- 5988
Qy uGlnArgHisSerIleAlaValSerCysLeu-----AspSerGlySerG1 2189
Db -----CTGCGGTACCAAGGGTCACTGACCTCTCCGCGAGGCCACCGGGAGCGA 6041
Qy nProArgLeuCysProSerSerLeuGlyGlnProLeuGlyGlyProGlyse 2209
Db CACGTGCTGAGCCAGCCAGCCAGCAG-CTCGCGGGGAGCTGCAGACCACGCTCGAGG 6100
Qy rArgProLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnG 2229
Db ACAGCCTGACCTGAGCGACAGACGCCCGCGG-----TGCCCTTG 6139
Qy ySerArgProProCysSer-----ProGlyValCysLeuArgArgAlaProAlase 2247
Db GCGCGCCCGCGCTGCTCCAGACCCCGCGGCGGCTGTCCCGCGGCTCGCCGCCGCC 6199
Qy rAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerProSerPr 2267
Db TGAGCCTGCGCGCGCGCGGCTCTTTCAGCCTGCGGGGCTGCGGGCGCATCAGCGCAGCC 6259
Qy oLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db ACAGCAGCGGGGCTCCACACAGCCCGGCTG 6290
```

RESULT 13

```
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1
Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.7% Conservative: 234
Best Local Similarity: 51.8% Mismatches: 494
Query Match: 45.1% Indels: 413
Gaps: 60
```

```
US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)
Qy 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db TCCCGCGCTCTCTCATCTGCAGCAGCCCGCCGCTGAGCCAGGAGTCACCCAGGAGCAG 266
Qy ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db CCGGAGCCCGG----- 278
Qy ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db -----AGCCCCCATCTCCCGCCAGGCTGAGGAGCCTCTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db CAGACCTGGCGCTATTGCTTCTGCTGCGCAGACACACAGCCCGCCGAACTGG 404
Qy CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db TGCATCAAGATGGTGTGCAACCGGTGTGAATGTGTGACATGCTGCTGATCTCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db AACTGCGTGACACTTGGCATGTACAGCGGTGCGACGACATGGACTGCTGTCCGACCGC 524
Qy 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaValIleMetVal 165
Db TGCAGATGCTGCGAGGTCTTTGATGACTTCATCTTTATCTTCTTTCATGAGATGGTG 584
Qy 166 VallysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
Db CTCAGATGCTGCGGCTGGGGATTTTGGCAAGAGTGTACTACCTCGGGGACACATGGAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db CGCCTGGATTTCTTTCATCGTCATGCGAGGATGGTCGAGTACTCCCTCGAGCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db ATCAACCTGTGAGCATCCCGCAGCGCTGCGGCTCTGAGGCCCTCAAAGCCATCAACCGC 764
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db GTGCCAGATGCGGATCTGTGTGAACCTGCTCTGGACACACATGCCCATCTCTGGGAAT 824
Qy 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db GTCCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db CCGGCGCTGCTGCGTAACCGCTGCTTCTTCTGAGGAGAACTTCACCATCAAGGGGATGTG 944
```

Qy 286 AspLeuGluProTyrThrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGCCCATACCTACAGCGGAGGAGATGATGAGATGCCCTTTCATCTGCTCCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGCGCAACAATGGGATGAGTGGCTGCATGAGATCCCGCTCAAGGAGCAG- 1058
Qy 326 GlyGlyProProCysSerLeu- 1111
Db 1059 -GGCCGTGAGTCTGCTGCTCAAGAGCAGCTCTACGACTTTGGGGGGGGCGCCAG 1115
Qy 340 SerSerAsnThrThr- 1111
Db 1116 GACCTCAATGCGACGCGCTCTGTGTCAACTGGAAACGTTACTACAAATGTGTGCGCAGC 1175
Qy 358 GlyGluHisProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCCCAACCCCAAGGGTGCATCAACTTTGACAACTCGGTATGCTTGGATT 1235
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTyrPheIleLeuLeuIleValGlySerPhePhe 397
Db 1236 GTCATCTTCAGGTGATCACTCTGGAAGCTGGGTGGAGATCATGTACTACGTATGAT 1295
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTCACTCTTTCACAACTTTCATCTTCTATCTGCTTATCATAGTGGCTCTTCTTC 1355
Qy 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGTTGTCATAGCAGCACCAGTTCTCGGAGACCAAGACGGGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACGGCTGATGTGGAGCAGCGCAGCTTACCTGTGCC-TCACAGCAGGTGGCCAGC 1472
Qy 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TAGCCCGAGCTGGCGACTGTACGAGGAGATCTTCAGATGATGTGCCACATCTCGGC 1532
Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGGCG- 1574
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC- 1577
Qy 518 HisArgArgLeuSerValHisLeuValHisHisHisHisHisHisHisHisTyr 537
Db 1578 -CGCGCCAGGCGCTG- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 - 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
Db 1602 - 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 - 1643
Qy 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACCAAGCTGTGCGCCGCAACATAGCCCGCTGATGCG- 1685
Qy 618 SerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLys 637
Db 1686 - 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657

Db 1698 -CTGGTGCG- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys- 676
Db 1731 -GATCCCGCAGCTGCCCTTGTGTCGAG 1757
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGACCGCGCGCGCTCGGGCTGGGCGACCGACTCGGGCGAGGAGGCTCG 1817
Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC- 1853
Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -GATGGGACGCGGGC- 1898
Qy 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGAAGGAGGAGGAGGAGGAGCAG- 1940
Qy 757 SerValLeuAla- 1974
Db 1941 GTCTGGCTGTGCGGGATGTGTGCGGGAGACGCGAGCCAAAGCTGCGCGGCATCGTGGAC 2000
Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGCATCATATGGCCATCTGTGTCACACCGTCAGATGGC 2060
Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCGAGCACCGAGCAGCGGAGGAGCTGACCAACATCTCGGAGATCTGCAATGTGTC 2120
Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPheGly 834
Db 2121 TTCACCAAGTATGTTGCCCTGGAGATGATCTGAAGCTGGCTGCAATTTGGCTCTTCGAC 2180
Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrpGlu 854
Db 2181 TACTTCGTAAACCCCTACAACATCTTCGACAGCATCATTTGTCATCAGCATCTGGAG 2240
Qy 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGCGAGGCGGAGCGTGGCTGCTGCGGACCTTCGGCTCTCGCGCTG 2300
Qy 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAAACTGTGGCTTCATGCTCCCTGCGCTGCGCGCAGCTCGTGTGCTCATGAAGACC 2360
Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914
Db 2361 ATGACAACTGGCGCACCTCTGCTGCTGCTCATGCTCTTCATCTTCATCTTCAGCATC 2420
Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp- 933
Db 2421 CTTGGGATGATATTTTGGCTGCAAGTTTCAGCTCCGCGCAGGACACTGGAGACACGCTG 2480
Qy 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCGACAGGAGAACTTCGACTCCCTGCTGCGCGCAGCTCGTGTGCTCATGTTCCCTCC 2540
Qy 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 973
Db 2541 ACCGAGGAGACTGGAACGCTGTTCTACAATGGCATGGCTCCACTTCTCCCTGGGCC 2600
Qy 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2601 TCCCTCTACTTGTGCGCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTCTGCTG 2660
Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013

2661	GCATCTCGTGGAGGCGCTTCCAGGCGGAGGGTGACGCCAATCGTCTCTACTCGGACGAG	2720
Db		
1014	AspPheSerProSerVal-----:::---:::---:::---:::---:::---AspGlyAsp	1023
Qy		
2721	GACCAGAGCTCATCCAACATAGAAGAGTTTTGATGAAGCTCCAGGAAGCGCTGGACGACG	2780
Db		
1024	GlyAspArgIysIysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys	1043
Qy		
2781	GGAGATCCCAAG-----CTCTGCCAATCCCATGATCCCAATGGCACTGGACCCOC	2834
Db		
1044	SerLeuLeuProProLeuLilleHisThr-----AlaAlaThrProMetSer	1059
Qy		
2835	AGTCTC-----CCACTGGGTGGCACACTAGTCTCTGTGGGCTCGGACCTGCC---	2885
Db		
1060	HisProIysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr	1079
Qy		
2886	---CCCCGACTCTCACTCAGCAGCGGACCCCATGCTGTGTGGCCCTCGGCTCCCGAAAG	2942
Db		
1080	SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer	1099
Qy		
2943	AGTGTCAATGCTCTA-----GGAGATGAGCTATACCAAGCGCTCCCTGTCTCAGC	2993
Db		
1100	AlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer	1119
Qy		
2994	TCCCGAGCTCTACTACGGGCCATGGCGCGCAGCGCGCCTGGGCCAGCCCTCGCTCC	3053
Db		
1120	SerArgAnSerLeuGlyArgAlaProSerLeuIysArgArgSerProSerGlyGluArg	1139
Qy		
3054	AGCTGGAA-----AGCTCAAGCACAAGCCGCCGCTCGCGGAGCAT	3095
Db		
1140	ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu	1158
Qy		
3096	GAGTCCCTGCTCTCTCGGAGCGCGCGCGCGCTCTCGAGGTTCGCGGAC	3155
Db		
1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----1169	
Qy		
3156	GAGGGCGCGCGCGCGCGCACCCCTGCACACCCACACCGCGAGCTGTCTCCGACACAGG	3215
Db		
1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181
Qy		
3216	CCCATCTGGCGCACCGCCACCGCCGAGCTGTCTCTCGACACAGGAC	3275
Db		
1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201
Qy		
3276	TCGGTGGACCTGGCGAGCTGTGTCGCCCGGTGGCGCCACCCCGCGCGCTCGAGG	3335
Db		
1202	SerSer-----AlaSerGluHisGlnAspCysAnclIysSerAlaSerGlyArgLeu	1219
Qy		
3336	CGCGAGCGCGCGCGCGCGCATGAGGACTGCAATGGCAGGATGCCACG-----ATC	3389
Db		
1220	AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
Qy		
3390	GCCAAAGACGCTTTCACCAAGATGGCGCACCGCGGGATCGCGGGAGGATGAGGAGAA	3449
Db		
1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
Qy		
3450	ATCGACTACACCTGTGCTTCCGCGTCCGCAAGATGATCGACGCTCTAATAGCCGACTG	3509
Db		
1259	CysArgGluArgAspSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeu	1278
Qy		
3510	TGCAGGTCCGCGAAGACTGGTGTCTACTCTCTCTCCGAGAACAGGTTCCGGGTC	3569
Db		
1279	LeuCysHisArgIleLilleThrHisLysMetPheAspHisValValLeuValIlePhe	1298
Qy		
3570	CTGTGTGAGACCATATTGCCCAAAACTCTTTCAGTACGTCTCTGGGCTTCATCTTT	3629
Db		
1299	LeuAnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
Qy		
3630	CTCAACTGTCATCACATCGCCCTCGAGCGGCTCGATCGAGCGCGCAGCAGCGAACGC	3689
Db		
1319	IlePheLeuThrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
Qy		
3690	ATCTTCTCACCGTCCAACTACTCTTACGGCCATCTTCAGGCCATCTTCGGGCGAGATG	3749
Db		

QY	1339	LyseValValAlaLeuGlyTyrCpCysPheGlyGluClnAlaTyrLeuArgSerSerTrrpAsn	1350
DB	3750	AAGGTAGTCTCGCTGGGCGCTTACTTTCGGCGAGCAGCGTACCTACGACAGCTGGAAC	3809
QY	1359	ValLeuAspGlyLeuLeuValLeuLeuSerValIleAspIleLeuValSerMetValSer	1378
DB	3810	GTGCTGATGGCTTCTTGTCTTCGTGTCATCATCGACATCGTGGTGTCCCTGGCCCTCA	3869
QY	1379	AspSerGlyThrIlysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
DB	3870	GCCGGGGAGCCCAAGATCTTGGGGGCTCCCGAGTCTTGGCGCTCCTGGCGACCCCTACGC	3929
QY	1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlnThrLeuMetSer	1418
DB	3930	CCCCTGGTGTATCATCACCGGGCGCGGGCTGAACTGTGTGTGGAGACATCATCTCC	3989
QY	1419	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1438
DB	3990	TCCCTCAAGCCCATCGSCAACATCGTCTCATCTGTGTGCCCTTCTTTCATCATCTTTGGC	4049
QY	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
DB	4050	ATCCTGGAGTGCAGCTTTCAAAGGCGAAGTCTTACCACTGTCTGGCGCTGGACACCCGC	4109
QY	1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrrpValArgHisLysTyr	1478
DB	4110	AACATCACCAACCGCTCGACTGCATGGCGCGCCAACTACCGCTGGTCCATCACAAATAC	4169
QY	1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
DB	4170	AACCTTCACAACCTGGGCCAGGCTCTGATGTCCCTCTTGTCTCGCATCCCAAGGATGGT	4229
QY	1499	TrrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
DB	4230	TGGGTGAACATCATGTACAATGAGACTGGATGCTTGTCTGTGACCGACGACCTGTGACC	4289
QY	1519	AsnHisAsnProTrrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
DB	4290	AACCACAAACCCCTGGATGCTGTACTTTCATCTCCTCTCCTGTCTCGTCAGCTCTTTT	4349
QY	1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln	1558
DB	4350	GTGCTCAACATGTTTGGGTGTCTGGTGTGGAGAACTTCCACAAGTCCGCGCAGCACCCAG	4409
QY	1559	GluGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArg	1578
DB	4410	GAGCTGAAGAGGACCGCGCGCTGAGGAGAGCGGCTGGCGGCGCTGGAGAGAAGCGC	4469
QY	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598
DB	4470	CGG-----AAGGCCACGCGGTGCCCTACTATGCACTATGT	4508
QY	1599	ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1618
DB	4509	CACACCGGGTGTCTATCCACTCCATGTGCACGACCACTACTGTGACATCTTTCATCACC	4568
QY	1619	GlyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1638
DB	4569	TTCATCATCTGCCTCAACGTTGGTCACCATGTCTTCGGAGCACTACAATCAGCCACCGTCC	4628
QY	1639	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer	1658
DB	4629	CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTTACCACCTGTCTTGTCTGGAGGCT	4688
QY	1659	ValPheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTrrpAsnGlnLeu	1678
DB	4699	GTGCTGAAGCTGGTGGCATTTGGTCTCAGGGGCTTCTTCAAGGACCGATGGAACACAGCTG	4748
QY	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
DB	4749	GACCTGGCCATTGGCTACTGTGAGTATGGGATATCCCTGGAGGAGATCGAGATCAAT	4808

1699	Qy	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1718
4809	Db	GCGCCCTCGCCCAATCCACCATCATCGCATCATGAGGTTCTGCGCATTGCCCGA	4868
1719	Qy	ValLeuLeuLeuLeuMetAlaValIglyMetArgAlaLeuLeuHisThrValMetGln	1738
4869	Db	GTGCTGAAGCTGTTGAAGATGGCCACAGGAATGCGGGCCCTGCTGGACACGGTGTGCCAA	4928
1739	Qy	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1758
4929	Db	GCCTTGGCCCGAGTGGGCAACCTGGGCTCTCTCTTCATGTCTCTTCTTTCATCATGTCT	4988
1759	Qy	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
4989	Db	GCTCTCGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACACGACGAGAACCCGTGCGAGGGC	5048
1779	Qy	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
5049	Db	ATGAGCCGGATGCCACTTCGAGACTTCGGCATGGCTTCTTCACACTCTTCTCCAGGTC	5108
1799	Qy	SerThrGlyAspAsnTrpAsnGlyIleMetIleAspProSerArgAspCys--AspGln	1817
5109	Db	TCCACGGGTGACAACTGGAACGGGATCATGAGACACCGTGGGACTGCACCCACGAC	5168
1818	Qy	GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1835
5169	Db	GAGCGCAGCTGCCTAGCAGCTGCTGTTGTGTGCGCGTGTACTTCGTGAGCTTCGTG	5228
1836	Qy	LeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetIleHisLeuGlu	1855
5229	Db	CTCACCGCGAGTTCGTGCTCATCAACGTGGTGGTGTGTGCTCATGAAGACACCTCGAC	5288
1856	Qy	GluSerAsnIleValLeuGluAlaGluLeuGluAlaGluLeuGluLeuGluMet	1875
5289	Db	GACAGCAACAGGAGGCGCAGGAGGACGCCAGATGATGCCGAGCTCGAGCTGGAGATG	5348
1876	Qy	---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly	1894
5349	Db	GCCATGGCTGGGCCCTGGCCGAGGCTGCCTACCGGCTCC-----	5390
1895	Qy	ValGluGlyValAsnSerThrAspSerProIleAlaProHisThrThrAlaHis	1914
5391	Db	-----CCGGCGCCCTCGCCGAGGCGCG-----	5414
1915	Qy	IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro-----	1930
5415	Db	---GGAGGGCGGGCGCGG- GGCGCAGACGAGGGCGGCTGTGCGCGGCTGCTACTC	5470
1931	Qy	-----HisProGluGluValProValPro	1938
5471	Db	GCCTGCCCGGACTCCTTGGAGGGGAGCTGACCATCATCGAACCTGTGGGCTCCAT	5530
1939	Qy	LeuGlyProAspLeuLeuThrValArgIleSerGlyValSerArgThrHisSerLeuPro	1958
5531	Db	CTTCCACCACTACTCTCTCGCTGCGGCTGCAAGAGTGCA-----CCA	5575
1959	Qy	AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly	1978
5576	Db	CGACAA-----GCAAGAGTGCAGCTGGCTGAGACGGA	5608
1979	Qy	TrpGlyLeuProIleAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp	1998
5609	Db	GGCTTCTCCTGAACTCAGACAGGCTCTCGTCCATCTGCTGGTGACACCTGAGTCT	5668
1999	Qy	ThrSerCysIleLeuGlnLeuProIleAspValHisTyrLeuLeuGlnProHisGlyAla	2018
5669	Db	CGAGGA-----CCCCACAGCCTG	5686
2019	Qy	ProThrTrpGlyAlaIleProLys-----	2026
5687	Db	CCACCTGG-----CCGCAAGGACAGCAAGGGTGAGCTGACCCACCTGAGCCCAT	5737
2027	Qy	---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla	2045

RESULT 14

RESOL 14
US-10-425-800-1

; Sequence 1, Application US/10425800

; Publication No. US20030180886A1

; GENERAL INFORMATION:

; APPLICANT: Dietrich, Paul S.

APPLICANT: McGivern, Joseph G

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/10/425,800

; CURRENT FILING DATE: 2003-04-29

; PRIOR APPLICATION NUMBER: US/09/404,650

; PRIOR FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

: SEO ID NO 1

: LENGTH: 6816

TYPE: DNA

ORGANTSM: Homo sapiens

ORGANISM.
FEATURE.

NAME/KEY:	CDS
FEATURE:	


```
Db 5797 ATCCAGAGAACTTCTCTGT---GTGAGATGGAGGAGATCCCAT-----TCAACC 5841
Qy ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIle 2085
Db 5842 CTGTCCGGTCTCTGGCTGAACATGACA----- 5868
Qy 2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
Db 5869 -----GCAGTCAAGCACCACCCCAAGTCCCTTCT 5895
Qy 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSerLeu 2125
Db 5896 CCC-----CGGATGCCCTCCAGCC----- 5913
Qy 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGlu 2145
Db 5914 -----CTCTCTGCCCATGCCAGCCAGCTTCTTCACCCCTG 5949
Qy 2146 ProLeuPhePro-----ArgAspLeuLysCysTyrSerValGluThrGlnSerCys 2163
Db 5950 CAGTGTCTGCCAGCAGAAAGGCGCAGAAAAGGCACTGGCACTGGAACCCCTCCCAAGA 6009
Qy 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
Db 6010 TTGGCGCTG-CAGGGCTCTCTGGGCATCT-----CTGCGGTCAACCAAGGTCAACTGT 6059
Qy 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
Db 6060 ACCCTCTCCGGCAGGCCACCGGAGGACACAGCTGCTGGAGCCGACCCCGCAGAG-CTC 6118
Qy 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProSer 2219
Db 6119 CGCGGGCAGCTCGACACCGCTCGAGGACAGCTGACCCCTGAGCGACAGCCCGCGCG 6178
Qy 2220 IleSerIleAspProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
Db 6179 -----TGCCCTGGGGCCCGCCGCGCTCTCTCCAGGACCCCGGC 6217
Qy 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCTGTCCCCCGCTCGCCCGCTGAGCCTGGCGGCGCGGGCCTCTTCAGCCT 6277
Qy 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGGCTGGGGCGCATCAGCGCAGCAGCAGCGGGGGCTCCACCAGCCCGGGCTG 6337
```

RESULT 15

```
US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. US2002015091A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McSivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3
Alignment Scores:
```

```
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 62.0% Conservative: 235
Best Local Similarity: 52.0% Mismatches: 500
Query Match: 45.1% Indels: 402
DB: 3 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-935-541-3 (1-6855)

Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCTTCTCATCTGCAGCAGCCCGCCGCTGAGCAGGAGTCCACCACGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyValAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCTGGAGAGCTCTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCTCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCTTCTGCTGCGCAGACCCAGCCAGCCCGCGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCAATGAAGTGGTGTGCAACCCGCTGTTGAATGTCTCAGCATGCTGGTGTATCCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCTGACACTTGGCATGTACCAGCCGTCGACGACCATGGAGTGCCTGCTCGACCGC 524
Qy 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaValIleGluMetVal 165
Db 525 TGCAAGATCTGCGAGGCTTTTGATGACTTCATCTTTATCTTCTTTCATGAGATGGTGTG 584
Qy 166 ValIleMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
Db 585 CTCAAGATGTGGCCCTGGGGATTTTGGCAAGAAGTGTACTACCTCGGGGACACATGGAAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCTGGATTTCTTCATGTCATGGCAGGATGCTCGAGTACTCTCTGGACCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTGAGCATCCGACCGTGGCTGCTGAGGCGCTCAAAGCCATCAACCGC 764
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCCATGATGGCGATCTGGTGAACCTGCTCTCGACACACTGCCCATCTCGGGGAA 824
Qy 246 ValLeuLeuLeuCysPhePheValPhePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCTCTGCTCTGCTTCTTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGCGCTGTGCGTAACCGCTGCTTCTGAGGAGAACTTCACCATACAAGGGGATGTG 944
Qy 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerCln 305
Db 945 GCCTTGGCCCCCATACTACCGAGCGGAGGATGATGAGTGCCTTCTCATCTGCTCCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGly 325
Db 1005 TCGGGCGACAATGGGATAATGGGCTGCGATGATCCCCCGCTCAAGGAGCAG----- 1058
```

Qy 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCCGTAGTGTGCTCTCCAGGACGACGTCTACGACTTTGGGGGGGGGGCCAG 1115
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATCCAGCGGCTCTGTGTCACTGGAACCGTTACTACATGTGTGCGCAGC 1175
Qy 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCCAAACCCCAAGGGTGCCATCACTTTGACAACTCGGTATGCTTGGATT 1235
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCCAGGTGATCACTCTGGAAGCTGGGTGGAGATCATGTACTAGTGATGGAT 1295
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1296 GCTCACTCTTCTACAACTTCATCTTCACTCTGCTTATCATAGTGGGCTCTCTTTC 1355
Qy 418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTCTGTGTATAGCGACCCAGTTCTCGGAGACCAAGCAACGGGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATCTGGAGACGGCAGCGCTACCTGTCC---TCAGCACCGGTGGCCAGC 1472
Qy 458 PheSerGluProGlySerCysTyrXGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TACGCCGAGCCTGGCAGCTGTCTACGAGGAGATCTTCCAGTAGTGTGTCACACATCTTGC 1532
Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCCCTGGGCTCTACACGGCCCTGCAG 1574
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
Qy 518 HisArgArgLeuSerValHisLeuValHisHisHisHisHisHisHisHisHisHis 537
Db 1578 ---CGGCCCGAGCCCTG----- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGGCCCGCCCAACCTGGGCC----- 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CACGCCAAG-----GAGCCC 1643
Qy 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACCACTGTGCGCGCAACATAGCCCCCTGGATGCG----- 1685
Qy 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACC----- 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGTGTCAG-----CCCATCCCGCCACGCTGGCTTCC----- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCAGCTGCCCTTGTGTCGAG 1757
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696

Db 1758 CATGAGACCGCCGGCGGCTCTGGGCTGGGACGACCGCTCGGGCCAGAGGGCTCG 1817
Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCGGCTGGTGGGAGACGAGGCG----- 1853
Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACCGGGCC-----CGGAGCAGCGAGGACGAGGCTCTCTCAGAA 1898
Qy 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGAGAGGAGGAGGAGGAGGAGCAG-----GCGGATGGGGCG 1940
Qy 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCTGGCTGTGCGGGGATGTGTGGCGGAGACGCGAGCCAAAGCTGCGCGCATCTGGAC 2000
Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGATCATGATGGCCATCTTGTCAACACCGTCGATGGGCG 2060
Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCGAGCACCGAGCAGCGGAGGAGTGACCAACATCTCTGGAGATCTGCAATGTGTC 2120
Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPheGly 834
Db 2121 TTCACGAGCATGTTTGGCCCTGGAGATGATCTCGAAGCTGGCTGCTTGGCTCTTCGAC 2180
Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrpGlu 854
Db 2181 TACTTCGTGTAACCCCTACAACATCTTCACAGCATATTGTCAATCATCAGCATCTGGAG 2240
Qy 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCTGGGGCAGCGGCGGCTGGCTGTCGGGTCTGCGGACCTTCCGGCTCTGCGGTG 2300
Qy 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAAACTGGTGGCTCTCATGCTGCGGCGGCGGCTGCTGGTGTCTCATGAAGACC 2360
Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914
Db 2361 ATGACAACTGGGCGACCTTCTGCTGCTGCTGCTGCTCTTCTTCTTCTTCTTCTTCT 2420
Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db 2421 CTTGGGATGCATATTTTGGCTGCAAGTTTCAGCTCGCACCGACACATGGAGACACGGTG 2480
Qy 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCGACAGGAAGAACTTCGACTCCCTGCTGGGCGCATGCTGCTGCTGCTTCCAGATCTC 2540
Qy 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCGAGAGGACTGGAACTGCTTCTTCAATGGCATGGCTCCACTTCTCTCTCTCTCTCT 2600
Qy 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2601 TCCCTCTACTTGTGCGCCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTGCTGTG 2660
Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluIleAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTCTGGTGGAGGCTTCCAGCGGAGGCTGACGCCAATCGCTCTCTTCTCTCTCTCT 2720
Qy 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGACTCATCCAACATAGAGAGTTCATAGCTCCAGGAGGCTTGACAGCAGC 2780
Qy 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043

Db 2781 GGAGATCCCAAG-----CTCTGCCCAATCCCATGACCCCAATATGGGCACCTGGACCCC 2834
Qy 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGGCACCTAGGTCTCTGGGCTGGCGGACCTGCC--- 2885
Qy 1060 HisProLysSerSerThrGlyValGlyAlaLeuLeuGlySerGlySerArgThr 1079
Db 2886 ---CCCCGACTCTCACTGCAGCGGACCCCATGCTGGTGGCCCTCCGAAAGAGC 2942
Qy 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCAATGCTCTA-----GGAGAGATGAGCTATGACACGCGCTCCCTGTCAGC 2993
Qy 1100 AlaArgSerSerProHisSerProTIPSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCGGAGCTCTACTACGGGCCATGGGGCGGACGCGCGCTGGGCCAGCGCTCGCTCC 3053
Qy 1120 SerArgHisSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
Db 3054 AGCTGGAAAC-----AGCCTCAAGCACAAGCGCGCTCGCGGAGCAT 3095
Qy 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGCTCTCTCGGAGCGCGCGCGCGCGCTCTCGGAGGTTGCGCGGAGC 3155
Qy 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGCG 3215
Qy 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATCTGGCGCACCGCCACCGCCACCGCGGACGCTGCTCCCTCGACAAAGGAC 3275
Qy 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGACCTGGCGGAGCTGGTGGCGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCG 3335
Qy 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 CGCGCAGCG 3389
Qy 1220 AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu 1238
Db 3390 GCCAAAGACGCTTCCACCAAGATGGCGCACCGCGGAGATCGCGGGAGGATGAGGAGAA 3449
Qy 1239 GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys 1258
Db 3450 ATCGACTACACCTGCTTCCGCGTCCGCAAGATGATCGACGCTTATAGCCCGACTGG 3509
Qy 1259 CysArgGluArgAspSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeu 1278
Db 3510 TGGAGTCCGCGAGACTGTGTCTACTCTCTCTCTCCGAGACAGGTTCCGGGTC 3569
Qy 1279 LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe 1298
Db 3570 CTGTGTCAAGACATTATGGCCACAAACTCTTCGACTACGTCTGCTGGCTTCTCATCTTT 3629
Qy 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
Db 3630 CTCAACTGCATCAACATCGCCCTGGAGCGGCTCAGATCGAGCGCGGACCGGACCGC 3689
Qy 1319 IlePheLeuThrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrVal 1338
Db 3690 ATCTTTCTACCGGTCCAACTACTATCTTCAGGCCATCTTCGTGGCGGAGATGACATTG 3749
Qy 1339 LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuArgSerTrpAsn 1358
Db 3750 AAGGTAGTCTCGCTGGCGCTGTACTCTCGCGGAGCAGCGGTACCTACGACGAGCTGGAAC 3809
Qy 1359 ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1378
Db 3810 GTGCTGATGGCTTTCTTGTCTTCTGCTTCATCATGACATCGTGGTGTCCCTGGCGCTCA 3869

Qy 1379 AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398
Db 3870 GCCGGGGAGCCCAAGATCTTGGGGGTCTCCGAGTCTTCGGGCTCTCGGCACCCCTACGC 3929
Qy 1399 ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1418
Db 3930 CCCCTGCGTCTCATCAGCGGGCGCGGCTTGAAGCTGTGTGGAGACACTCATCTCC 3989
Qy 1419 SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly 1438
Db 3990 TCCCTCAAGCCCATCGGCAACATCGTCTCATCTGCTGTGCCCTTCTTCATCACTTTGGC 4049
Qy 1439 IleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArg 1458
Db 4050 ATCTTGGGAGTGCAGCTCTTCAAGGCCAAGTTCTACCATGCTCTGGGCGTGGACCCGC 4109
Qy 1459 AsnIleThrAsnLysSerAspCysAlaGluAsaSerTrpArgTrpValArgHisLysTrp 1478
Db 4110 AACATCACCACCGCTCGGACTGCATGGCGGCCAACTTACCGCTGGGTCCATCAAAATAC 4169
Qy 1479 AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 1498
Db 4170 AACTTCGACAACTGGGCCAGGCTCTGATGTCCCTCTTGTCTGGCATCCAAGATGGT 4229
Qy 1499 TrpValAspIleMetTrpAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet 1518
Db 4230 TGGGTGAACATCATGTACATGACTGGATGCTGTTGCTGTGGCAGCAGCCTGTGACC 4289
Qy 1519 AsnHisAsnProTrpMetLeuLeuTrpPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db 4290 AACCCAAACCCCTGGATGCTGTGCTACTTCATCTCTCTCTGCTCATCTGTCAGCTTTT 4349
Qy 1539 ValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGln 1558
Db 4350 GTCTCAACATGTTTGGGTGTGTGGTGGAGAACTTCCCAAGTCCCGGAGCACCAG 4409
Qy 1559 GluGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg 1578
Db 4410 GAGGTGAAGAGGACGCGCGCTGAGGAGAGCGGCTGCGCGCTGGAGAGAGAGCGC 4469
Qy 1579 ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTrpTrpSerAspTrpSer 1598
Db 4470 CGG-----AAGGCCACGCGCTGCCCTACTATATGCCATTTGT 4508
Qy 1599 ArgPheArgLeuLeuValHisHisLysThrSerHisTrpLeuAspLeuPheIleThr 1618
Db 4509 CACACCGGCTGTCTCATCTCATCTGTCACGACGACCTTACCTGGACATCTTCATCACC 4568
Qy 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTrpGlnGlnProGlnIle 1638
Db 4569 TTCATCATCTCGCTCAACGTTGTCACCATGCTCCCTGGAGCACTACAATACGCCACCTCC 4628
Qy 1639 LeuAspGluAlaLeuLysIleCysAsnTrpIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACGCGCTCAAGTACTGCAACTATATTTTCCACCACTGTCTTTGTGGTGGAGCT 4688
Qy 1659 ValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeu 1678
Db 4689 GTCTGAAGCTGTGTGGCAITTTGCTGAGGCGCTTCTTCAAGGACCGATGGAACCACTG 4748
Qy 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsn 1698
Db 4749 GACTTGGCCATTTGCTACTGTCTGATCATGGGCATCACCTGGGAGGATCGAGATCAAT 4808
Qy 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db 4809 GCGGCGCTGCCCATCAATCCACCATCATCCGATCATGAGGTTCTGCGCATTTGCCGA 4868
Qy 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db 4869 GTCTGAAGCTGTGTGAAGATGGCCACAGGAATGCGGCGCTTCTTGGACACGCTGGTCA 4928

Qy	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheLeuPheAla	1750
Db	4929	GCCTTGGCCAGGTGGGCAACCTGGGGCTCCTCTTCATGCTGCTCTCTTCATCTATCTGCT	4988
Qy	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
Db	4989	GCTCTGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACACGACGAGAACCCGCTCGAGGGC	5048
Qy	1779	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATGAGCCGGATGCCACTTCGAGAACTTCGGCATGGCCTTCTTCACACTTTCAGGTC	5108
Qy	1799	SerThrGlyAspAsnTrpAsnGlyIleMetIleAspProSerArgAspCys---AspGln	1817
Db	5109	TCCACGGGTGACAACTGGAACGGGATCATGAAGGACACGCTGCGGGACTGCACCCACGAC	5168
Qy	1818	GluSerThrCysTyrrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1835
Db	5169	GAGCGCAGCTGCCTGACGACGCTGCAGTTGTGTGCGCGCTGTACTTCTGTGAGCTTCGTG	5228
Qy	1836	LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu	1855
Db	5229	CTCACCGCGAGTTCTGTGCTCATCAACGTGTGTGTGTGTCTCATGAAGACCTTCGAC	5288
Qy	1856	GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMet	1875
Db	5289	GACAGCAACAGGAGGCGCAGGAGGACGCCGAGATGGATGCCGAGCTCGAGCTGGAGATG	5348
Qy	1876	---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro---	1893
Db	5349	GCCCATGGCTTGGCCCTGGCGCCGAGCTGCCTACCGGCTCCCGGGCGCC---CCTGGC	5405
Qy	1894	-----GlyValGluGlyValAsnSerThrAsp-----	1902
Db	5406	CGAGGGCGGGAGGGCGGGCGGGGGCGCACACCGAGGGCGGCTGTGCCGGCGCTGC	5465
Qy	1903	---SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla	1917
Db	5466	TACTCGCTGC-CACAGGAGAACCTGTGGCTGGACAGCGTCTCTTTAATCATCAAGGACTC	5524
Qy	1918	AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVal	1937
Db	5525	CTTGAGGG---GGAGCTGACCAT-----CATCGACAAACCTGTCGGGCTC	5566
Qy	1938	ProLeuGlyProAspLeuLeuThrValArgLysSerClyValSerArgThrHisSerLeu	1957
Db	5567	CATCTTCCACACACTCTCTCTCGCTCGCGCTGCAAGAAGTGCA-----	5611
Qy	1958	ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg	1977
Db	5612	CCACGACNA-----GCAAGAGGTGCAGCTGGCTGAGAC	5644
Qy	1978	GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla	1997
Db	5645	GGAGGCTTCTCCCTGAACTCAGACAGGTCTCTGCTCCATCCTGTGGTGACGACCTGAG	5704
Qy	1998	AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly	2017
Db	5705	TCTCGAGGA-----CCCCACAGC	5722
Qy	2018	AlaProThrTrpGlyAlaIleProLysLeuProPro-----	2029
Db	5723	CTGCCCACCTGG-----CCGCAAGACAGCAGGGTGAGCTGACCCACTGAGCC	5773
Qy	2030	-----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla	2044
Db	5774	CATGCGTGTGGAGACCTGGGCGCAATGCTTCTCCCTTGT-CCTCTACGGCGCTCTCGC	5832
Qy	2045	AlaIleArgThrAspSerLeuAspValClnGlyLeuGlySerArgGluAspLeuLeuSer	2064
Db	5833	CGGATCCACAGAACTTCTGT---GTGAGATGGAGGAGATCCCCAT-----TCA	5877
Qy	2065	GluValSerGlyProSerCysProLeuThrArgSerSerPheThrProGlyGlySerSer	2084

Db	5878	ACCCTGTCGGGTCTCTGGCTGAACATGACA	5907
Qy	2085	IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleAlaArgLeuPro	2104
Db	5908	-----GCAGTCAAGCACCCCCAAGTCCCT	5931
Qy	2105	AlaProCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSer	2124
Db	5932	TCTCCC-----CGGATGCTCCAGCC-----	5952
Qy	2125	LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu	2144
Db	5953	-----CTCTCTGCCATCGCAGCGCGAGTCTTCCACC	5985
Qy	2145	GluProLeuPhePro-----ArgAspLeuLysCysTrpSerValGluThrGlnSer	2162
Db	5986	CTGCAGTGTCTGCACGACCCAGAAAGGCCACTGGCACTGGGAACCTCCCCA	6045
Qy	2163	CysArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSer	2182
Db	6046	AGATTGCGCTG-CAGGGCTCTCTGGCATCT-----CTGCGGTCAACAAGGGTCAAC	6095
Qy	2183	CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer	2198
Db	6096	TGTACCTCTCTCGGACGGCCACCGGAGCGACACGTCTGACGCGACCCCGACGAG-	6154
Qy	2199	LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro	2218
Db	6155	CTCCGCGGGCAGCTTGACAGCACCGCTCGAGGACAGCGTCACTGAGCGACGCCCGC	6214
Qy	2219	SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro	2236
Db	6215	GCG-----TGCCCTTGGGGCGCCCGCGCTGCTCCAGGACCCCG	6253
Qy	2237	GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer	2256
Db	6254	GGCGGGCTGTGCCCCCGCTGCCGCCCTGAGCGCTCGGGCGCGGGGCTCTTTCAG	6313
Qy	2257	ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly	2276
Db	6314	CCTCGGGGGCTGCGGGCGCATCAGCCGACCCACAGCAGCGGGGGCTCCACGACCCGGG	6373
Qy	2277	Leu 2277	
Db	6374	CTG 6376	

Search completed: July 10, 2006, 09:44:03
Job time : 5447.64 secs

QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGCACAAGCTGCTGGAGACACAGATACAGTGCTGCCAAAGCTCTTGCAGA	2320
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2321	TCTCCAGCCCTTGCTTTGAAAGCAGACAGATGGAGCCTGTGTCTCAGACAGCTGCCCTACT	2380
QY	702	ysAlaArgThrGlyAlaGluProGluSerAlaAspHisValMetProAspSerAspS	722
Db	2381	GTCCCCGGCGGGCAGGGAGGTGGAGCTGCCCGACCGTGAAATGCCTTGACTCAGACA	2440
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHis	742
Db	2441	GCAGGCGAGTTTATGAGTTCACACAGGATGCCCGACACAGCGACCTCCCGGACCCCCACA	2500
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2501	GC---CGGCGCAACCGAGCCTGGGCCAGATGCAGAGCCAGCTCTGTGCTGGCCTTCT	2557
QY	762	rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	2558	GGAGGCTAAATCTGTGCACCTTCGAAAGATTTGGGACAGCAAGTACTTTGGCGGGGAA	2617
QY	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802
Db	2618	TCAATGATCGCCATCCTGGTCAACACACTCAGCATGGGCATCGAATACACAGCAGCCCG	2677
QY	802	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2678	AGGAGCTTTACCAACGCCCTAGAAATCAGCAACATCGTCTTACACAGCCTCTTTGGCCCTGG	2737
QY	822	luMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
Db	2738	AGATGCTGCTGAAGCTGCTTGTGTATGTCCTTGGCTATCATCAAGAAATCCCTTACAA	2797
QY	842	lePheAspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnGlyG	862
Db	2798	TCITCGATGTTGTCATTTGTTGTCATCAGCGTGGAGATCGTGGCGCAGCAGGGGGCG	2857
QY	862	lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	2858	GCCTGTGCGTCTGCGGACCTTCGCGCTGATGCGTGTGCTGAAGCTGGTGGCTTCTGTC	2917
QY	882	roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	2918	CGGCGCTGCAGCGGACGCTGGTGTGCTCATGAAGACCATGGACACGTGGCCACCTTCT	2977
QY	902	ysMetLeuLeuMetPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
Db	2978	GCATGCTGCTTATGCTCTTTCATCTTCATCTTCAGCATCTGGGCATCATCTCTTCGGCT	3037
QY	922	ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
Db	3038	GCAAGTTTGGCTCTGAGCGGATGGGACACCCCTGCCAGACCCGGAAGAAATTTTGACTCCT	3097
QY	942	eulLeuTpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTyrAsnLysValL	962
Db	3098	TGCTCTGGGCGCATCGTCATGCTCTTCAGATCTTCAGACCCAGGAGACTTGAACAAAGTCC	3157
QY	962	eutYrAsnGlyMetAlaSerThrSerSerTyrAlaAlaLeuTyrPheIleAlaLeuMetT	982
Db	3158	TCTACATGATGGCTCCACCGTCTGCTGGCGGGCCCTTTATTTTCATTTGCCCTCATGA	3217
QY	982	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
Db	3218	CCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTGGCCATTCCTGGTGGAGGGCTTCCAGG	3277
QY	1002	laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG	1022
Db	3278	CGGAGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTTCTTCACCCAGCCTGGATG	3337

QY	1022	lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA	1042
Db	3338	GTGATGGGACAGAAAGATGCTTGGCCTTGTGTCTCCCTGGGAGAGCACCCGAGCTGC	3397
QY	1042	rgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetSerHisProL	1062
Db	3398	GGAAGAGCCTGTGCGCCTCTCATTCACACGGCCGCCACCCATGTGCTGCTGCCCA	3457
QY	1062	ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSerS	1082
Db	3458	AGAGCACAGCAGCGGCTGGCGAGCGCTGGCCCTCGCTCGCGCCGACACAGCAGCA	3517
QY	1082	erGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSerAlaArgS	1102
Db	3518	GCGGGTGGCAGACCTGGGGCGGCC--CACAGATGAAGTCAACCGCCAGCGCCGCCA	3574
QY	1102	erSerProHisSerProTyrSerAlaAlaSerSerTyrThrSerArgArgSerSerArgA	1122
Db	3575	GCTCTCGCACAGCCCTGGAGCGCTGCAAGCAGCTGGACAGCAGCGCTCCAGCCGGA	3634
QY	1122	snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL	1142
Db	3635	ACAGCCTCGGCCGTGCCACAGCCTGAGCGGAGAGCCCAAGTGGAGAGCGCGGTCCC	3694
QY	1142	eulSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAspArgA	1162
Db	3695	TGTTGTGGGAGAGGCCAGGAGCAGCAGATGAAGAGGAGAGCTCAGAAGAGAGCGGG	3754
QY	1162	laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerS	1182
Db	3755	CCAGCCTCGGGCAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGAGGCCAAGAGTT	3814
QY	1182	erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS	1202
Db	3815	CTTTGACCTGCCAGACACTGCAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAG	3874
QY	1202	erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT	1222
Db	3875	GGTCTGCTTCTGAGCACCAGGACTGCAATGGCAAGTCGGCTTCAGGGCGCTGGCCCGGG	3934
QY	1222	hrLeuArgThrAspAspProGlnLeuAspGlyVAspAspAspAsnAspGluGlyAsnLeuS	1242
Db	3935	CCCTGGCGCTGATGACCCCCCACTGGATGGGATGACCGCGATGACAGGGCAACCTGA	3994
QY	1242	erLysGlyGluArgIleGlnAlaTyrPValArgSerArgLeuProAlaCysCysArgGluA	1262
Db	3995	GCAAGGGGAACGGTCCGCGCTGGATCCGAGCCGCACTCCCTGCTGCTGCCTCGAGC	4054
QY	1262	rgAspSerTyrSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCysHisA	1282
Db	4055	GAGACTCTGGTCAGCCTACATCTTCCTCTCAGTCCAGGTTCCGCTCTCTGTGTCAAC	4114
QY	1282	rgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI	1302
Db	4115	GGATCATCACCAAGATGTTCCACCACGTGTCTTGTTCATCATCTTCTTAACTGCA	4174
QY	1302	leThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuT	1322
Db	4175	TCACCATCGCATGGAGCGCCCAAAATTCACCCACAGCGCTGAACGCATCTTCTCTGA	4234
QY	1322	hrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValValA	1342
Db	4235	CCCTCTCCAATTACATCTTCACCGCAGTCTTCTGGCTGAAATGACAGTGAAGTGGTGG	4294
QY	1342	laLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTyrAsnValLeuAspG	1362
Db	4295	CACCTGGCTGGTCTTCGGGAGCAGCGGTACCTTCGGAGCAGTGTGAAACGTGTGACG	4354
QY	1362	lyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyT	1382
Db	4355	GGCTGTGGTGCTCATCTCCGTCATCGACATCTTGGTGTCCATGCTCTCTGACAGCGCA	4414
QY	1382	hrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgV	1402

Db 4415 CCAAGATCTGGGCGATGCTGAGGGTGTCTGGCGTCTGGCGACCTGGCGCGCTCAGGG 4474
Qy 1402 allleSerArgAlaGlnGlyLeuIysLeuValValGluThrLeuMetSerSerLeuIysP 1422
Db 4475 TGATCAGCGGGCGCAGGGGCTGAAGCTGGTGGTGGAGACGCTGATCTCTCACTGAAC 4534
Qy 1422 rolleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyV 1442
Db 4535 CCATCGGCAACATTTGATGATCATCTGCTGTGCTCTTCATCATTTTCGGCATCTGGGG 4594
Qy 1442 alGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsnIleThrA 1462
Db 4595 TGCAGCTCTTCAAGGAGAGTTTTTCGTGTGCCAGGGCGGAGATACCAAGNACATCACCA 4654
Qy 1462 snLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspA 1482
Db 4655 ATAAATCGGACTGTGCCGAGGCCAGTTACCGTGGGTCCGGCACAAAGTACAACTTTGACA 4714
Qy 1482 snLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspI 1502
Db 4715 ACCTTGGCCAGGCCCTGATGCTCCCTGTTCGTCTTTGGGCTCCAGGATGGTTGGGTGGACA 4774
Qy 1502 leMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnP 1522
Db 4775 TCATGTACGATGGGCTGGATGCTGTGGGCGTGGACAGCAGCCCATCATGAACCCACAACC 4834
Qy 1522 roTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnM 1542
Db 4835 CCTGGATGCTGCTACTCTACTCTCGTTCTCTGCTCAATTGTGGCTTCTTTGCTCGAACA 4894
Qy 1542 etPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG 1562
Db 4895 TGTGTGGGTGTGGTGTGGAGAACCTTCCACAAGTGTCCGACAGCACAGGAGGAAGG 4954
Qy 1562 luAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgSerLysG 1582
Db 4955 AGGCCGGCGCGGGAGAGAGCGCTACGAAGACTGGAGAAAAGAGAAGAGTAAGG 5014
Qy 1582 luLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgL 1602
Db 5015 AGAAGCAGATGGCTGAAGCCAGTGCAAACCTTACTCTCGACTACTCTCCGCTTCGCGC 5074
Qy 1602 euLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleG 1622
Db 5075 TCCTCGTCCACACTGTGACACAGCCACTACCTGGACCTCTTATCACAGGTGTATCG 5134
Qy 1622 lyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluA 1642
Db 5135 GGCTGAACGTGTCACCATGGCCATGGAGCACTACCAAGCAGCCAGATTCTGGATGAGG 5194
Qy 1642 laLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysL 1662
Db 5195 CTCTGAAGATCTGAACCTACATCTTCACTGTCATCTTTGTCTGGAGTCAGTTTTCAAAC 5254
Qy 1662 euValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaI 1682
Db 5255 TTGTGGCCCTTTGGTTTCGTCGGTTCTTCCAGGACAGGTGGAACCAAGCTGGACCTGGCCA 5314
Qy 1682 leValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuP 1702
Db 5315 TTGTGCTGCTCTCCATCATGGGCATCAGCTGGAGGAAATCGAGTCAACGCCCTCGCTGC 5374
Qy 1702 rolleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysL 1722
Db 5375 CCATCAACCCACCACCATCATCCGCATCATGAGGGTGTGCGGATTTCCCGAGTGTGAAGC 5434
Qy 1722 euLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProG 1742
Db 5435 TGCTGAAGATGGCTGTGGGCAATGGGGCGCTGTCTGGACACCGGTGATGACGGCCCTGCCCC 5494
Qy 1742 lnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaLeuGlyV 1762

Db 5495 AGGTGGGAAACCTGGGACTTCTCTTCATGTTGTTGTTTTTTCATCTTTGCAGCTCTGGCG 5554
Qy 1762 alGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgH 1782
Db 5555 TGGAGCTCTTTGGAGACCTTGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGCGCGTC 5614
Qy 1782 isAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyA 1802
Db 5615 ATGCCACCTTTCGAACTTTGGCATGGCCTTCTTAACCTCTTCCGAGTCTCCACAGGTG 5674
Qy 1802 spAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrCyst 1822
Db 5675 ACAATTGAATTGGCATTTATGAAGGACACCCCTCCGGGACTGTGACAGAGTCCACCTGCT 5734
Qy 1822 yrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValL 1842
Db 5735 ACAACAGCGTCATCTCGCTTACTTGTGTCTTGTGCTGACGGCCAGTTCGTGTC 5794
Qy 1842 euValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaL 1862
Db 5795 TAGTCAACGTGGTGATCGCGTCTGTATGAAGCACCTGGAGGAGGACACCAAGAGGCCA 5854
Qy 1862 ysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnP 1882
Db 5855 AGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTCAGCCCCCAGC 5914
Qy 1882 roHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrA 1902
Db 5915 CCCACTCGCACCTGGGCGAGCCCTTCTCTGGCTGGGGTGGAGGGCCCCAGAGCCCCG 5974
Qy 1902 spSerProLysProGlyValAlaProHisThrThrAlaHisIleGlyValAlaSerGlyPheS 1922
Db 5975 ACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACCGAGATCAGCCTCCCATTTT 6034
Qy 1922 erLeuGluHisProThr----- 1927
Db 6035 CCCTGGAGCACCCACGACGAGCAGCTGTTGTGACACCATATCCCTGCTGATCCAGGSGCT 6094
Qy 1927 ----- 1927
Db 6095 CCCTGGAGTGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCACAGGGGCCAGGCCCTCTG 6154
Qy 1927 ----- 1927
Db 6155 CCTTCCCTTCTGCCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAGATGG 6214
Qy 1927 ----- 1927
Db 6215 AGGCTCTGCTCTGACGTGACAGATTTGTGTGTAACCGTCTCTGCTCTTAGCTCTGACGG 6274
Qy 1928 -----MetV 1929
Db 6275 ATGACTCTTTCCTGTATGACATGCACACACTTCTTACTTAGTGCCTGGAGAGCAATATGC 6334
Qy 1929 alProHisProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLysS 1949
Db 6335 AGCCCCACCCACGAGCTGCCA-----GCACAGACTTACTGACTGTGCGAAGT 6385
Qy 1949 erGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerT 1969
Db 6386 CTGGGGTCAGCCGAACGACTCTCTGCCCAATGACAGCTACATGTGTGGCATGGGAGCA 6445
Qy 1969 hrAlaGluArgSerLeuGlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerI 1989
Db 6446 CTGCCGAGGGGCCCTTGGGACAGGGGCTGGGGCTTCCCCAAGACTCAGTCAGGCTCCG 6505
Qy 1989 leLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspV 2009
Db 6506 TCTTGTCCGTTCCTCCAGCCAGCAGATACCAGCTACATCTCTGAGCTTCCCAAAGATG 6565
Qy 2009 alHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProp 2029
Db 6566 CACTCATCTGCTCCAGCCCCACAGCGCCCCCAACCTGGGGCACCATTCCCCAAACTGCCCC 6625

5007 -----AAGGCCAGCGCGGCCCTACTATGCGACTACTCGCCC 5045
1600 PheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGly 1619
15046 ACGCGCGCTCCATTACTCGCTGTGCACCAAGCACTATCTCGACCTCTTCATCACCTTC 5105
1620 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu 1639
15106 ATCATCTGTGTCAACGTATCACCATGTCCATGAGGACATATAACCAACCAAGTCGCTG 5165
1640 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerVal 1659
15166 GACGAGGCCCTCAAGTACTGCACTACGTCTTCAACATCGTGTGTTCCTTCGAGGCTGCA 5225
1660 PheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTyrAsnGlnLeuAsp 1679
15226 CTGAAGCTGGTAGCATTTGGGTTCGTCGGTCTTCAAGGACAGGTGGAAACAGCTGGAC 5285
1680 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu 1699
15286 CTGGCCATCGTGTCTGTCTACTCATGGGCATACGCTGGAGGAGATAGATAGAGGCC 5345
1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719
15346 GCGCTGCCCATCAACCCCAACCATCATCGCATCGCGTGTCTCGCATTTGCCGCTGTG 5405
1720 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739
15406 CTGAAGCTGTCTGAAGATGGCTACGGGCATGCGCGCCCTGCTGGACACTGTGTGTGCAAGCT 5465
1740 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAla 1759
15466 CTCCTCCAGGTGGGAACCTGGGCTCTTTTCATGCTCTCTTTTATCTATGCTGCG 5525
1760 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1779
15526 CTGGAGTGGAGCTGTCTCGGAGGCTGGAGTGCAGTGAAGACAACCCCTGCGAGGCGCTG 5585
1780 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1799
15586 AGCAGGCACGCCACCTTCAGCAACTTCGGCATGGCTTCCTCAGCTGTTCGCGTGTCC 5645
1800 ThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys-----Asp 1816
15646 ACGGGGACAACTGAACGGGATCATGAAGACACGCTGCGCGAGTGTCTCCGTGAGGAC 5705
1817 GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu 1836
15706 AAGCACTGCCGTGAGCTACTGCGGCGCTGTGCGCGCTACTTCTGCTGACCTTGTGTCTG 5765
1837 ThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGlu 1856
15766 GTGGCCCAAGTTCGTGCTGAACGTGTGTGTGGCGGTGCTCATGAACCACTGGAGGAG 5825
1857 SerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuMetLys 1876
15826 AGCAACAAGGAGGACGAGGAGTCCGAGCTGGACGCGGAGATCGACTGGAGATGCGG 5885
1877 ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlu 1896
15886 -----CAGGGCCCCGGG 5897
1897 GlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly 1916
15898 AGTGACGCCCGGTGGACGCGGAGGCT----- 5927
1917 AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValPro 1936
15928 -----CCCTTCCCCAGGAGAGTCCG 5948
1937 ValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer 1956
15949 GCGCGCAGGAGCGCCCAAACTGGTTGCAAGAGGTGTCGTTGTCCAGGATGCTCTCG 6008

1957 LeuProAsnAspSerTyrMetCysArgAsnGlySerThrAla----- 1970
6009 CTGCCCCAACACAGCTACATGTTTCAGGCCCGTGTGTGCTCGCTCGGCGCCACCCCGCGC 6068
1971 -----GluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGly 1987
6069 CCGCTGCAGAGGTGGAGATGGAGACCTATGGGCGCGCACCCCC-----TTGGGC 6119
1988 SerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuLeuGlnLeuProLys 2007
6120 TCCGTTCCCTCTGTGCACTCTCCGCGCGCAGAGTCTGTGCTCCCTCCCATATCCCATTTG 6179
2008 AspValHis-----TyrLeuLeuGlnProHisGlyAla 2018
6180 GCTGTGTGTCGCCAGCAGAGCGGCGAGCCCTCCACGCCCTGTCCCTTCGGGGGACA 6239
2019 ProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2038
6240 -----GCCCGCTCCCCCAGTCTCAGCGG 6263
2039 ProLeuArgArgGlnAlaIleAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2058
6264 CTGCTCTGCACACAGGAGGTGTGCACACCGATTCCTTGAAGGGAAG---ATTGACAGC 6320
2059 ArgGluAspLeuLeuSerGluVal-----SerGlyProSerCysProLeuThr 2074
6321 CCTAGGACACCTCGGATCTCTGCAGAGCTGTGTGAGAAACCCCGGTGAGCCCGTGACC 6380
2075 ArgSerSerPheTrpGlyGlySerSerIleGlnValGlnArgSerGlyIleGln 2094
6381 CAG-----GGGGCTCCCTGCAGTCCCCACCACTGCCCGCCCGCC 6422
2095 SerLysVal-----SerLysHis-----IleArgLeuProAlaPro 2106
6423 GCCACGCTCCGCACTCTGTAAGCATACCTTCGGACAGCGCTGCGTCTCCAGCCGCGCGCG 6482
2107 CysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSerLeuGlu 2126
6483 GCGCCAGCGGAGGAGGCGGAGCTCGACCA----- 6518
2127 LeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro---SerSerGlnGluGlu 2145
6519 GCGCAGCAGGAGGTGAGCCACATCACCAGCTCCGCTCGCCCTGCGCACCCACAGCCGAG 6578
2146 ProLeuPhePro-----ArgAspLeuLysCysTyr 2156
6579 CCCCATGCCCCGAAGCTCTCCGCTGCGCGCGCGAGCGGACCTGCGCAGGCTCTAC 6638
2157 SerValGluThrGlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArg 2176
6639 AGCTGTGATGTCAGGGCTTCTCGACACGCGGCG---CGGCGACAGCAGCAGTGGCGG 6695
2177 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerPro 2196
6696 CCCTCGCGGAG-----CTGGCAGCGGGGAG-----CCTGGGGAG 6731
2197 SerSerLeuGlyGlyGlnProLeuGlyGlyPro-----GlySerArgProLysLys 2214
6732 GCGAAGCGCTGGGCG---CCTGAGCGCGAGCCCGCTGTGGTGGCGCAGAAAGAGAG 6788
2215 LeuSerProProSerIleSerIleAspProPro---GluSerGlnGlySer---ArgPro 2232
6789 ATGAGCCCCCTGCACTCTCGTGGAAACCCCTTCGGGAGGACGAGGGCTCTCGCGCGGCC 6848
2233 ProCysSerProGly-----ValCysLeuArgArgAlaProAla----- 2246
6849 TCCGCGGAGGCGCGGCGAGCACCACTGAGGGCGAGACCCCGCTCTGTGTGAGGCCACG 6908
2247 -----SerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSer 2264
6909 CCTCACAGGGACTCCCTGGAGCCCAAGAGGGCTCAGGCGCGGGGGGAGCCCTGACGCC 6968


```
Qy 2265 -----ProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6969 AAGGGGAGCGCTGGGCCAGGCTCTCTGCGGGCTGAGCACCTTGACCGTCCCGAGCTTT 7028
Qy 2278 SerSerAspProThrAspMet-----AspPro 2286
Db 7029 GCCTTTGAGCGCTGGACCTCGGGTCCCGCAGTGGAGACCT 7070

RESULT 3
US-11-350-336-3
; Sequence 3, Application US/11350336
; Publication No. US20060135751A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/11/350,336
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
US-11-350-336-3

Alignment Scores:
Pred. No.: 1,31e-74 Length: 7376
Score: 1743.50 Matches: 660
Percent Similarity: 37.9% Conservative: 362
Best Local Similarity: 24.5% Mismatches: 882
Query Match: 14.5% Indels: 792
DB: 8 Gaps: 83

US-09-611-257A-24 (1-2287) x US-11-350-336-3 (1-7376)

Qy 5 ArgValProArgCysValArgThrProProLeuArg-----GlySerAlaArg 20
Db 84 CGCGCCCGCGC-----CCTCCCTGCGGGCGCGCTGGCGCGGGGATGCACGC 131
Qy 21 ProSerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu 40
Db 132 GGGGCGCGGAGCCAT--GGTCCG-----CTTCGGGAGCAGCTGGCGCGCGCTATGG 183
Qy 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
Db 184 AGGCGCGCGCGGAGAGCGGGCCG-----GGCGCGCGGGCGCGCGGGGGGG 237
Qy 61 ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla 80
Db 238 CCCGGGTCCCGGGGGCTGAGCCCGCGCGCGCTCTCTACAAGCAATCGATCGCGCA 297
Qy 81 GluGlyLeuProTyrProAlaLeuAla-ProVal----- 91
Db 298 CGCGCGCGGACCATGGCGCTGTAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGT 357
Qy 92 -----ValPheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgTh 109
Db 358 CAACCGCTCGCTCTTCGTTTCAGCGAGGACCAACGCTCGTCCGCAAAATACGGAAGCGCAT 417
Qy 109 rValCysAsnProTrpPheGluArgValSerMetLeuValLeuLeuAsnCysValTh 129
Db 418 CACCGAGTGGCTCCATTTCGAGTATATATCTCTGGCCACCATCATCTGCCAACTGCATCGT 477
```

```
Qy 129 rLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLe 149
Db 478 GCTGGCCCTG-----GAGCAGCACCTCCCTGATGGGACAAACGCCCATGTC 525
Qy 149 uGlnAlaPheAspAsp-----PheIlePheAlaPhePheAlaValGluMetValva 166
Db 526 CGAGCGGCTGGACGACACACGAGGCCCTATTTTCATCGGATCTTTTGTCTCGAGCAGGAT 585
Qy 166 lLysMetValAlaLeuGly--lIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAs 185
Db 586 CAAATCATCGCTCTGGCTTTGTCTTCCACAGGGCTCTTACCTCGGAGACGCTGGAA 645
Qy 185 nArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer-----LeuAs 202
Db 646 CGTCATGAGCTTCGTGCTGCTCTCACAGGATCCTTGCACGCGCTGGAAGTACTGCTGA 705
Qy 202 pLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAl 222
Db 706 CCTGCCA-----ACACTGAGGGCTGTGCTGTGCTGAGGCCCTTGAAGCT 750
Qy 222 alIeAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMe 242
Db 751 GGTGCTCTGGGATTCCAAGTTTGAGGTGGTCTCAAGTCCATCATGAAGGCCATGGTTC 810
Qy 242 tLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyVa 262
Db 811 ACTCTGCAGATTGGGCTGCTCTCTCTTTTGGCATCTCTCATGTTTGCATCATGTCCT 870
Qy 262 lGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuPr 282
Db 871 GGAGTTCTACATGGCAAGTTCCACAAAGGCTGTGTTT-----CC 909
Qy 282 oLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIl 302
Db 910 CAACAGCACAGATCGGAGCCCGTG----- 934
Qy 302 eCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGl 322
Db 934 ----- 934
Qy 322 yGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAs 342
Db 935 -----GGTCACTTCCCTCTGGCAAGAGAGCCCGCGCGCTGTGCGAGGCGCA 984
Qy 342 nThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnPr 362
Db 985 CACTGAGTGC-----CGGAGTACTGGCCA-----GGACC 1014
Qy 362 oPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnVa 382
Db 1015 CAACTTTGGCATCACCAACTTTGACAATATCTGTTTGGCCATCTTGACGGTGTTCAGTG 1074
Qy 382 lIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp---AlaHisSerPh 401
Db 1075 CATCACCATCGAGGGCTGGACTGACATCTCTATAATACAAACGATCGCGCGCAACAC 1134
Qy 401 eTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLe 421
Db 1135 CTGGAATGGCTCTACTTTCATCTCTCATCATCGGCTCTCTTCTTCATGCTCAACCT 1194
Qy 421 uCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer----- 438
Db 1195 GGTGCTGGGCTGCTCTCGGGGAGTTTGGCAAGGAGGAGAGGGTGGAGAACCCCGC 1254
Qy 439 -----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLe 455
Db 1255 CGCCTTCCTGAAGCTCGCGCGAGCAGCAGCATCGAG----- 1291
Qy 455 uAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeuValTyrIl 475
Db 1292 -----CGAGAGCTCAACGGGTACCTTGGATGGAT 1320
```

Qy	475	eLeuArgLysAlaalaArgLeuGluValSerArgAlaIleGlyValArgAlaGl	495
Db	1321	CTTCAAGCGGAGGAAGTCATGCTGGCCGAGGAGAC-----	1357
Qy	495	yLeuLeuSerSerProValalaaArgSerGlyGlnGluProGlnProSerGlySerCysTh	515
Db	1358	: -----AGGAATGCAGAGAGAAGTCCCTTTTGACGTGTGAA	1395
Qy	515	rArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHi	535
Db	1396	: GAGAGCGGCCAACGAAGACGAATACTGATCCAC-----	1435
Qy	535	sHisTyrrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluLeuGlnAs	555
Db	1436	: -----GCAGAGGAGGAGAGGA	1452
Qy	555	pArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSe	575
Db	1453	: CCGCTTTTGCAGAT-----	1465
Qy	575	rGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrrHisAlaAspCysHisLe	595
Db	1465	-----	1465
Qy	595	uGluProValArgCysGlnAlaProProArgCysProSerGluAlaSerGlyArgTh	615
Db	1465	-----	1465
Qy	615	rValGlySerGlyLysValTyProThrValHisThrSerProProGluLeuLeuLy	635
Db	1465	-----	1465
Qy	635	sAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAs	655
Db	1465	-----	1465
Qy	655	nileProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAl	675
Db	1465	-----	1465
Qy	675	aCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGl	695
Db	1466	-----CTCTGTGTGTGTGGATCCCCCTTCGCCGCCGACC-----	1501
Qy	695	yProAspSerCysProTyrcysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHi	715
Db	1502	-----CTCAAGAGCGGGGAAGACAGAGACTCGTCATA	1533
Qy	715	sValMetProAspSerAspSerGluAlaValTyrgluPhethrGlnaspAlaGlnHisse	735
Db	1534	CTTC-----	1537
Qy	735	rAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluPr	755
Db	1538	-----CSGAGGAGGAGAAG-----	1552
Qy	755	oSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSe	775
Db	1553	-----ATGTTCCGGTTTTTT-----ATCCGGCGCATGGTGAAGGC	1597
Qy	775	rLysTyrrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIl	795
Db	1588	TCAGAGCTTCTACTGGGTGGTGTGGTGGTGGCTGNACACACTGTGTGTGGCCAT	1647
Qy	795	eGluTyrrHisGluInProGluGluLeuThrAsnAlaLeuGluLeuSerAsnIleValph	815
Db	1648	GGTGCATTACAACCAAGCCGCGCGCTTACCACGACCTGTATTTTGACAGAGTTGTTTT	1707
Qy	815	eThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrglyProPheGlyTy	835
Db	1708	CCTGGGTCTCTCTCACAGAGATGTCCCTGAAGATGATCGCTGGGGCCCAGAAGCTA	1767
Qy	835	rIleLysAsnProTyrrAsnIlePheAspGlyValIleValValIleSerValTrpGluil	855

Db	1768	CTTCGGGTCTCTTCAACTGCTTCGACTTTGGGTCATCGTGGGAGCGCTCTTTGAAGT	1827
Qy	855	evAligYgln-----GlnGlyGlyLeuSerValLeuArgThrPheAr	870
Db	1828	GGTCTGGCGGCCATCAAGCGGGAAGCTCTTTGGATCAGTGTCTGGCGCCCTCCG	1887
Qy	870	gLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValVa	890
Db	1888	CTGCTCAGGATCTTCAAAGTACGAAGTACTGGAGCTCCCTCGGAACCTGGTGTGTC	1947
Qy	890	lLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePh	910
Db	1948	CTGCTGAACCTCCATGAAGTCCATCATCACCTGCTCTTCTTCTCTTCCTGTTCATTGT	2007
Qy	910	eIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGl	930
Db	2008	GGTCTTCGGCCCTGCTGGGATGACGCTGTITGGGACAGTTCACCTCCAGGATGAGAC	2067
Qy	930	yAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPh	950
Db	2068	TCCACA-----ACCAACTTCGACACCTTCCCTGCCGCCATCCTCACTGTCTT	2115
Qy	950	eGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMet-----	966
Db	2116	CCAGATCTCAGCGGAGGACTGGAATGCAGTGCATGATACAGGGATCGAATCGCAAGG	2175
Qy	967	---AlaSerThrSerSerTrpAlaLeuTyrPheIleAlaLeuMetThrPheGlyAs	985
Db	2176	CGGCGTCAGCAAGGCATGTTCCTGCTCTTTTACTTCAITGTCTGACACTGTTCGAAA	2235
Qy	985	nTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAs	1005
Db	2236	CTACACTCTGCTGAATGCTTTCTGGCCATCGCTGTGGACAACCTGSCCAACGCCAAGA	2295
Qy	1005	pAlaThrLysSerGluSerGluProAsp-----	1014
Db	2296	GCTGACCAAGGATCAAGAGGAGATGGAAGAGCAGCAATCAGAAGCTTCTCTCTGCAAAA	2355
Qy	1015	-----Phe-PheSerProSerValAspG	1022
Db	2356	GGCCAAAGAGTGGCTGAAGTCAGCCCATGTCTGCCGCGAACAATCTCCATCGCCGCAG	2415
Qy	1022	lyAspGlyAspArgLysLysArg-LeuAlaLeuValAlaLeuGlyGluHisAla-----	1039
Db	2416	GCACGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGCGCCAGCTACGGCT	2475
Qy	1040	-----GluLeuArgLysSerLeuLeu-----ProPro	1048
Db	2476	GCAGAACTCGCGGCCAGCTCGAGGCGCTGTACAGCGAGATGGACCCCGAGGAGCGGCT	2535
Qy	1049	LeuIleIleHisThrAlaAlaThrProMetSerHisProLysSerSerThrGlyVal	1068
Db	2536	CGCTCTCGCCACTACGGCGCCACCTCGCGCCGACATGAAGACGCACCTGACCGCGCGCT	2595
Qy	1069	GlyGluAla-LeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGl	1088
Db	2596	GGTGGTGGAGCTGGGCCCGCAGCGCGCGCGGGGGCCGTGGAGGCCAAAGCCCGACCTGA	2655
Qy	1088	yAlaAla-----HisHis-----G1	1093
Db	2656	GGCTGCGGAGGCCCCCGAGGGCGTCGACCCTCGCGCAGGCACACCGGCACCGCGACAA	2715
Qy	1093	uMetLysCPro-----	1097
Db	2716	GGACAAGACCCCGCGCGGGGACCAAGGACCGAGCAGAGCCCGGAAGCGGAGACGG	2775
Qy	1098	---ProSerAlaArgSerSer-----ProHisSerProTrpSerAlaAlaSerSe	1113
Db	2776	GGAGCCCGGTCCCGGAGGAGCGCGCGCGCGCCGACCGCAGCCACAGGAGGCGCG	2835
Qy	1113	rTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgAr	1133

Db 2836 G-----GGGCCCCCGGAGCGCGGACGAGCGCGCGCGGCCCCA----- 2875
Qy 1133 gSerProSerGlyGluArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspG1 1153
Db 2876 -GGCCCCGAGCGCGCGCGGACACCGCGCGGCTCCCGGAGGAGCGCGCGAGCG 2934
Qy 1153 uGlu-----GluSerSerGluGluAspArgAlase 1163
Db 2935 GGAAGCCCCGAGCGCGCGCGCACCGCGCACCGAGATCCGAGCAAGGAGTGCGCGCGCG 2994
Qy 1163 rProAlaGlySerAspHisArgHisArgGlySerLeuGlu-----ArgGluAlaLy 1180
Db 2995 CAAGGGCGAGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGGAGCGGA 3054
Qy 1180 sSerSerPheAspLeuProAspThrLeuGlnValProGly---LeuHisArgThrAlase 1199
Db 3055 GAGCGGG-----GAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 3093
Qy 1199 rGlyArgSerSerAlaSerGlu-----HisGlnAspCysAsnGlyLysSerAlaseG1 1217
Db 3094 CAAGGGCGAGCG 3153
Qy 1217 yArgLeuAla-----ArgThrLeuArgThrAspAspProG1 1229
Db 3154 GAAGGAGGCTGAGATAGTGAAGCCGACAAAGGAAAGGAGCTCCGGAACACCGAGCGCGCG 3213
Qy 1229 nLeuAspGlyAspAspAspAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAl 1249
Db 3214 GGAGCCACACTGACTGAGACCTGAGACCTGGAGCTGGAGCTGACTGTGGGTCCC----- 3262
Qy 1249 aTrpValArgSerArgLeuProAlaCysCysArgGluArg----- 1262
Db 3263 -----ATGCACACACTGCCAGCACCTGTCTCCAGAAGGTGGAGGAACAGCGAGGA 3315
Qy 1263 -----AspSerTrp----- 1265
Db 3316 TGCAGACAATACGCGGAACGTCACCTCGCATGGGCAGTCAGCCCCCGACCGAACAACATAT 3375
Qy 1265 ----- 1265
Db 3376 TGTACATATCCAGTGATCTGACGGCGCCCTCTTGGGGAGCCAGCCAGCTGTTCCAGTGG 3435
Qy 1265 ----- 1265
Db 3436 TAACGTGGACCTGGAAAGCCAAAGCAGAGGGGAAGAGGAGGTGGAGCGGATGACGTGAT 3495
Qy 1266 -----SerAlaTyrllePheProProGlnSe 1274
Db 3496 GAGGAGCGCGCGCGCGGCTATCGTCCCATACAGCTCCATGTTCTGTTTAAGCCCCACCAA 3555
Qy 1274 rArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLe 1294
Db 3556 CTGTCTCGCGCGCTTGCACATCATCTGACCATCAGGACTTTCGAGGTGTGTCATCT 3615
Qy 1294 uValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHi 1314
Db 3616 CGTGTCTACCTCGCTGAGCAGCATCGCCCTGGCTGCTGAGGACCA-----GTGCGCACAGA 3672
Qy 1314 sSerAlaGluArgIlePheLeuThrLeuSerAsnTyrllePheThrAlaValPheLeuAl 1334
Db 3673 CTCGCCGAGGAACAACGCTCTGAAATACCTGGATTACATTTTCACTGGTGTCTTACCTT 3732
Qy 1334 aGluMetThrValLysValValAlaLeuGlyTyrllePheGlyGluGlnAlaTyrlleuAr 1354
Db 3732 TGAGATGGTAAAGATGATCGACTTGGGAGCTGCTGCTTCAACCTCGAGCGCTATTTCGG 3792
Qy 1354 gSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIle---Le 1373
Db 3793 GGACTTGTGGAACATCTGACACTTTCATTTGTGTGTCAGTGGCGCGCTGTGGGTGTTGCTT 3852
Qy 1373 uValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLe 1393
Db 3853 CTCGAGCTTCTGTGGGAGGATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGT 3912

Qy 1393 uLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValVa 1413
Db 3913 CTTTCGTGCTCTCGGCGCCCTCAAGACCATCAAAACGGCTGCCCAAGCTCAAGGCTGTGT 3972
Qy 1413 lGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaph 1433
Db 3973 TGACTGTGTGGTGAACCTCCCTGAAGAATGTCTCAACATCTTGAATGTCTACATGCTCTT 4032
Qy 1433 ePheIleIlePheGlyLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG1 1453
Db 4033 CATGTTTCATATTTGCCGTCAATCGGTGTCAGCTCTTCAAGGGAAGATTTTCTACTGCAC 4092
Qy 1453 nGlyGlu-----AspThrArgAsn-----IleThrAsnLysSerAs 1465
Db 4093 AGATGAATCCAAAGGAGCTGGAGAGGAGCTGCAGGGGTCACTATTTGGATTATGAGAAGGA 4152
Qy 1465 pCysAlaGluAlaSerTyrlleArg---TrpValArgHisLysTyrlleAsnPheAspAsnLeuG1 1484
Db 4153 GGAAGTGGAGAGCTCAGCCCGAGGAGTGGAGAAATACGACTTTCTACTACGACAATGTGCT 4212
Qy 1484 yGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTy 1504
Db 4213 CTGGGCTCTGCTCAGCTGTTTCAGGTCCACGGGAGAGGCTGGCCCATGGTGTGCTGAA 4272
Qy 1504 rAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMe 1524
Db 4273 ACACCTCGGTGATGCCACCTATCAGGAGCAGGGTCCAAAGCCCTGGGTACCGCATGGAGCT 4332
Qy 1524 tLeuLeuTyrllePheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheVa 1544
Db 4333 GTCCATCTTCTACGTGCTTACTTTGTGTCTTTCCTCTTCTTCGTCAACATCTTGT 4392
Qy 1544 lGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaAr 1564
Db 4393 GGCTTTGATCATCATCACCTTC-----CAGGAGCAGGGGGACAAAGGT 4434
Qy 1564 gArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgSerLysGluLysG1 1584
Db 4435 GATGTCTGAA-----TGCAGCCTGGAGAGACGAGAGGCTTGCATGACTT 4482
Qy 1584 nMetAlaGluAlaGlnCysLysProTyrlleSerAspTyrlleSerArg-----PheArgLe 1602
Db 4483 CGCCATCAGCGCCCAAAACCCCTGACCGGTACATGCCCAAAACCGCGAGTGTTCAGATA 4542
Qy 1602 uLeuValHisLysLeuCysThrSerHisTyrlleLeuAspLeuPheIleThrGlyValIleG1 1622
Db 4543 TAAGACGTGGACATTTGTGTCTCCCGCCCTTTGAATCTTATCATGCGCATGATAGC 4602
Qy 1622 yLeuAsnValValThrMetAlaMetGluHisTyrlleGlnGlnProGlnIleLeuAspGluAl 1642
Db 4603 CCTCAACACTGTGTGCTGATGATGAATTCATGATGCACCTTATGATGACGAGCTGAT 4662
Qy 1642 aLeuLysIleCysAsnTyrllePheThrValIlePheValPheGluSerValPheLysLe 1662
Db 4663 GCTGAAATGCTGAACATCGTGTTCACATCCATGTTCTTCCATGGAATGCGTGTGGAAGT 4722
Qy 1662 uValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaI1 1682
Db 4723 CATCGCTTTGGGGTGTGAACATTTTCAGAGATGCTCGGAATGCTCTTGTGACTTGTTCAC 4782
Qy 1682 eValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu-----Va 1697
Db 4783 TGTGTTGGGAAGTATTACTGATATTTTGTAGTAACAGAGATTCGCGAAACGAAATTCAT 4842
Qy 1697 lAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAl 1717
Db 4843 CAACCTCAGC-----TTCTCGCGCTCTTTCGAGTGC 4875
Qy 1717 aArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMe 1737
Db 4876 GCGGCTGATCAAGCTGCTCCGCGAGGCTACACCATCCGATCTCTGTGTGGACCTTGT 4935

Qy	1737	tGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePh	1751
Db	4936	CCAGTCTTCAAGGGCCCTGCCTACGTGCTGCTCATTCGCCATGCTGTTCTTCATCTA	4995
Qy	1757	eAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGln	1777
Db	4996	CGCCATCATCGGCATGAGTGTTGGGAATATTGCCCTGGATGATGAC-----AC	5046
Qy	1777	uGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheAr	1797
Db	5047	CAGCATCAACGGCCACAACTCCGGACGTTTTTGCAGCCCTGATGCTGCTGTTCAG	5106
Qy	1797	gValSerThrGlyAspAsnTrpAsnGlyIleMetLysAsp-----ProSerArgAspCy	1815
Db	5107	GAGCGCACGGGGAGGCGCTGGCAGCAGATCATGCTGCTGCTGAGCAACACGACGCTG	5166
Qy	1915	sAspGlnGlu-----SerThrCysTyrAsnThrValIleSerProIleTyrPheValSe	1933
Db	5167	TGATGAGCAGGCCAATCCACCCAGAGTGTGAAGTGACTTTTGCCTACTCTTCTACTCTC	5226
Qy	1933	rPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet----	1951
Db	5227	CTTCATCTCTGTGCTCCCTTTCGATGTTGAACCTCTTTGTGGCTGTGATCATGACAA	5286
Qy	1952	-----LysHisLeuGluGlu-SerA	1958
Db	5287	TTTTGAGTACTCACGGGGACTCTTCCATCTTAGGTCTCACCATTTGGATGAGTTCT	5346
Qy	1958	snLysGluAlaLysGluGluAlaGluLeuGluLeuGluLeuMetLysThrL	1978
Db	5347	CCGGGTCTGGGCTGAATACGACCCGGCTGGGTGGGGCGCATCAGTTTACAATGACATGTT	5406
Qy	1978	eu-SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGly	1997
Db	5407	TGAGATGCTGAACACATGCTCCCGCTCTGGG-----GCTGGGGGAAGAAATG	5454
Qy	1998	ValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHisIleGlyAla	1917
Db	5455	CCCTGCTCGATTCCTTACAAGCCCTGGTTGCG--CATGAACATGCCATCTCCAACGA	5511
Qy	1918	AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVal	1937
Db	5512	GGACATGACTGTTCACTTTCACGCTCCACGCTGATGGCCCTCATCCGGACGCACTGGAGAT	5571
Qy	1938	ProLeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeu	1957
Db	5572	CAAGCTGGCCCCAGCTGG-----GACAAAGCAGCATCAGTGTGACGGGAGATT	5619
Qy	1958	ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGly----	1975
Db	5620	GAGGAAGGAGATTTCCTGTTGT--GTGGGCCAATCTGCCCCAGAGACATTTGGACTTGCT	5676
Qy	1976	-----HisArgGlyTrpGlyLeuProLysAlaGlnSer	1986
Db	5677	GGTACCACCCCATTAAGCCTGATGAGATGACAGTGGGAAGGTTTATGCAGCTCTGATGAT	5736
Qy	1987	GlySerIleLeuSerVal-----HisSerGlnPro-----	1996
Db	5737	ATTTGACTTCTPACAAGCAGAACAAAACACAGAGACCCAGATGACAGCGAGCTCTGGAGG	5796
Qy	1997	-----AlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGln	2014
Db	5797	CCTCTCCAGATGGGTCTGTGCTCTGTTCCACCCTCTGAGGCCAC-----	5844
Qy	2015	ProHisGlyAlaProThrTrpGlyAlaIleProLysLeuPro-----	2028
Db	5845	--CCTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGCCCGGGTTTTCTTCGACAGAA	5901
Qy	2028	-----	2028
Db	5902	GAGTTCACCTCTCCTACGAAATGCGGGGGCCATACAAAACAGAGAGTGGCATCAAGA	5961
Qy	2029	-----ProPro	2030

Db	5962	GTCTGTCTCTGGGGCACTCAAAAGGACCCACAGGATGACACCCCATAGAGCCACAGGCCACCCCT	6021
Qy	2031	GlyArgSerProLeu-AlaGlnArgProLeuArgArgGlnAlaAlaileArgThrAsp--	2049
Db	6022	GGACGTGGGCATCCACAGAGATCCCTGTGGGGCGGTGAGAGACACTGGCTGGACCGT	6081
Qy	2050	-----SerLeuAspVa	2053
Db	6082	TCAGATGCAGACATAACCCGGAGGGGCCCTGATGGGAGACCCACGCTGGGTGGAGAG	6141
Qy	2053	lGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPro-----Se	2070
Db	6142	CCAGGGTCGAGCGCCTCCATGCCCCCGCTTGGCGCGAGACTCAGCCCTGCACATGC	6201
Qy	2070	rCysProLeuThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnAr	2090
Db	6202	CAGCCCCATGAAGCGCTCCATCTCC-----ACGCTGGCCACGCG	6240
Qy	2090	gSerGlyIleGlnSerIysValSerIysHisIleArgLeuProAlaProCysProGlyLe	2110
Db	6241	GCCCCGTGG-GACTCATCTTTGACGACACACCCCGGACCGCCACCCCTTAGCAGCGCGT	6299
Qy	2110	u-----GluProSerTrpAlaIysAspProProGlu-ThrArgSerSerLeuGluLeuA	2128
Db	6300	CGTCGCACACACCCACCACCGCTGCCACCCCGCAGGACAGAGACAGAGATCCCTGG	6359
Qy	2128	spThrGluLeuSerTrpIleSerGlyAspLeu-----LeuProSerSerGlnGluGluP	2146
Db	6360	AGAAAGGGGCCAGC--CTGTCTGCCGATATGATGGCGCACCAAGCAGTGTGTGGGC	6416
Qy	2146	roLeuPhePro-----ArgAspLeuLysLysCysTyRS	2157
Db	6417	CGGGGCTGCCCCCGGGAGAGGGCGCTACAGGCTGCCGGCGGGAACAGAGCGCGCGGAGG	6476
Qy	2157	erValGluThrGlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArgH	2177
Db	6477	AGCGGGCGCGTCCAGAGCGGAGGAGCCCTACTCTCTCTCGGAGACGACGCGCT	6536
Qy	2177	isSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProS	2197
Db	6537	TC-----TACTCTCGACCGCTTTGGGGCGCGTGAGCGCCCCGAAGCCCAAGCCCT	6587
Qy	2197	er-----	2197
Db	6588	CCCTCAGAGCCACCCAAAGTGGCCACAGCTGGCCAGAGCGCGGACCCACCCACAGG	6647
Qy	2198	-----SerLeuGlyGlyGlnProLeu-----	2204
Db	6648	GCAGTGGTTCGTGAATGGGAGCCCTTGCTGTCAACATCTGTGTGTAGCACCCCGGCC	6707
Qy	2205	--GlyGlyProGlySerArgProLysLysLysLeuSerPro-----ProSerIleSerIleA	2223
Db	6708	GCGTGGGGGAGGAGCAGTCCCCAGACGCCCCCTGACTCCCGCCCGCAGCATCACCACAC	6767
Qy	2223	spProProGluSer-----GlnGlySerArgProProCysS	2235
Db	6768	AGACGGCCAACTCTCCACCATCCACTTGGCGGGGCTCAGACAGGCTCCCTGCTCTCT	6827
Qy	2235	erProGly-----ValCysLeuArgArgAlaProA	2246
Db	6828	CCCCAGCGCGGCTCAGCGCGTGGGCTTTCCGAACACACACGCGCTGTGCAGAGAGACCCCC	6887
Qy	2246	laSerAsp-----SerLysAspProSerValSerSerProL	2258
Db	6888	TCAGCCAGCCCTCGGCCCTTGCTCGAAATGGCTCTGACCCCTTACTCTGGGCGAGCGTC	6947
Qy	2258	euAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeu-----	2274
Db	6948	TGGACATGTAGGCGCTCTGTCCACCGCCCTGCTGAGGACACGCTCACTTTCGAGGAGGCTG	7007
Qy	2275	-----SerGlyLeuSerSer	2279

```
Db      7008 TGGCCACCAACTCGGGCGCTCTCTCC 7033
RESULT 4
US-11-350-336-5
; Sequence 5, Application US/11350336
; Publication No. US20060135751A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/11/350,336
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7162
US-11-350-336-5

Alignment Scores:
Pred. No.:      2,03e-74      Length:      7364
Score:          1739.50      Matches:    662
Percent Similarity: 37.9%      Conservaive: 358
Best Local Similarity: 24.6%      Mismatches: 880
Query Match:      14.5%      Indels:     796
DB:                8         Gaps:        84

US-09-611-257A-24 (1-2287) x US-11-350-336-5 (1-7364)
Qy      5 ArgValProArgCysValArgThrProLeuArg-----GlySerAlaArg 20
Db      84 CGCGCCCGCGC-----CCTCCCTGCGGGCGCGCTGGCGCGGGATGCAACGC 131
Qy      21 ProSerSerAspProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu 40
Db      132 GGGCGCGGGAGCCAT--GGTCCG-----CTTCGGGAGCAGCTGGCGCGCGCTATGG 183
Qy      41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
Db      184 AGGCGCGCGCGCGAGAGCGGGCCG-----GGCGCGGGCGCGCGCGGGCGGGGG 237
Qy      61 ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla 80
Db      238 CCGGGGTCGCGGGGGCTGAGCGCGCGCCGCGCGCGCGCTCTTACAAGCAATCGATCGCGCA 297
Qy      81 GluGlyLeuProTyrProAlaLeuAla--ProVal----- 91
Db      298 CGCGCGCGGACCATGGCGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTACCGGT 357
Qy      92 -----ValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgTh 109
Db      358 CAACCGCTCGCTCTTCGCTTTCAGCGAGGACCAACGTCGTCGCAAAATACGGAAGCGCAT 417
Qy      109 rValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValTh 129
Db      418 CACCGAGTGGCCCTCCATTCGAGTATATGATCCTCGGCCACCATCATCGCAACTGCATCGT 477
Qy      129 rLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLe 149
Db      478 GCTGGCCCTG-----GAGCAGACCTCCCTGATGGGACAAACGCCCATGTC 525
Qy      149 uGlnAlaPheAspAsp-----PheIlePheAlaPheAlaValGluMetValVa 166

526 CGAGCGGCTGGACACACGAGCGCCCTATTTTCATCGGATCTTTTGTCTCGAGGAGGAT 585
166 lLysMetValAlaLeuGly---lIlePheGlyLysCysTyrLeuGlyAspThrTrpAs 185
586 CAAAATCATCGCTCTGGGCTTTGTCTTCCACAGGGCTCTTACCTGCGGAACGCTGGAA 645
185 nArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer-----LeuAs 202
646 CGTCAAGACTTCGTGGTCTCTCACAGGATCCCTTGCACGCGCTGGAAGTCACTCGA 705
202 pLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAl 222
706 CTTGCCA-----ACACTGAGGCTGTGCTGTGCTGAGGCGCCCTGGAAGCT 750
222 alIeAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMe 242
751 GGTGCTCTGGGATTCCAAGTTTGAGGTGGTCTCAAGTCCATCATGAAAGCCATGGTTC 810
242 tLeuGlyAsnValLeuLeuLeuCysPhePheValPheIlePheGlyIleValGlyVa 262
811 ACTCTGCAGATTGGGCTGCTTCTCTTTTGGCATCTCATGTTTCCCATCATGCGCT 870
262 lGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuPr 282
871 GGAGTTCTACATGGCAAGTTCACCAAGGCTGTTC-----CC 909
282 oLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIl 302
910 CAACAGCACAGATCGGAGCCCTGT----- 934
302 eCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGl 322
934 ----- 934
322 yGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAs 342
935 -----GGTGACTTCCCTGTGGCAAGAGAGGCCCGCGCGCTGTGCGAGGCGCA 984
342 nThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnPr 362
985 CACTGAGTGC-----CGGAGGACTTGCCCA-----GGACC 1014
362 oPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnVa 382
1015 CAACTTTGGCATCACCACATTTGACAATACTCTGTTTGGCATCTTGACGGTGTTCAGTG 1074
382 lIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp---AlaHisSerPh 401
1075 CATCACCATGGAGGCTGGACTGACATCTCTATAATACAAACGATCGCGCGGCAACAC 1134
401 eTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLe 421
1135 CTGGAAGTGGCTCTACTTCTCATCTCTCATCATCATCGGCTCTCTTCTTCTGCTCAACT 1194
421 uCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer----- 438
1195 GGTGCTGGGCTGCTCTCGGGGAGTTTGCAGAGGCGAGAGAGGGTGGAGAACCGCGCG 1254
439 -----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLe 455
1255 CGCCTTCTGAAGCTCGCGCGGAGCAGCAGATCGAG----- 1291
455 uAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyl 475
1292 -----CGNAGACTCAACGGGTACCTGGAGTGGAT 1320
475 eLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGl 495
1321 CTTCAAGGCGGAGGAAGTCATGCTGGCGGAGGAGGAC----- 1357
495 yLeuLeuSerSerProValAlaAlaArgSerGlyGlnGluProGlnProSerGlySerCysTh 515
```


Db	4984	CGCCATCATCGGCATG	CAGGTGTTGGGAATATTGGCCCTGGATGATGAC-----AC	5038	
Qy	1777	uGlyLeuGlyArgHisAlaThrPheArgAsn	PheGlyMetAlaPheLeuThrLeuPheAr	1797	
Db	5035	CAGCATCAACCGCCACAACAACTCCGGAGCGTTTTC	CAAGCCCTGATGCTGCTGTTTCAG	5094	
Qy	1797	gValSerThrGlyAspIenTrpAsnGlyIleMet	LysAsp-----ProSerArgAspCy	1815	
Db	5095	GAGCGCACCGGGAGCGCTGGCACAGATCATCTGCT	TGCTGAGCAACACCGGCGTG	5154	
Qy	1815	sAspGlnGlu-----SerThrCysTyrAsnThr	ValIleSerProIleTyrPheValSe	1833	
Db	5155	TGATGAGCGGCCAATGCCACCGAGTGGNAAGT	GACTTTCCTACTTCTACTTCGTC	5214	
Qy	1833	rPheValLeuThrAlaGlnPheValLeuValAsn	ValIleAlaValLeuMet-----	1851	
Db	5215	CTTCATCTTCCTGTGCTCTTCTGATGTTGAACCT	CTTTGTGCTGTGATCATGGACAA	5274	
Qy	1852	-----	-----LysHisLeuGluGlu-SerA	1858	
Db	5275	TTTTGAGTACCTCAGCGGGGAGCTCTTCATCT	CTAGTCTCACACCTTGGATGAGTTCAT	5334	
Qy	1858	snLysGluAlaLysGluGluAlaGluLeuGluAla	GluLeuGluLeuMetLysThrL	1878	
Db	5335	CCGGCTGTGGCTCAATACGACCCGGCTGCGTGT	GGCGCATCAGTTACAATGACATGTT	5394	
Qy	1878	eu-SerProGlnProHisSerProLeuGlySerPro	PheLeuThrProGlyValGluGly	1897	
Db	5395	TGAGATGCTGAAACACATGCTCCCGCCTCTGGG	-----GCTGGGGAAGAATG	5442	
Qy	1898	ValAsnSerThrAspSerProLysProGlyAla	ProHisThrAlaHisIleGlyAla	1917	
Db	5443	CCCTGCTCGAGTCTTACAAGCGCTGGTTCG--	--CATGAACATGCCCATCTCCAAGA	5499	
Qy	1918	AlaSerGlyPheSerLeuGluHisProThrMet	ValProHisProGluGluValProVal	1937	
Db	5500	GGACATGACTGTTCACTTTCAGCTCCACGCT	GATGGCCTCATCCGGACGGCACTGGAGAT	5559	
Qy	1938	ProLeuGlyProAspLeuLeuThrValArgLys	SerGlyValSerArgThrHisSerLeu	1957	
Db	5560	CAAGCTGCCCCACGCTGG-----	-----GACAAAGCAGCATCAGTGTGACGCGGAGTT	5607	
Qy	1958	ProAsnAspSerTyrMetCysArgAsnGlySer	ThrAlaGluArgSerLeuGly-----	1975	
Db	5608	GAGGAAGGAGATTTCCGTTGT--GTGGCCAA	TCTGCCCAGAAAGACTTTGGACTTGCT	5664	
Qy	1976	-----	-----HisArgGlyTrpGlyLeuProLysAla	GlnSer	1986
Db	5665	GGTACCACCCCATTAAGCCTGATGATGACAGT	GGGGAAGTTTATGCGAGCTCTGATGAT	5724	
Qy	1987	GlySerIleLeuSerVal-----	-----HisSerGlnPro-----	1996	
Db	5725	ATTTGACTTCTACAAGCAGAAACAAACCACC	CAGAGACAGATGCAGCAGGCTCTCGGAGG	5784	
Qy	1997	-----AlaAspThrSerCysIleLeuGlnLeu	ProLysAspValHisTyrLeuLeuGln	2014	
Db	5785	CCTCTCCAGATGGGTCTGTGCTCTTCCACCC	CTGTAAGCCAC-----	5832	
Qy	2015	ProHisGlyAlaProThrTrpGlyAlaIle	ProLysLeuPro-----	2028	
Db	5833	---CCTGGAGCAGACACAGCCGGTGTGCTCC	GAGGACCCGGGTTTCCTTCACACAGAA	5889	
Qy	2028	-----	-----	2028	
Db	5890	GAGTTCCACCTCCCTCAGCAATGGCGGGCC	ATCAAAACCAAGAGATGGCATCAAGA	5949	
Qy	2029	-----	-----ProPro	2030	
Db	5950	GTCTGTCTCTGGGCACTCAAGAGACCCAGAT	GCACCCCATGAGCCAGGCCACCCCT	6009	
Qy	2031	GlyArgSerProLeu-AlaGlnArgProLeuArg	GlnAlaAlaIleArgThrAsp--	2049	
Db	6010	GGAGCTGGCCACTCCACAGAGATCCCTGTGGG	CGGTTCAGAGCACTGGCTGTGGACGT	6059	

QY	2050	-----SerLeuaspva	2050
Db	6070	TCAGATGCAGAGCATAAACCCGGAGGGCCCTGATGGGAGCCCGACGCTGGGTGGAGAG	6129
QY	2053	lGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPro-----se	2070
Db	6130	CCAGGGTCAGAGCGCTCCATGCCCCGCTTGGCGCGGAGACTCAGCCCGTCACAGATGC	6189
QY	2070	rCyseProLeuThrArgSerSerPheTrpGlyGlySerIleGlnValGlnGlnAr	2090
Db	6190	CAGCCCATGAAGCGCTCCATCTCC-----ACGCTGCCCCAGCG	6228
QY	2090	gSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLe	2110
Db	6229	GCCCGGTG-CACTCATCTTTGCAGCACCACCCCGGACCGCCACCCCTAGCCAGCGT	6287
QY	2110	u-----GluProSerTrpAlaLysAspProGlu-ThrArgSerSerLeuGluLeuA	2128
Db	6288	CGTCGCACCAACCCACCCGCTGCCACCGCGCGCAGGAGCAAGAGAGTCCTCTGG	6347
QY	2128	spThrGluLeuSerTrpIleSerGlyAspLeu-----LeuProSerSerGlnGluGluP	2146
Db	6348	AGAAGGGGCCAGC---CTGCTCCGATATGATGGCGCACCAAGCAGTGTGTGGGCG	6404
QY	2146	roLeuPhePro-----ArgAspLeuLysCysTyrs	2157
Db	6405	CGGGGCTGCCCGGGAGAGGGCCCTACAGGCTGCCGGCGGGAACGAGAGCGCGCAGG	6464
QY	2157	erValGluThrGlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArgH	2177
Db	6465	AGCGGGCCGCTCCAGAGGGAGGAGCCCTCATCTCTCTCGGAGAAGCAGCGCT	6524
QY	2177	isSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProS	2197
Db	6525	TC-----TACTCTGGCAGCGCTTTGGGGCGCTGAGCGCCCGGAAGCCCAAGCCCT	6575
QY	2197	er-----	2197
Db	6576	CCCTCAGAGCCACCAACGTCGCCACAGCTGGCCAGAGCGGGACCCACCCACAGG	6635
QY	2198	-----SerLeuGlyGlyLnpProLeu-----	2204
Db	6636	GCAGTGGTTCCGTGAATGGAGGCCCTTGCTGTCAACATCTGGTGTAGCACCCCGGCC	6695
QY	2205	--GlyGlyProGlySerArgProLysLysLysLeuSerPro---ProSerIleSerIleA	2223
Db	6696	CGGTTGGCGGAGCAGCTCCCCAGAGCCCTTGACTCCCGCCCGCAGATCACCTACA	6755
QY	2223	spProProGluSer-----GlnGlySerArgProProCysS	2235
Db	6756	AGACGGCCAACTCCTCAACCATCCACTTCGCCGGGGCTCAGACAGCGCTCCCTGCCTCT	6815
QY	2235	erProGly-----ValCysLeuArgArgArgAlaProA	2246
Db	6816	CCCAGAGCGGCTCAGCGTGGGCTTCCGAACACACAGCCCTGTCTCAGAGAGACCCCC	6875
QY	2246	laSerAsp-----SerLysAspProSerValSerSerProL	2258
Db	6876	TCAGCCAGCCCTTGGCCCTTGCTCGAATTTGGCTCTGACCCCTTACCTGGGGCAGCGTC	6935
QY	2258	euAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeu-----	2274
Db	6936	TGGACGTAGCGCTCTGTCCACCGCCCTGCTGGGACACGCTCCTTTTCGAGGAGGCTG	6995
QY	2275	-----SerGlyLeuSerSer	2279
Db	6996	TGGCCACCAACTCGGGCGGCTCTCTCC	7021

RESULT 5
US-11-350-336-7
; Sequence 7, Application US/11350336
; Publication No. US20060135751A1

```

; GENERAL INFORMATION:
; APPLICANT: Lipecombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/11/350,336
; CURRENT FILING DATE: 2006-02-07
; PRIOR FILING DATE: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 7177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..6856
US-11-350-336-7

Alignment Scores:
Pred. No.: 1.52e-73 Length: 7177
Score: 1721.00 Matches: 656
Percent Similarity: 38.2% Conservative: 356
Best Local Similarity: 24.8% Mismatches: 873
Query Match: 14.3% Indels: 765
DB: 8 Gaps: 84

US-09-611-257A-24 (1-2287) x US-11-350-336-7 (1-7177)

Qy 5 ArgValProArgCysValArgThrProProLeuArg-----GlySerAlaArg 20
Db 84 CGCGCCCGCGC-----CCTCCCTGCGGGGCGCGCTGGCGCGGGGATGCACGC 131

Qy 21 ProSerSerProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu 40
Db 132 GGGCCCGGAGCCAT--GGTCCG-----CTTCGGGACGAGCTGGCGCGCGCTATGG 183

Qy 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
Db 184 AGGCCCGCGCGCGAGCGGCGCG-----GGCGCGCGCGCGCGCGCGCGGGGG 237

Qy 61 ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla 80
Db 238 CCCGGGTCCCGGGGGCTCGACGCCCGCGCGCGCTCTTACAAGCAATCGATCGCGCA 297

Qy 81 GluGlyLeuProTyrProAlaLeuAla-ProVal----- 91
Db 298 CGCGCGCGGACCATGGCGCTGTGTACACCCCATCCCGGTCAAGCAGAACTGCTTACCGT 357

Qy 92 -----ValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgTh 109
Db 358 CAACCGCTCGCTCTTCGTTTCAGCGAGGACAACGTCGTCGCAAAATACGCGAGCGCAT 417

Qy 109 rValCysAnProTrpPheGluArgValSerMetLeuValleLeuLeuAnCysValTh 129
Db 418 CACCGAGTGGCTCCATTCGAGTATATGATCCTCGGCACCATCATCCCAACTGCATCGT 477

Qy 129 rLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLe 149
Db 478 GCTGGCCCTG-----GAGCAGCAGCTCCCTGATGGGACAAACGCCCATGTC 525

Qy 149 uGlnAlaPheAspAsp-----PheIlePheAlaPhePheAlaValGluMetValVa 166
Db 526 CGAGCGGCTGACGACACGAGGCCCTATTTCATCGGGATCTTTTCTTCGAGGAGCGGAT 585

Qy 166 lLysMetValAlaLeuGly-----IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAs 185
Db 586 CAAATCATCGCTCTGGGCTTTGTCTTCCACAAGGGCTCTTACCTGCGGAACGCGTGAA 645

185 nArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer-----LeuAs 202
646 CGTCATGAGCTTCGTGTGCTCTCACAGGATCCTTGCCACGCTGGAAGTACTGCTCGA 705

202 pLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAl 222
706 CTTGCGCA-----ACACTGAGGGTGTGCGTGTGAGGGCCCTTGAAGCT 750

222 aIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMe 242
751 GGTGCTCTGGGATCCAAAGTTTGAGGTGGTCTCAAGTCCATCATGAGGCCATGGTTCC 810

242 tLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyVa 262
811 ACTCTGCAGATTGGGCTGCTTCTCTTCTTGGCATCTCATGTTTCCCATCATGGCCT 870

262 lGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAnPheSerLeuPr 282
871 GGAGTTTCTACATGGCAAGTTCACAAGGCTGTGTTTC-----CC 909

282 oLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIl 302
910 CAACAGCACAGATCGGAGCCCGTG----- 934

302 eCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGl 322
934 ----- 934

322 yGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAnSerSerSerAs 342
935 -----GGTGACTTCCCTGTCGCAAGAGGCCCGCCGCGCTGTGCGAGGCGCA 984

342 nThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnPr 362
985 CACTGAGTGC-----CGGAGTACTCGCCA-----GGACC 1014

362 oPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnVa 382
1015 CAACTTTGGCATCACCACATTTGACAATATCCTGTTGTCATCTTGACGGTGTTCAGTG 1074

382 lIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp---AlaHisSerPh 401
1075 CATCACCATCGAGGGCTGGACTGACATCTCTATAATACAAACGATCGCGCCGCAACAC 1134

401 eTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLe 421
1135 CTGGAACCTGCTCTACTTCTCATCTCTCATCATCATCGGCTCTCTTCTTCTCATGCTCA 1194

421 uCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer----- 438
1195 GGTGCTGGGCTGCTCTCGGGGAGTTTGCAGGAGCGAGAGGGTGGAGAACCCGCG 1254

439 -----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLe 455
1255 CGCCTTCCTGAAGTGC CGCGAGCAGCAGCATCGAG----- 1291

455 uAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIl 475
1292 -----CGAGACTCAACGGGTACCTGGAGTGGAT 1320

475 eLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGl 495
1321 CTTCAAGGCGGAGGAGTGCATGCTGGCGGAGGAGGAC----- 1357

495 yLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysTh 515
1358 -----AGGAATGCAGGAGGAGGAGTCCCTTTTGGACGCTGCTGAA 1395

515 rArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHi 535
1396 GAGAGCGGCCCAACGAAGAGCAGAAATGACCTGATCCAC----- 1435
```

Qy	535	sHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluLeuGlnAs	555
Db	1436	-----GCAGAGGAGGAGGAGGA	1452
Qy	555	pArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSe	575
Db	1453	-----CCGGTTTGACAGAT	1465
Qy	575	xGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLe	595
Db	1465	-----	1465
Qy	595	uGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgTh	615
Db	1465	-----	1465
Qy	615	rValGlySerGlyLysValTyrProThrValHisThrSerProProProGluLeuLeuLy	635
Db	1465	-----	1465
Qy	635	sAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAs	655
Db	1465	-----	1465
Qy	655	nIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAl	675
Db	1465	-----	1465
Qy	675	aCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGl	695
Db	1466	-----CTCTGTGTGTGGATCCCTTTCGCCCGCGCCAGC	1501
Qy	695	yProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHi	715
Db	1502	-----CTCAGAGCGGGAACACAGAGAGCTGCTGCATA	1533
Qy	715	sValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSe	735
Db	1534	CTTC-----	1537
Qy	735	rAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluPr	755
Db	1538	-----CGGAGAAGGAGAAG	1552
Qy	755	oSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSe	775
Db	1553	-----ATGTTCGGTTTTTT	1587
Qy	775	rLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIl	795
Db	1588	TCAGAGTTCTACTGGGTGGTGCTGCGTGGTGGCCCTGAACACACTGTGTGGCCAT	1647
Qy	795	eGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluLeuSerAsnIleValPh	815
Db	1648	GGTGCAITTACAAACCAGCGCGCGCGCTTACCACACCCCTGATTTTTCAGAGTTTGT	1707
Qy	815	eThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTy	835
Db	1708	CCTGGGTCTCTCTCTCACAGAGATGTCCCTGAAGATGTATGGCTGGGGGCCCAAGACTA	1767
Qy	835	rIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGluIl	855
Db	1768	CTTCGGGTCCCTTCAACTGCTTCGACTTGGGGTTCATCGTGGGAGCGCTCTTTGAAGT	1827
Qy	855	eValGlyGln-----GlnGlyGlyGlyLeuSerValLeuArgThrPheAr	870
Db	1828	GGTCTGGCGGCCCATCAAGCGGGAAGCTCTTTGGGATCAGTGTGTGGCGGCCCTCCG	1887
Qy	870	gLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValVa	890
Db	1888	CCTGCTGAGGATCTTCAAGTACAGAGATCTCGGAGCTCCCTCGGAACTCTGGTGTG	1947
Qy	890	lLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePh	910

[illegible]

Db 2995 CAAGGGCAGCGCGCGCCGACCGCGCGGCCCGCCGAGCGGGCGCCCGGAGCGGCA 3054
Qy 1180 sSerSerPheAspLeuProAspThrLeuGlnValProGly---LeuHisArgThrAlaSe 1199
Db 3055 GAGCGGG-----GAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 3093
Qy 1199 rGlyArgSerSerAlaSerGlu-----HisGlnAspCysAsnGlyLysSerAlaSerG1 1217
Db 3094 CAAGGGCAGCGCTGCTCAGCGAGGTGTGGAGAGGAGACACCGAGAGAGGAGCGCACGGA 3153
Qy 1217 yArgLeuAla-----ArgThrLeuArgThrAspAppProG1 1229
Db 3154 GAAGGAGGCTGAGATAGTGAAGCCGACAGAGAAAGAGGCTCGGAAACACACGAGCGCCG 3213
Qy 1229 nLeuAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAl 1249
Db 3214 GGAGCCACACTGTGACCTGAGACCACTGGAGCACTGTCTCCAGAAAGGTGGAGGAGCGG 3262
Qy 1249 aTrpValArgSerArgLeuProAlaCysCysArgGluArg- 1262
Db 3263 -----ATGCACACACTGCCAGCACCTGTCTCCAGAAAGGTGGAGGAGCGGAGGA 3315
Qy 1263 -----AspSerTrp----- 1265
Db 3316 TGCAGACAATCAGCGGAACGTCACCTCGCATGGCGAGTCAGCCCCCAGACCCGAACTAT 3375
Qy 1265 ----- 1265
Db 3376 TGTACATATCCAGTGTGCTGACGGGCCCTCTTGGGGAGGCCACCGTCTGTTCCAGTGG 3435
Qy 1265 ----- 1265
Db 3436 TAACGTGACCTGGAAGCCAGCAGAGGAGGAGGAGGTGGAGCGGATGACGTGAT 3495
Qy 1266 -----SerAlaTrpIlePheProProGlnSe 1274
Db 3496 GAGGAGCGCGCGCGGCTATCGTCCCATACAGCTCCATCTCTGTTTAAGCGCCCAACAA 3555
Qy 1274 rArgPheArgLeuLeuCyHisArgIleIleThrHisLysMetPheAspHisValValLe 1294
Db 3556 CTGCTCGCGCGCTTCTGCACCTACATCTGGACCATCAGGTACTTTCAGGTGTCTATCT 3615
Qy 1294 uValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHi 1314
Db 3616 CGTGTCTATCGCTTGAGCAGCATCGCCCTGGCTGTGTGAGGACCCA---GTGCGCACAGA 3672
Qy 1314 sSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaValPheLeuAl 1334
Db 3673 CTGCCCCAGGAACAACGCTCTGAAATACCTGGATTACATTTTCACTGGTGTCTTTACCTT 3732
Qy 1334 aGluMetThrValIysValAlaLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuAr 1354
Db 3733 TGAGATGGTGAATAAGATGATCGACTTGGGAGTCTGCTCTCACCCCTGGAGCCTATTCCG 3792
Qy 1354 gSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuVa 1374
Db 3793 GGACTTGTGGACATCTGGAC-----TTCACTTGTGTGAGTGGCGCCCTGGT 3840
Qy 1374 lSerMetVal---SerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLe 1393
Db 3841 GGCGTTTGTCTTCTCAGGATCCAAAGGAAAGACATCAATACCATCAAGTCTCTGAGAT 3900
Qy 1393 uLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValVa 1413
Db 3901 CCTTGTGTCTGCGGCCCTCAAGACCATCAAAACGGCTGCCCAAGCTCAAGGCTGTGTT 3960
Qy 1413 lGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleValIleCysAlaPh 1433
Db 3961 TGACTGTGTGTGAATCCCTGAGAGATGTCCTCAACATCTTGATTGCTACATGCTCTT 4020
Qy 1433 ePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysG1 1453
Db 4021 CATGTTCATATTTGCGGTCATTTGGGTGCAGCTCTTCAAAAGGGAAGTTTTTCTACTGCAC 4080

Qy 1453 nGlyGlu-----AspThrArgAsn-----IleThrAsnLysSerAs 1465
Db 4081 AGATGAATCCAAGGAGCTGGAGGAGCTCCAGGGGTCACTATTGGATTATGAGAAGGA 4140
Qy 1465 pCysAlaGluAlaSerTrpArg---TrpValArgHisLysTrpAsnPheAspLeuG1 1484
Db 4141 GGAAGTGGAGCTTCAGCCAGGAGTGGAGAAATACGACTTTTCATACCAATGTGCT 4200
Qy 1484 yGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTy 1504
Db 4201 CTGGGCTCTGCTGACCGCTGTTACAGTGTCCAGGGAGAGGCTGCCCATGTGCTGAA 4260
Qy 1504 rAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMe 1524
Db 4261 ACACCTCGTGGATGCCACCTATGAGGAGCAGGGTCCAAGCCCTGGGTACCGCATGGAGCT 4320
Qy 1524 tLeuLeuTrpPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheVa 1544
Db 4321 GTCCATCTTCTACGTGCTCTACTTTGTGTCTTTCCTCTTCTCTCTCAACATCTTTGT 4380
Qy 1544 lGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaAr 1564
Db 4381 GGCTTTGATCATCATCACCTTC-----CAGGAGCAGGGGGACAAGGT 4422
Qy 1564 gArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgSerLysGluLysG1 1584
Db 4423 GATGCTGAA-----TGCAGCCTGGAGAGACGAGAGGGCTTGCACTTGACTT 4470
Qy 1584 nMetAlaGluAlaGlnCysLysProTrpTrpSerAspTrpSerArg-----PheArgLe 1602
Db 4471 CGCCATCAGCGCCAAACCCCTGACCGTACATGCCCCAAACCGGCGAGTCGTTCAGTA 4530
Qy 1602 uLeuValHisLeuCysThrSerHisTrpLeuAspLeuPheIleThrGlyValIleG1 1622
Db 4531 TAAGAGTGGACATTTGTGTCTCCCGCCCTTTGAATACTTTCATCATGCGCATGATAGC 4590
Qy 1622 yLeuAsnValValThrMetAlaMetGluHisTrpGlnGlnProGlnIleLeuAspGluAl 1642
Db 4591 CCTCAACACTGTGTGCTGATGATGAATTCATATGTCACCCCTATGAGTACGAGCTGAT 4650
Qy 1642 aLeuLysIleCysAsnTrpIlePheThrValIlePheValPheGluSerValPheLysLe 1662
Db 4651 GCTGAAATGCTCAACATCGTGTTCATCATCCATCTTCTCCATGGAATCGCTGCTGAAGT 4710
Qy 1662 uValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaI1 1682
Db 4711 CATCGCTTTGGGTGCTGAACATATTTCAGAGATGCTTGAATGTCTTTGACTTGTCTAC 4770
Qy 1682 eValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu-----Va 1697
Db 4771 TGTGTTGGGAAGTATTACTGATATTTAGTAAACAGAGATTGCGGAAACGAACATTTTCAT 4830
Qy 1697 lAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAl 1717
Db 4831 CAACCTTCAG-----TTCTCCGCTCTCTTCGAGCTGC 4863
Qy 1717 aArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuHisThrValMe 1737
Db 4864 CGCGCTGATCAAGCTGCTCCGCGAGGCTACACCATCCGCTCTCTGCTGTGGACCTTTGT 4923
Qy 1737 tGlnAlaLeuProGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPheIlePh 1757
Db 4924 CCACTCTTCAAGCCCTGCCCTACGTGTCTGCTCATTTGCCCATGCTGTTCTTCACTA 4983
Qy 1757 eAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysG1 1777
Db 4984 CGCCATCATCGCATCGAGGTGTTGGGAATATTGCCCTCGCATGATGAC-----AC 5034
Qy 1777 uGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheAr 1797
Db 5035 CAGCATCAACCGCCACAAACATTCGCGAGCTTTTTCGAAGCCCTGTGCTGCTGTTTCAG 5094

Db 1277 GAAATGACCT----- 1286
Qy 625 lHisThrSerProProGluIleLeuLeuAspLysAlaLeuValGluValAlaProSe 645
Db 1286 ----- 1286
Qy 645 rProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHi 665
Db 1286 ----- 1286
Qy 665 sLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr 685
Db 1287 -----CATCC 1291
Qy 685 oCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCys-----ProTyrCys- 702
Db 1292 ATGCAGAAGAGGGGAGGACCGGTTTGTAGACCTCTGTGCTGGGTCTCCCTTCTGCTC 1351
Qy 703 --AlaArgThrGlyValaGlyGluProGluSerAlaAspHisValMetProAspSerAsps 722
Db 1352 GTGCAGCCTCAAGATGGGAAGACAGAGACTCATCGTACTTC----- 1395
Qy 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHiss 742
Db 1395 ----- 1395
Qy 742 erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db 1396 --CGAGGAGGAGAAG-----ATGT 1414
Qy 762 rPArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db 1415 TCCGGTTCCTT-----ATCCGTCTGTATGGTGAACACACAGACTTCTACTGGGTGG 1465
Qy 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
Db 1466 TACTGTGGTGGTGGCCCTGAACAGTGTGTGGCCATGCTATATAATCAGCCTC 1525
Qy 802 luGluLeuThrAsnAlaLeuGluIleSerAniIleValPheThrSerLeuPheAlaLeuG 822
Db 1526 AGCGGCTTACCACCTGCACCTGTACTTGCAGAGTTTGTTCCTGGGTCTCTTCCTCAG 1585
Qy 822 luMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAniI 842
Db 1586 AGATGTCCCTGAAGATGTACGGTCTAGGGCCACAGAGCTACTTCCGGTCTCTTCAACT 1645
Qy 842 lePheAspGlyValIleValIleSerValTrpGluIleValGlyGln----- 858
Db 1646 GCTTTGACTTTGGGGTGATTGGGGAGTATCTTTGAAGTAGTCTGGGCTGCCATCAAGC 1705
Qy 859 -----GlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysL 877
Db 1706 CAGGAACCTCTTCGGAATCAGTGTGCTGGGGCTCTCCGACTGCTGAGGATTTCAAAG 1765
Qy 877 euValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspA 897
Db 1766 TCACCAAGTATTGGAACCTCCCTGAGGAACCTGGTTGTTTCCCTCTCAACTCCATGAAGT 1825
Qy 897 snValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyM 917
Db 1826 CCATCATCAGGCTTCTCTCTCTGCTTTTCTCTTTTCTTTTCTTTTCTTTCTTTCTTTG 1885
Qy 917 etHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgL 937
Db 1886 TGCAGCTGTTGGGGGAGAGTTTCAACTTTCAAGATGAGACTTCCAAACC-----A 1933
Qy 937 ysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluA 957
Db 1934 CCAATTTTGTATACCTTCCAGCTGCCATCTCTACTGTGTTTCAGATTCTGACAGGAGAG 1993
Qy 957 spTrpAsnLysValLeuTyrAnGlyMet-----AlaSerThrSerSert 972
Db 1994 ACTGGAAATCGATCATGTATCGGATTTGAGTCAAGAGGAGGAGTCAAGAAAGGCATGT 2053

Qy 972 rpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuL 992
Db 2054 TTTATCTCTTTTACTTCTCTCTGACTGTTTGGAAACTACACCTGTGTGAACGTTT 2113
Qy 992 euValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerG 1012
Db 2114 TCTTGGCCATTGTGTGGACAACCTTCCCAATGCCAGGAGTTGACCAAGATCAAGAGG 2173
Qy 1012 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032
Db 2174 AGATGGAAGAGGAGCC-----AATCAGAAGCTTCTCTC 2206
Qy 1032 euValAlaLeuGlyGluHisAlaGluLeu----- 1041
Db 2207 TTCAGAAAGCCCAAGAAGTAGTGAAGTACAGCCCATGTCTGTGCCAACATCTCCATTG 2266
Qy 1042 -----ArgLysSerLeuL 1046
Db 2267 CTGCCAGCAGCAGAACTCGGCCAAGCGCGCTCAGTATGGAGCAGCGGCCAGTCAGC 2326
Qy 1046 eu----- 1046
Db 2327 TAAGGCTCCAGAACCTCGTCCAGCTGTGAGGCATGTATAGTGAGATGGACCCGAGG 2386
Qy 1047 -----P 1047
Db 2387 AGCGCTTCGTTATGCCAGCAGCGCCACGTGAGGCCAGACATGAAGACACACATGGACC 2446
Qy 1047 roProLeuIleIleHis----- 1052
Db 2447 GACCCCTAGTGTGGAACCTGTCGGATGCGCTGCGGGACCCGCCGGGAACAAGTCAA 2506
Qy 1053 -----ThrAlaAlaThr-----ProMetSerHisProLys----- 1062
Db 2507 AGCCTGAGGACAGGAGGCCACCGAAGTGGGATCCACCACGCCGACACCCCGGCATC 2566
Qy 1063 -----SerSerSerThrGlyValGly----- 1069
Db 2567 GTGATAGGACAAGACCTCAGCCTCAACCCCTGTGGAGGGCAACAGGACAGACACT 2626
Qy 1070 -----GluAlaLeuGlySerGlySerArg-----ArgThrSerSerS 1082
Db 2627 GCCCAAGGCCGAAAGCAACGAGACCGGGCCCGGAGGAACGTGCGCGCTCGTCGAA 2686
Qy 1082 erGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProSerAlaArgS 1102
Db 2687 GTCACAGCAGGAGGCTCCAGGGGCTGACACACAAGTGTGTGTGAGCGCAGTAGACGTC 2746
Qy 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg----- 1118
Db 2747 ACCACCGCGCGGATCCCGGAGGAGGCCACTGAACCGGAACCTCGCGCCACCGTGCCC 2806
Qy 1119 -----SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysA 1132
Db 2807 ACCGGCAGCAGCAGGACTCAAGCAAGGAAGCAAGGAGGAGGCACTGCACCGGTGTTT 2862
Qy 1132 rgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGlu-----GlyGlnG 1149
Db 2863 -----GTACCCAAAGGGGAGCGTCCGCAAGACATCGAGGCCCGGTACGGGCCCGCGTG 2917
Qy 1149 luSerGlnAspGluGluSerSerGluGluAspArgAla-SerProAlaGlySerAsp 1168
Db 2918 AGACAGAACACAGTGAAGGCCACACGCGGACCGCTGCAAGACATGAAGGTGCCACCAA 2977
Qy 1169 His-----ArgHisArgGlySerLeuGluArgGlu----- 1178
Db 2978 CACTGTAGCCCCCAGAGAGGAGGTTCGACAGAGAAGGAGAGCAACGTGTGGAAGGGGATA 3037
Qy 1179 AlalysSerSerPheAspLeuProAspThrLeuGlnVal-ProGlyLeuHisArgThrAl 1198
Db 3038 AGGAAACTCGAAATCACCGGCCCAAGNACCTCGCTGTGACCTGGAGGCCAT-----TG 3091

Db 5187 CATTCGGCTCTGGCTGAATACAGCCAGCTGCGTGTGGCGCATCAGTTACATGACAT 5246
Qy 1873 -LeuGluMet---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLe 1891
Db 5247 GTTTGAGATGCTGAACACATGCTCCCA- - - - -CCTCTGGGTTTGGGGAA-GA 5293
Qy 1891 uTriProGly- - - - -ValGluGlyValAsnSer- - - - - 1900
Db 5294 AATCCCGGCTCGAGTTGCATACAGCGCTGGTTGCAATGAACATGCCCATATCCCAATG 5353
Qy 1901 - - - - -ThrAspSerProLysPro- - - - - 1906
Db 5354 AGGACATGACGGTACACTTTATACACTGATGGCCCTCATCCGAGCGCACTGGAGA 5413
Qy 1906 - - - - - 1906
Db 5414 TCAAGCTTGGCCCGGAGGGAACAAACAGCACCAATGTGATGCTGAGCTGAGGAAGGAGA 5473
Qy 1907 - - - - -GlyAlaProHisThrThraAlaHisIleGlyAlaAla- - - - - 1918
Db 5474 TCTCTTGTGTGGCTAATCTGCCCCAGAAAGACTCTGGACTTACTGGTGCCACCCCA 5533
Qy 1919 - - - - -SerGlyPheSerLeu- - - - - 1923
Db 5534 AACCTGACGAGATGACAGTGGGAAGGTCTATGCGGCTCTCATGATATTTGACTTCTACA 5593
Qy 1924 - - - - -GluHisProThrMet- - - - -ValProHisPr 1932
Db 5594 AACAGAAACAAACACACAGAGATCAGACTCACCAGCTCTCTGGAGGCTGTGCCAGATGG 5653
Qy 1932 oGluGluValProValProLeu- - - - -GlyProAspLeu- - - - -LeuTh 1945
Db 5654 GTCCGTGTTCCCTATTCATCTCTGAAGGCCACCTGGAGCAGACACAGCCCGCTGTGC 5713
Qy 1945 rValArgLysSerGlyValSerArgThr- - - - - 1954
Db 5714 TCCGAGGAGCTCGGTTTTCTTCGACAAAGAGTGCAACTTCCCTCAGCAATGGGGCG 5773
Qy 1955 -HisSerLeuProAsnAspSerTyr- - - - - 1962
Db 5774 CCATACAAACCCAGGAAGTGCGCATCAAGAGTCCCTGTCTGTGGGCACGACGAGGACCC 5833
Qy 1963 - - - - -MetCysArgAsnGlyse 1968
Db 5834 AGGACGTACTTTATGAGCCACAGACCTCTAGAACGTGGCCATCTTCGAGAGATCCCTG 5893
Qy 1968 rThrAlaGluArgSerLeuGlyHisArg- - - - - 1977
Db 5894 TGGGCGACCCAGGAGCACTGGCTGTAGATGTCCAGATGCAGAACATGACATTGAGAGGAC 5953
Qy 1978 -GlyTriProGlyLeupro- - - - -LysAlaGlnSerGlySerIleL 1990
Db 5954 CGGATGGGGAGCCCGCAGCTCGCTGGAGAGCCAGGCGCGGCTCTATGCGACGCC 6013
Qy 1990 euSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValH 2010
Db 6014 TGGGGCGAGAACAACAGCCGGCCCTAATGCCAGC- - - - -CCCATGAAGCGCTCCATCT 6067
Qy 2010 iSTyrLeuLeu- - - - -GlnProHisGlyAlaProThrTriProGlyAlaIleProLysLeuProp 2029
Db 6068 CCACACTGGCTCCAGCCCGCATGGACTCAGCTTTGCAACACAGACTCTGGACCGGCCAC 6127
Qy 2029 roProGly- - - - -ArgSerProLeuAlaG 2037
Db 6128 CTCCTAGCCAGGTGTCCCATCACCAACCCCGCTGCCACCGGCGCAGGACAGGAAGC 6187
Qy 2037 InArgProLeuArgGlnAlaIleArgThrAspSerLeuAspValGlnGlyLeuG 2057
Db 6188 AGAGTCCCTGGAAAGGGCCAGCCGCTGTCTGTTGACACA- - - - - 6228
Qy 2057 LysrArgGluAspLeuLeuSerGluValSerGlyPro-SerCysProLeuThrArgSer 2076
Db 6229 - - - - -GAAGGTGCACCAAGTACTGTGTCAGGATCTGGCTTGCCTGCCCATGAGAAGGGT 6280

Qy 2077 SerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLys 2096
Db 6281 CCACAGGCTCCGGCGGGAGC- - - - - 6301
Qy 2097 ValSerLysHisIleArgLeuPro-AlaProCysProGlyLeuGlu- - - - - 2111
Db 6302 GTAAGCAAG- - - - -AGCGAGCGCGTCCCAAGGAGCGGAGCGAGCCCTCTCTCT 6349
Qy 2112 - - - - -ProSerTrp-AlaLysAspProProG 2120
Db 6350 CTTCTTCAGAGAAAGCAGCGCTTCTATTCTGTGACCGCTTTGGAGCGCGGAGCCCCAC 6409
Qy 2120 luThrArgSerSerLeuLeuLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuP 2140
Db 6410 AACCTAAG- - - - - 6418
Qy 2140 roSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTy-SerValGluT 2160
Db 6419 CTTCCCTCAGTAGCACCCCATATCGCA- - - - - 6447
Qy 2160 hrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleA 2180
Db 6447 - - - - - 6447
Qy 2180 laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG 2200
Db 6448 -ACAGCGGCACTAGACAGCAGGCCACCCACCCGAG- - - - -GGCAGTGGTTCCGTTA 6496
Qy 2200 lyGlyGlnProLeu- - - - -GlyGlyProGlys 2209
Db 6497 ATGGAGCCCTTGATGTCAACATCTGGTGTAGCACGCGCGGCGGAGGTGGCGGAGGC 6556
Qy 2209 erArgProLysLysLeuSerPro- - - - -ProSerIleSer- - - - - 2221
Db 6557 AGCTCCCCAGACTCCCTGTACCCACGCCCGCCAGCATCACCCTACAAGACGCGCAATTCCT 6616
Qy 2222 - - - - -IleAspProProGluSerGlnGlySerArgProProCysSerProGly- - - - - 2237
Db 6617 CGCTGTCCACTTTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 6676
Qy 2238 - - - - -ValCysLeuArgArgAlaProAlaSerAsp- - - - - 2248
Db 6677 GCGCGGCTTTCTGAACAACAATGCCCTGTCTCCAGAAAGAGCCCTGAGCCAGCTCTAG 6736
Qy 2249 - - - - -SerLysAspProSerValSerSerProLeuAspSerThrAlaA 2263
Db 6737 CTTCTGGCTCCCGCATTTGGCTCTGACCCCTTACCTAGGGGAGCGCTCTGGACAGTGGCCCT 6796
Qy 2263 laSerProSerProLysLysAspThrLeuSerLeu- - - - -SerG 2276
Db 6797 CTGCCCCAACCTCCCTGAGGATACACTCACCTTTGAAGAGCGCGTGGCCACCAACTCTG 6856
Qy 2276 lyLeuSerSer 2279
Db 6857 GCGCTCTCTCC 6867

RESULT 7

US-11-313-450-9
; Sequence 9, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
; APPLICANT: Adorante, Joseph S.
; APPLICANT: Ehring, George R.
; TITLE OF INVENTION: High-Throughput Screens For Identifying
; FILE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers
; FILE REFERENCE: 17407 CIP (AP)
; CURRENT APPLICATION NUMBER: US/11/313,450
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/989797
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252771
; PRIOR FILING DATE: 2000-11-22

Qy 601 ln----- 601
Db 1633 GATGATGAAACAGCAGCAGCGGGGAGAGCAGAGCCACACACATCACTCTCGTGGTCCC 1692
Qy 602 --AlaPro---ProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620
Db 1693 TGGCCCTTGGCGCGGACAGTGCAGGAGCCAGCCAGTCCCGGAACCTCGGCTCC--- 1748
Qy 620 ysValTyPro-ThrValHis----- 626
Db 1749 -----TGGCCACGCCCTCCATGGCAAAAGAACAGCACTGTGGACTGCAATGGGGTGGTC 1803
Qy 627 -----ThrSerProProGluIleLeuLysAsp 636
Db 1804 TCATTACTGGGGGAGGGACCCAGAGCCACATCCCCAGGAAGCCACTCTCCGCCCT 1863
Qy 637 LysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIle 656
Db 1864 GTGATGCTA-----GAGCACCGCCAGACACGACGACCCAGCCATCGGAGGAG 1908
Qy 657 ProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys 676
Db 1909 CCAGCGGGCCC-----CAGATGCTGACCTCCAC----- 1938
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1939 -----GCTCCGTGTGATGGCTT-CGAGGA----- 1964
Qy 697 AspSerCysProTyrcysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1965 -----GCCAGGAGCAGCAGCGGGCCCTCAGCGCAGTCAGCGT--- 2003
Qy 717 MetProAspSerAspSerGluAlaValTyrgluPheThrGlnAspAlaGlnHisSerAsp 736
Db 2003 ----- 2003
Qy 737 LeuArgAspProHisSerArgArg---ArgGlnArgSerLeuGlyProAspAla----- 753
Db 2004 -----CTCACCAGCGACTGGAAGAGTTAGAGGAGTCTGCCACAGTGTCCACC 2054
Qy 754 -----GluProSer-----SerValLeu-AlaPheThrArgLe 764
Db 2055 ATGCTGGAACCGTCTCGCCCGCAGCGTACCTGATCTGGGAGTGTCTGCCCGTGTGGATGTC 2114
Qy 764 uIleCysAspThrPheArgLysIleValAspSerLysTyrgluArgGlyIleMetI 784
Db 2115 CATCAAGCAGGAGTGAAGTTGGTGTATCGAGCCCGTTTACTGACCTCCACCATCACTAT 2174
Qy 784 eAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrgluHisGluGlnProGluGluLe 804
Db 2175 GTGCATCGTACTACACACTCTTCATGGCGCTGGAGCACTACAACATGACAGTGAATT 2234
Qy 804 uThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLe 824
Db 2235 CGAGGAGATGCTGCAGGTGCGGAACCTGGTCTTCACAGGATTTTTCACAGCAGAGATGAC 2294
Qy 824 uLeuLysLeuValTyrglyProPheGlyTyrglyIleLysAsnProTyrgluPheAs 844
Db 2295 CTTCAAGATCATGCTCCCTCGACCCCTACTACTTCCAAAGGCGCTGGAACATCTTCGA 2354
Qy 844 pGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuLeu 864
Db 2355 CAGCATCATCTCATCTTAGCTCATGGAGCTGGCGCTGCTCCCGCATGAGCAACTTGTGTC 2414
Qy 864 rValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLe 884
Db 2415 GGTGTGGCTCTCTTCGCGCTGCTGCGGGTCTTCAAGCTGGCCAAATCATGGCCACCCCT 2474
Qy 884 uGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLe 904
Db 2475 GAACACATCATCAAGATCATCGGAACTCATGTGGGGGCACTGGGGAACTGACACACTGGT 2534
Qy 904 uLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPh 924

Db 2535 GCTAGCCATCATCGTGTTCATCTTGTCTGTGGTGGCATGACGCTCTTTGGCAAGAACTA 2594
Qy 924 eAlaSerGluArgAspGlyAspThr---LeuProAspArgLysAsnPheAspSerLeuLe 943
Db 2595 CTGGAGCTGAGGACAGCAGCTCAGGCCTGCTCGCTCGCTGGCACATGATGGACTTCTT 2654
Qy 943 uTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTy 963
Db 2655 TCATGCTTCTCATCATCTTCGCGCATCTCTGTGGAGAG---TGGATCGAGACCATGTG 2711
Qy 963 rAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrgluPheIleAlaLeuMetTh 982
Db 2712 GGACTGATGAGGTGTGGGGCAGTCATTATGCTGCTGCTCTTCTGTTGTTATGGT 2771
Qy 982 rPheGlyAsnTyrgluValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnAl 1002
Db 2772 CATTTGGAACCTTGTGCTCTGAATCTCTTCTGGCCTTGTGCTGCTGCTCAGCTCCTT 2831
Qy 1002 aGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspGl 1022
Db 2832 AGACAACCTCAGACCCCTGATGAGGA-CAGAGAGATGAACAACCTCAGCT-----GG 2884
Qy 1022 yAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHis----- 1038
Db 2885 CCCTGGCCCGCATCCAGAGGGCGCTGCGCTT---TGTCAGCGGACCACTGGGATTTCT 2941
Qy 1039 -----AlaGluLeuArgLysSerLeuLeuProProLeuIleI 1051
Db 2942 GCTGTGTCTCTCTGCGCAGCGCTCAGAAAGCCGCGAGCCC-TTGGCGCCAGGGCCAG 3000
Qy 1051 eHisThrAlaAlaThrPro-----MetSerHisProLysSerSerSerThrGlyVa 1068
Db 3001 CTGCCAGCTGCTGTCACCCCTACTCCTCCCGCCACCCCGAGAGCGGAGAGTGCCT 3060
Qy 1068 lGlyGluAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGl 1088
Db 3061 CCCACCCGCAAGGAAACACACGGTTTGAGGAAGCGGCGAGCAACAGGCGGACCCCGGG 3120
Qy 1088 yAlaAlaHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTr 1108
Db 3121 G---ATCCAGAGCCCGTGTGTGTCCTCA-----TCCGTGTG 3153
Qy 1108 pSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaPr 1128
Db 3154 GCCGAGTCAGACAGATGACCAAGAGAGATGAGAGACAGCAGCTGGGACCG----- 3208
Qy 1128 oSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGl 1148
Db 3209 -----AGGAGGAGTCCAGCAGCAGCAGGAATCCAGCCTGTG-TCCGGTGGGCC 3257
Qy 1148 nGlu-----SerGlnAspGluGluGluSerSerGluGluAs 1160
Db 3258 AGAGGCCCTCCCGAATTCAGGACCTGGAGCAGGTGTACGCGACTGCTCTCTGAGGC 3317
Qy 1160 pArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLy 1180
Db 3318 CGAGCCAGTGCATCTCAGGCCGACTGCGGCGCAGCAGTGGAAAGCGGAACCCAGGCC 3377
Qy 1180 sSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGl 1200
Db 3378 AGGTGCGGTGAGACCCAGAG----- 3399
Qy 1200 yArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAl 1220
Db 3400 ---GACAGTGTCTCCAG-----GGCAGCACAGCAGACATGACCAACAC 3440
Qy 1220 aArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspGluGlyAs 1240
Db 3441 CGCTGAGCTCTGGAGCAGATCCCTGACCTCGGCCAGGATGTCAAGGACCCAGGAGCTG 3500
Qy 1240 nLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysAr 1260

Db 3501 CTTCACTGAAGGC-----TGTCGCGG---CGCTGTCCTGCTGCGGT 3542
QY 1260 gGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeuCy 1280
Db 3543 GGCACACACACAGCCCGGAGGAGTCTGG-----TGCGGTGGCGAAGACCTG 3593
QY 1280 sHisArgIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAs 1300
Db 3594 CTACCACATCGTGAGCAGACAGCTGGTTGAGACATTATCATCTTCATGATCTACTCAG 3653
QY 1300 nCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePh 1320
Db 3654 CAGTGAGCGCTGCGCTTCGAGACATCTACCTAGAGGCGGAGAACCATCAAGGTCT 3713
QY 1320 eLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysVa 1340
Db 3714 GCTTGAGTATGCCGACAGATGTTACATATGTTCTTCGTCGAGATGCTGCTCAAGTG 3773
QY 1340 lValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValle 1360
Db 3774 GGTGGCC-----TACGGCTTCAAGAAGTACTTCACCAATGCTGGTGGCT 3821
QY 1360 uAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSe 1380
Db 3822 CGACTTCCTCATCGTAGACGTCTCT-----CTGGTCAGCCTGGTGCCCAAC 3869
QY 1380 r---GlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPr 1399
Db 3870 CTTGGGCTTTGCGAGATGGGCCCCCAATCAAGTCACTGCGAGCGTGGTGCACTCCGTCC 3929
QY 1399 oLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValIcluThrLeuMetSerSe 1419
Db 3930 TCTGAGAGCTCTGTACAGATTTCAGGGCATGAGGGTGTGTCAATGCTCCCTGTGGGCGC 3989
QY 1419 rLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIl 1439
Db 3990 CATCCCGTCCATCATGAACCTCTCTGCTGCTGCTCATCTTCTGGCTCATCTTCAGCAT 4049
QY 1439 eLeuGlyValGlnLeuPheLysGlyLysPhePheValCys-----GlnGlyG1 1455
Db 4050 CATGGGCGTGAACCTCTTTCCGGGAAGTTTGGAGGTGATCAACACAGACAGAGGAGA 4109
QY 1455 uAspThrArgAsnIleThr-----AsnLysSerAspCysAlaGluAlaSerTyrAr 1472
Db 4110 CTTGCCCTTTGAACATACACCATCTGTGAACAACAAGAGCCAGTGTGAGTCTTGAACTTGAC 4169
QY 1472 g-----TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMe 1488
Db 4170 CGGAGAAATTGTACTGGACCAAGGTGAAGTCAACTTTTGACAAACGTGGGGCCCGGTACCT 4229
QY 1488 tSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAs 1508
Db 4230 GGCCCTTCTCAGGTGGCAACATTTAAAGCTGGATGGACATTATGTATCAGCTGTGGA 4289
QY 1508 pAlaValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPh 1528
Db 4290 CTCAGGGGGTATGAAGAGAGCGCTCAGTGGGAATACAACTCTACATGTATATCTATT 4349
QY 1528 eIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValva 1548
Db 4350 TGTCAATTTTCATCATCTTTGGGTCTTTCTTCAACCTGAACTCTTATTGTTGTCATCAT 4409
QY 1548 lGluAsnPheHisLysCysArgGlnHisGlnGluGluAlaAala---ArgArgG1 1567
Db 4410 TGACAACTTCAACCAACAGAAAGAAAGTTAGGGGGCCAGGACATCTTTCATGACAGAGGA 4469
QY 1567 uGluLysArgLeuArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaG1 1587
Db 4470 GCAGAAAGTACTACAAATGCCATGAAGAGCTGGGCTCCAAGAAGCCCCAG----- 4521
QY 1587 uAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLe 1607
Db 4522 -----AAGCCCATCCACGCGCCCTGAAACAGTACCAGGCTTTCATATTTCGACAT 4571

QY 1607 uCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValth 1627
Db 4572 TGTGACCAACAGCAGCGCTTTGACGTCAACCATCATGTTTCTGATCTGCTTGAATATGGTGAC 4631
QY 1627 rMetAlaMetGlu---HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCy 1646
Db 4632 CATGATGGTGGAGACAGATGACCAAAAGTCTTGAGAAAATCAACATCTTGGCCAAAGATC-- 4689
QY 1646 sAsnTyrIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAl 1666
Db 4690 -AACCTGCTCTTTGTGGCCATCTTCACAGCGAGTGTATTGTCAAGTGGCTGCCCTGCG 4748
QY 1666 aPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSe 1686
Db 4749 C---CACTACTACTTCCACCAACAGCTGGAATATCTTCGACTTCTGCTGTTGTCATCTCTC 4805
QY 1686 rIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProth 1706
Db 4806 CATCTGGGCACCTGCTCTCTCGAGCATCATCCAGAACTACTTC-----TTCCTCCCGAC 4859
QY 1706 rIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAl 1726
Db 4860 GCTCTTCCAGTCTCCGCTGCGCCGAATAGCCCGCATCTCAGACTGATCCGAGGGC 4919
QY 1726 aValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLe 1746
Db 4920 CAAGGGATCCGACGCTGCTCTTTCCTCATGATGTCCCTGCTGCTGCTCTTCAACAT 4979
QY 1746 uGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheG1 1766
Db 4980 CGGGCTGCTGCTCTTCTGCTCATGTTTCTACTCATCTTTGGCATGGCCAACTTCG 5039
QY 1766 yAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheAr 1786
Db 5040 TTATGTCAAGTGGAG-----GCTGGCATCGACGACATGTTCAACTTCCA 5084
QY 1786 gAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnG1 1806
Db 5085 GACCTTCCGCAACAGCATGCTGTGCTCTTCCAGATCACCACGTCGCGCGCTGGGATGG 5144
QY 1806 yIleMetLys-----AspProSer-----ArgAs 1814
Db 5145 CTTCTCCAGCCCCATCTCAACACTGGGCGCCCTACTGCGACCCCATCTGCCCCAACAG 5204
QY 1814 pCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPh 1834
Db 5205 CAATGGCTCTGGGGGACTGCGGGAGCCCGGCGGCGGCGCATCTCTTCTTCCACCCTA 5264
QY 1834 eValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLe 1854
Db 5265 CATCATCATCTCTCTCTCATCTGTTCAACATGTATCTTCCATCATCTCTGGAGAACTT 5324
QY 1854 uGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeu-G 1874
Db 5325 CAGCGTGGCCAGCAGAGAGACCCGCGCCCTGAGT---GAGGACGACCTTCGATATGTT 5381
QY 1874 luMetLysThr-----LeuSerProGlnProHisSerProLeuGly-----SerP 1889
Db 5382 CTATGAGATCTGGGAGAAATTTGACCAGGAGGCCACTCAGTTTATTGAGTATTCGGTCT 5441
QY 1889 roPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaP 1909
Db 5442 GTCTGACTTTCGCG---ATGCCCTGTGTAGCCACTCCGATCGCAAGCCCAACACAGAT 5498
QY 1909 roHisThrThrAlaHis-----IleGlyAlaAlaSer-----GlyP 1921
Db 5499 AAGCCTCATCAACATGCACCTGCCCATGTGTGAGTGGGGACCGCATCCATTGTCATGGACAT 5558
QY 1921 heSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGly- 1940
Db 5559 TCTCTTTG-----CCTTCACAAAGAGGTCTCTGGGGGAGTCTGGGGA 5600

```
Qy 1941 -----ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuP 1958
Db 5601 GATGAGCCCTGAAGATCCAGATGGAGGAGATTTCATGGCAGCCCAACCATCCAGAT 5660
Qy 1958 roAsnAspSer-TyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5661 CTCCTACGAGCCCATCCACCACACTCCGGCGCAAGCAGCAGAGAGGTGTGGCCAT-- 5717
Qy 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db 5718 -----GGTTATCCAGAG-----AGCCTTCGCGAGGCACCTGCT 5750
Qy 1998 AspThr-----SerCysIleLeuGlnLeuPro----- 2006
Db 5751 GCAAGCTCTTTGAAGCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5810
Qy 2007 -----LysAspValHisTyrLeu-----LeuGln 2014
Db 5811 CGAAGAGGATGCCCTGAGCGAGAGGGCTCATCGCTACGTGATGAGTGAGAACTTCTC 5870
Qy 2015 ProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgSerPro 2034
Db 5871 CCGACCCCTTGGCCACCCCT-CCAGCTCTCTCCATCTCTCCACTCTCTCCACCCCTCT 5929
Qy 2035 LeuAlaGlnArgProLeuArgGlnAlaIleArgThrAspSerLeuAspValGln 2054
Db 5930 ATG-----ACAGTGTCACTAGAGCCACCA 5953
Qy 2055 GlyLeuGlySerArgGluAspLeuLeuSerGluValSer-----GlyProSerCys 2071
Db 5954 CGGATAACCTCCAGTGGGGGTCTGACTACAGCCAGTGAAGATCTCGCCGACTTCC 6013
Qy 2072 ProLeuThrArgSerSer 2078
Db 6014 CCCCTTCTCCGAGCGGACC 6034
```

RESULT 8

```
US-11-266-748A-29006
; Sequence 29006, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Patrick
; APPLICANT: Johnstone, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266.748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29006
; LENGTH: 7193
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29006
```

```
Alignment Scores:
Pred. No.: 4,54e-70 Length: 7193
Score: 1648.50 Matches: 627
Percent Similarity: 38.5% Conservative: 354
Best Local Similarity: 24.6% Mismatches: 781
Query Match: 13.7% Indels: 788
DB: 8 Gaps: 85

US-09-611-257A-24 (1-2287) x US-11-266-748A-29006 (1-7193)
Qy 14 ProLeuArgGlySerAlaArgProSerSerAspProProGlyProArgLeuAlaArgGly 33
Db 215 CCTCTTTCTGTTGAGGACCAACTTCTCAGCCGAATAGCTCCAGCAAGATGTCTCTGTCT 274
Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 275 TGG-----CAAGCTGCAATCGATGCTGTAGACGAGCCCAAGGCTGCCCAAACT 322
Qy 54 SerSerThrThrCysProGlyProGlyAlaAlaGlyAlaGlySerThrGluLysAspPro 73
Db 323 ATGAGCACCTCTGCACCCCCACCT-----GTAGGATCTCTCTCCCAAGAAACGTCAG 376
Qy 74 GlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValAlaPhe 93
Db 377 CAATACGCCAAGAGCAAAAAACAGGGTAACCTCGTCCAAACAGCCGACCTGCCCGCCCTT 436
Qy 94 PheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnPro 113
Db 437 TTCTGTATTATACATCAATAACCCCATCCGAAGAGCCCTGCATTAGTATAGTG-----GAA 490
Qy 114 Trp-----PheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGly 131
Db 491 TGGAAACCAATTGACATATTATATATTGCTATTTTTGCCTAATTTGTCGCTTAGCT 550
Qy 132 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 151
Db 551 ATTTACATCCCAATTCCTCGAAGATGATTCTAATTCACAAAT-----CATACTTCGAAAA 607
Qy 152 PheAspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeu 171
Db 608 GTAGAATATGCTTCTCGATTATTTTACAGTCGAGACATTTTTCAGAGATTATAGCGTAT 667
Qy 172 Gly---IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePhe 190
Db 668 GGATTATTGCTACATCCTAATGCTTATGTTAGGAATGGATGAATTTTACTGGAATTTGTT 727
Qy 191 IleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSer----- 207
Db 728 ATAGTAATAGTAGGATTG-----TTTAGTGTAAATTTTGGAAACAATTAACCAAGAAACA 781
Qy 208 -----PheSerAlaValArgThr 213
Db 782 GAAGCGGGAACCACTCAAGCGGCAATCTGGAGGCTTTGATGTCAAGGCTCTCGTGCC 841
Qy 214 ValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVal 233
Db 842 TTTGAGTGTGTCGACCACTTCGACTAGTGTGCGGGGTGCCCACTTTTACAGATTGTCTGT 901
Qy 234 ThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheVal 253
Db 902 AACTCCATTATAAAGGCATGGTTCCCTCTCTCCATAGCCCTTTGGTATTATTATTGTA 961
Qy 254 PhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCys 273
Db 962 ATCATATCTATGCTATTATAGGATTGGAACTTTTATTGGAAAAATGCACAAACATGT 1021
Qy 274 PheLeuProGlnAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnThr 293
Db 1022 TTTTGTGCTGACTCA-----GATATC-----GTA 1045
Qy 294 GluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSer 313
Db 1046 GCTGAAGAGGACCAGCTCCATGTGCGTCTCA----- 1078
```

QY	314	CysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuAsp	333	QY	669	uThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAl	689
DB	1079	-----GGGAATGGACGCCAGTGT-----	1096	DB	1677	-----AACTCAGC	1684
QY	334	TyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrThr	353	QY	689	aAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyG1	709
DB	1097	-----ACTGCCAATGCG-----ACG	1111	DB	1685	CGACGCTGGCGTCCGTGGAAACCGATTCAAT-----	1714
QY	354	AsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsnIleGly	373	QY	709	uProGluSerAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheTh	729
DB	1112	GAATGTAGGAGTGGCTGGTGGCCCAAGCGGAGCATCACCACCTTTGATACTTTGCC	1171	DB	1714	-----	1714
QY	374	TyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyr	393	QY	729	rGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLe	749
DB	1172	TTTGGCCATGCTTACTGTGTTTCAGTGCCATCACCATGGAGGCGTGGACAGCGTCTCTAC	1231	DB	1715	-----CGCAGAAGATGTAGG-----	1729
QY	394	PheValMetAspAlaHisSerPhe---TyrAsnPheIleTyrPheIleLeuLeuIle	412	QY	749	uGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPh	769
DB	1232	TGGTAAATGATCGATAGGATGGAAATGGCCATGGGTGTATTGTTAGTCTGATCATC	1291	DB	1730	-----GCCGCGTGAAGTCTGTACGTTTACTTGGCTGGTTATC-----	1768
QY	413	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	432	QY	769	eArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAs	789
DB	1292	CTTGGCTCATTTTCGTCCTTAACCTGTTCTTGGTGTCTTAGTGAGAAATTTCAAAG	1351	DB	1769	-----GTCTGGTGTTCGTGAA	1785
QY	433	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	452	QY	789	nThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuG1	809
DB	1352	GAAGAGAGAGGCAAAAGCACGGGAGATTTCAGAAAGCTCCGG-----	1396	DB	1786	CACCTTAAACCATTTCTCTGAGCATTACATACAGCCAGATTGGTTGACACAGATTCAAGA	1845
QY	453	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	472	QY	809	uLleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuVa	829
DB	1397	-----GAGAAGCAGCAGCTGGAGGAGGAGTCTAAAGGGCTACTTG	1435	DB	1846	TATTGCCAAACAAAGTCTCTTGGCTCTGTTCACCTGCGAGATGCTGTTAAATAATGTACAG	1905
QY	473	ValTyrIle-----LeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaI1	490	QY	829	lTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal--	848
DB	1436	GATTGGATCACCAGCTGAGGACATCGATCCGAGAAATGAGGAAGAGGAGGAGG--	1493	DB	1906	CTTGGGCGCTCCAGCATATTTCGTCTCTCTCTTTCAACCGTTCATTGCTCGGGGTG	1965
QY	490	eGlyValArgAlaGly---LeuLeuSerSerProValAlaArgSerGlyGlnGluProG1	509	QY	849	-----ValIleSerValTrpGluIleValGlyGlnGlnGlyGlyG1	862
DB	1494	-----AAGGCAACAAATACTAGCATGCCACACGAGCAGTGTGTGACACACA	1546	DB	1966	TGGTGAATCAGTACGAGACGATCCTGGTGAACCTGGAATCATGTCTCCCTCG-----	2019
QY	509	nProSerGlySerCysThrArgSerHisArgArgLeuSerValHisHisValHisH1	529	QY	862	yLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuPr	882
DB	1547	GAGAACG---TCAGCGGTGAAGCGGAGAACCGAGCGTCTGTGTG-----	1586	DB	2020	GATCTCTGTGTTTCGGTGTGCGCCTCTTAAAGAACTCTTCAAAGTGACCGGACTCGAC	2079
QY	529	sHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAl	549	QY	882	oAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCy	902
DB	1586	-----	1586	DB	2080	TTCCCTGAGCAACTAGTGGCATCTTATTAACTCCATCAAGTCCATCGCTTCGCTGT	2139
QY	549	aSerProGluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeuProProPr	569	QY	902	sMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMethHisLeuPheGlyCy	922
DB	1587	-----GAAGTCTCTGCTGCTGGTGAGAGCGGAGAGCGCGG-----	1622	DB	2140	GCTTCTGCTTTTCTCTTCATTATCATCTTTCTCTTGGGATGCGAGCTGTTTGGCGG	2199
QY	569	oSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTy	589	QY	922	sLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLe	942
DB	1623	-----CCAAGCGGGGCGCT-----	1637	DB	2200	CAAGTTTAATTTTGTAT-----GAAACGCAAAACCAAGCGGAGCACCTTTGACAATTT	2250
QY	589	rHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgCysProSe	609	QY	942	uLeuTrpAlaIleValTrpValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLe	962
DB	1637	-----	1637	DB	2251	CCCTCAAGCACTTCTCACAGTGTTCAGATCTTGACAGGCGAGACTGGATGCTGTGAT	2310
QY	609	rGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerPr	629	QY	962	uTyrAsnGlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTy	976
DB	1638	-----CTGGGTGTGGCGGTGG-----	1655	DB	2311	GTACGATGGCATCATGGCTTACGGGGGCCCATCTCTTTCAGGAATGATCGTCTGCATCTA	2370
QY	629	oProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProPr	649	QY	976	rPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLe	996
DB	1656	-----GTCAAGCCATCTCAAAATCCA--	1676	DB	2371	CTTCATCATCCTTCTTCTTGTGTGTAATAATATTCTACTGAATGCTCTTCTTGGCCATCGC	2430
QY	649	oThrLeuThrSerPheAsnIleProProGlyProPhePheSerSerMethHisLysLeuLeuG1	669	QY	996	uValGluGlyPhe-----GlnAlaGluGlyAspAlaThrLysSerGluSerGluPr	1013
DB	1676	-----	1676	DB	2431	TGTAGACAATTTGGCTGATGCTGAAAGTCTGAAACACTGCTCAGAAAGAGAGCGGAA--	2488
QY	1676	-----	1676	QY	1013	oAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuVa	1033

Qy	1728	yMetArgAlaLeuLeuHisThrValMet	-----GlnAlaLeuProGlnValGlyAs	1745
Db	4183	CATCCGACATATGCTGTGGACTTTTATTAAGATCCCTTTTCAGCGCTCCCGTATGTG		4237
Qy	1745	nLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuValGluLeuPhe		1765
Db	4238	-----GCCCTCTCATAGCCATGCTGTTCTTCATCTATGCGGTCAATGGCATGCAGATGTT		4293
Qy	1765	eGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPh		1785
Db	4294	TGGAAAGTTGCCATGAGATACAAACCAG		4344
Qy	1785	eArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAs		1805
Db	4345	CCAGACGTTTCCCAGGCGGTGCTGCTCTTCAGGTGTGCACACAGGTGAGCGCTGGCA		4404
Qy	1805	nGlyLeuMetLysAsp	-----ProSerArgAspCysAspGlnLysSer	1819
Db	4405	GGAGATCATGCTGGCCGTGCTCCCGAGGAAGCTCTGTGACCTCGAGTCAGATACAAACC		4464
Qy	1820	-----ThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheVa		1835
Db	4465	CGGGAGGAGTATACATGT	-----GGGAGCAACTTTGCCATTTGCTCTATTTCATCAGTTTTTA	4521
Qy	1835	lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet		1851
Db	4522	CATGCTCTGTGCATTTCTGATCATCAATCTGTTGTGGCTGTCTCATCGATTAATTCGA		4581
Qy	1852	-----LysHisLeuGluGluSerAsnLysG		1860
Db	4582	CTATCTGACCCGGGACTGGTCTATTTTGGGCGCTCACCATTTAGATGAATTC		4638
Qy	1860	uAlaLysGluGluAlaGluLeuAlaGlu	-----LeuGluLeuGluMetLysTh	1877
Db	4639	AATATGTGCAATATACACCTGAGGCAAGGGAAGGATAAACCCTTGATGGTGCAC		4698
Qy	1877	rLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro	-----GlyValGluGlyValAs	1899
Db	4699	TCTGCTTCGACGCATCCAGCTCCCTCGGGTTTGGGAAGTTATGTCCACACAGGTAGC		4758
Qy	1894	-----GlyValGluGlyValAs		1924
Db	4759	GTGCAAGAGATTAGTTGCCATGAACATGCCTCTCAACAGTCAGCGGACAGTCATGTTAA		4818
Qy	1899	nSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlase		1919
Db	4819	TGCNACC	-----CTGTTTGCTTTGTTGTCGACGGCTCT	4851
Qy	1919	rGlyPheSerLeuGlu	-----	1924
Db	4852	TAAGATCAAGACCGAAGGAACCTGGAGCAAGCTAATGAAGAACTTCGGCTGTGATAAA		4911
Qy	1925	-----HisProThrMetValProHisProGluValProValProLeuGlyPr		1941
Db	4912	GAAATTTTGAAGAAAACACGATGAAATTAATTGACCAAGTTGTCCTCCAGCTGTGTA		4971
Qy	1941	oAspLeuLeuThrValArgLys	-----	1948
Db	4972	TGATGAGGTAACCTGGGGAAGTTCTATGCCACTTTCCTGATACAGGACTACTTTAGGAA		5031
Qy	1948	-----	-----	1948
Db	5032	ATTCAAGAAAACGGAAGAAACAAGGACTGGTGGGAAGTACCTTCGGAAGAACACCAAT		5091
Qy	1949	-----SerGlyValSerArgThrHisSerLeu	-----	1957
Db	5092	TGCCCTACAGCGGGATTAAGGACACTGTCATGACATTTGGGCCAGAAATCCGGCGTGTAT		5151
Qy	1958	-----ProAsnAspSerTy	-----	1962
Db	5152	ATCGTGTGATTTGCAAGATGACGAGCTGTAGGAAACAAAACGAGAAAGAAAGATGATGT		5211

Qy	1962	rMetCysArgAsnGly	-----SerThrAlaGluAspSerLeuGlyHisArgGlyTrpGlyLe	1981
Db	5212	GTTCAAAGAAATGGTGCCCTGCTGTGAAACCAATGTCATGTTAAATAGTATAGGAG	5271	
Qy	1968	-----SerThrAlaGluAspSerLeuGlyHisArgGlyTrpGlyLe	1981	
Db	5272	AGATTCCCTTCAGCAGACCAATACCCACCGTCCCTGCATGTCCAAAGGCCCTCAAT	5331	
Qy	1981	uProLysAlaGln	-----SerGlySerIleLeuSerVa	1992
Db	5332	TCCACCTGCAAGTGATACTGAGAAACCGCTGTTTCTCCAGCAGGAGAAATCCGGTG	5388	
Qy	1992	lHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTrpLe	2012	
Db	5389	TCATAACCATCATACCAATAATTCCATAGAAAGCAAGTTCCCAACCTCCAAACAATGCCAA	5448	
Qy	2012	uLeuGln	-----ProHisGly	2024
Db	5449	TCTCAATATGCCAATATGTCCAAAGCTGCCATGGNAAGCGGCCGACGATTGGGAACCT	5508	
Qy	2024	eProLysLeuProProGly	-----ArgSerProLeuAl	2036
Db	5509	TGAGCATGTGCTGAAATGGGCATCATCTTCCCAACGATGACCGGAGCCTCAGAG	5568	
Qy	2036	gAlnArgProLeuArgArg	-----GlnAlaAlaIleArgThrAspSerLeuAs	2052
Db	5569	AAGCTCCAGTGTGAAAGAAACCGCGCTATTATGAACCTTACATTAGTTCGCACTCAGAGA	5628	
Qy	2052	pValGln	-----GlyLeuGlySerArgGluAspLeuSerGluValSerGlyProSerCy	2071
Db	5629	TGAACAGCTCCCAACTATTTCGCGGGAAGAC	5674	
Qy	2071	sProLeuThrArg	-----SerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgs	2091
Db	5675	-----TATTTTCAGGACCCCTGCTTGGGGAGCAGGAGTATTTCAGTA	5720	
Qy	2091	erGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuG	2111	
Db	5721	-----GTGAGGAATGCTACGAGGATGACAGCTCGCGCCACCTGGAGCAG	5763	
Qy	2111	luProSerTrpAlaLysAspProGluThrArgSerSerLeuGluLeuAspThrGluL	2131	
Db	5764	GCAAAACTATGGCT	5802	
Qy	2131	euSerTrpIleSerGly	-----AspLeuLeuProSerSerGlnGluGluProLeuPheProArg	2150
Db	5803	CATCGACTTGAGAGGCCCGCAGGCTACCATCATCC	5859	
Qy	2151	AspLeuLysLysCysTrpSerValGluThrGlnSerCysArgArgArg	2166	
Db	5860	TGACTCCCGCTTGTCTATGAT	5916	
Qy	2167	-----ProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAs	2185	
Db	5917	CACCCAGCA	5964	
Qy	2185	pSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG	2205	
Db	5965	-----CCGGCAGACGACCGAGAGAGGTCCCGTCTCTCCATCTT	6017	
Qy	2205	yGlyProGlySer	-----ArgProLysLysLys	2214
Db	6018	CGGCGCTGCTCTGCATCTAATGCGCAACAGATCATGGCAGTTGCGCGCTAGATTCAA	6077	
Qy	2214	sLeuSerProProSerIle	-----SerIleAspProProGluSerGlnGlySerArgPr	2232
Db	6078	GTAAGCCCAAGATGACTACCGAGTCACTCGACCCCGGTGCTGGGCCACCCCTCCAGCAA	6137	
Qy	2232	oProCysSerProGlyValCysLeu	-----ArgArgArg	2243
Db	6138	CCCCCTCCTACCGGAGCTGGACACCGTGCTACACCCCTGATCCAAAGTCGAGCAGTCAG	6197	
Qy	2243	gAlaProAlaSerAspSerLysAspProSerValSerSerPro	2262	

Qy	433	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	452
Db	1352	GAAGAAGAGAAGGCAAAAGCACGGGGAGATTTCAGAAAGTCCGG	1396
Qy	453	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	472
Db	1397	-----GAGAACAGCAGCTGGAGAGGATCTAAAGGCTACTTG	1435
Qy	473	ValTyrIle-----LeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaIle	490
Db	1436	GATTGGATCACCACCAAGCTGAGGACATCGATCCGAGAAATGAGGAAGAGGAGAGG--	1493
Qy	490	eGlyValArgAlaGly---LeuLeuSerSerProValAlaArgSerGlyGlnGluProGly	509
Db	1494	-----AAGCAACACGAAATACTAGCATGCCACCAACCGAGAGCTGAGTCTGTGAACACA	1546
Qy	509	nProSerGlySerCysThrArgSerHisArgArgLeuSerValHisIleLeuValHisIle	529
Db	1547	GAGAACG---TCACCGGTGAAGGCGAGAACCGAGGCTGTGTG	1586
Qy	529	sHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAla	549
Db	1586	-----	1586
Qy	549	aSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProPr	569
Db	1587	-----GAAGTCTCTGCTGCTGGAGACGGAGAGCGCGG	1622
Qy	569	oSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTy	589
Db	1623	-----CCAAAGCGGGGCCCT	1637
Qy	589	rHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgCysProSe	609
Db	1637	-----	1637
Qy	609	rGluAlaSerGlyArgThrValGlySerGlyLysValTyProThrValHisThrSerPr	629
Db	1638	-----CTGGGTGTGGCGGTGGG	1655
Qy	629	oProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProPr	649
Db	1656	-----GTCAAGCCATCTCAAATCCA	1676
Qy	649	oThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGl	669
Db	1676	-----	1676
Qy	669	uThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerIysAl	689
Db	1677	-----AACTCAGC	1684
Qy	689	aAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGl	709
Db	1685	CGACGTCGGGTCCGCTGGAACCGATTCAAT	1714
Qy	709	uProGluSerAlaAspHisValMetProAspSerAspSerCluAlaValTyrGluPheTh	729
Db	1714	-----	1714
Qy	729	rGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLe	749
Db	1715	-----CGCAGAGAGATCTAGG	1729
Qy	749	uGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPh	769
Db	1730	-----GCCCGCTGAAGTCTGTACACCTTTTACTGGCTGTTATC	1768
Qy	769	eArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAs	789
Db	1769	-----GTCTGGTGTTCCTGAA	1785
Qy	789	nThrLeuSerMetGlyIleGluTyrHisGluGlnProGluLeuThrAsnAlaLeuGl	809

[illegible]

Db 1743 TGAGAGCAGAGGGGCTCACTGTTTGTGCCCCACAGACCCAGGAGCGACGACGATAA 1802
Qy 617 lySerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspL 637
Db 1803 CATCAGCCAG----- 1813
Qy 637 ysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleP 657
Db 1814 -----C 1814
Qy 657 roProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysH 677
Db 1815 CAGTAGTCCC-----C 1826
Qy 677 isSerSerCysLysIleSerSerProCysSerLysAla---AspSerGlyAlaCysGlyP 696
Db 1827 ACCAATGCTCCGGTGAACGGGAAATGCAGCTGTGGACTGTCACCGTGTGGTCTC 1886
Qy 696 ro-----AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1887 CCTGTTGATGGAGCGCTCAGCCCTCATGCTCCCC-AATGGACAGCTTCTGCCAGAGGCCA 1945
Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 1946 CGACCAATCAAAATACACAAGAAAGCGTTGTAGTTCTCTCTCTCTCTCTCTCTCTCTCT 2004
Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2005 -----CTGAATGATCCCACTCAAGCAAGCAAGCAAGT- 2040
Qy 753 laGluProSerSerValLeuAla----- 760
Db 2041 -----AGAGCAAGCATATTAAACAACACTGTGGAAGAACTTGAAGAGTCCAGACAAAAT 2095
Qy 761 -----PheTyrArgLeuIleCysAsp- 767
Db 2096 GTCCACCTTGGTGGTACAGATTTCACACAAAATCTTTGATCTGGAAT-----TGCTCTC 2149
Qy 768 -----ThrPheArgLys-----IleValAspSerLysTyrPheGlyA 780
Db 2150 CATATTGGATAAAATTCAAAAGTGTATCTATTATTATGTAATGGATCCTTTGTAGATC 2209
Qy 780 rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG 800
Db 2210 TTGCAATTACCATTTGTCATAGTTTAAACACATTATTATTTATGGCTATGGAACACACCACAA 2269
Qy 800 lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA 820
Db 2270 TGACTGAGGAATTCAAAAATGTACTTCTATAGGAAATTTGGTCTTTACTGGAATCTTTG 2329
Qy 820 laLeuGluMetLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT 840
Db 2330 CAGCTGAATATGGATTAAACTGATTCGCCATGGATCCATATGAGTATTTTCAAGTAGGCT 2389
Qy 840 yrAsnIlePheAspGlyValIleValValIleSerValTyrGluIleValGlyGlnGlnG 860
Db 2390 GGAATATTTTGACAGCTTTATGTGACTTTAAGTTAGTGGAGCTCTTTCTACAGATG 2449
Qy 860 lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgP 880
Db 2450 TGAAGGATTTGTCAGTTCTGCGATCAATTCAGACTGCTCCGAGTCTTCAAGTTCGCAAAAT 2509
Qy 880 heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaIat 900
Db 2510 CCTGGCCAACATTGAACATGCTGATTAAAGATCAATGGTAATCTAGTAGGGGCTCTAGGTA 2569
Qy 900 hrPheCysMetLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuP 920
Db 2570 ACCTCACCTTAGTGTGGCCATCATCGTCTTCATTTTGTGTTGCTGGCATGCGACTCT 2629
Qy 920 heGly-----CysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2630 TTGGTAAGAGCTACAAAGAAATGTGCTGCAAGATC-----AATGATGACTGTACGC 2680

Qy 933 euProAspArgLysAsnPheAspSerLeuLeuTyrPalaIleValThrValPheGlnIleL 953
Db 2681 TCCCA---CGGTGGCACAATGACGACTCTTCCACCTCTTCTGATGTTGTGTGGCGTGC 2737
Qy 953 euThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMet---AlaSerThrSerSerT 972
Db 2738 TGTGTGGAGAG---TGGATAGAGACCATGTGGAGCTGTATGGAGGTCGCTGGTCAAGACTA 2794
Qy 972 rpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuL 992
Db 2795 TGTGCTTATTTTACATGATGTCATGTCATTGGAACCTTGGTGGTCTTAAACCTAT 2854
Qy 992 euValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerG 1012
Db 2855 TTCTGCGCTTATTATTAGAGCTCATTTAGTTTTCAGAC---AATCTTACAGCAATTCGAAGA 2911
Qy 1012 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaL 1032
Db 2912 ACCCTGAT-----GCAAAACAACCTCCAGATTGCAG 2941
Qy 1032 euValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleH 1052
Db 2942 TGACTAGAAATTAAGGGAATAAATATGTGAAACAAACCTTACGTGAATTTATTCTAA 3001
Qy 1052 isThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaL 1072
Db 3002 AAGCA-----TTTTCAAAAGGCCAAAGATTTCCAGGAGATAAGACAACGAG 3049
Qy 1072 euGlySerGlySerArgArg-----ThrSerSerSerGlySerAlaGluProGlyA 1089
Db 3050 AAGATCTGAAATTAAGGGAATAAATATGTGAAACAAACCTTACGTGAATTTATTCTAA 3109
Qy 1089 laAlaHisHisGluMetLysCysProSerAlaArgSerSerProHisSerProTrps 1109
Db 3110 AAGCTCACAATTTCTCCCAAG-----GAAAAAGATAAAATCA 3145
Qy 1109 erAlaAlaSerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAla--- 1127
Db 3146 GTGGTTTGAAGCAGCGTGGACAAACACACTTGATGGAAGACAGTGTGGTCAATCATTTA 3205
Qy 1128 -----ProSerLeuLysArgSerProSerGlyGluArgArgSerLeuLeuSerG 1145
Db 3206 TTCACAATCCAGCCTCACAGTGCAGAGTGCCA-----ATTCACACTG 3247
Qy 1145 lyGluGlyGlnGluSerGlnAspGluGluSerSerGluAspArgAlaSerProA 1165
Db 3248 GGGAA-----TCCGATTTGGAAAATATGAAATGCTGAGAACTTAGCAGTGTGAT 3295
Qy 1165 laGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspL 1185
Db 3296 CGGATAGTGAATAC----- 3309
Qy 1185 euProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaS 1205
Db 3310 -----AGCAAAAGTGAGATTAAACCGGTCAAGCTCT 3340
Qy 1205 erGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgT 1225
Db 3341 CAGAG-----TGAGC-----A 3352
Qy 1225 hrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyG 1245
Db 3353 CAGTTGATAACCTTTGCTGGAGAGGAGAGAGGAGGCTGAACCTTATGATATCCG 3412
Qy 1245 luArgIleGlnAlaTyrValArgSer-----ArgLeuProAlaCysCysArgGluA 1262
Db 3413 ATGACCCAGAGGCGCTGTTTTCACAGATGGTTGTGTACGAGGTTCTCATGTGCCAAGTTA 3472
Qy 1262 rg---AspSerTyrSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCysH 1281
Db 3473 ACATAGAGTCCGGAAGGAAAAAATCTGG-----TGAACATCAGGAAAAACCTGCT 3523


```

Db 5507 AGCGTGTGTTGGGT-----GAGAGTGGGAGATGGATT 5539
QY 1991 erValHisSerGlnProAlaAspThr-SerCysIleLeuGlnLeuProLysAspValHis 2010
Db 5540 CTCTTCGTTACAGATGGAAGAAGGTTCTATGTCTGCAAAATCCTTCCAAAGTGTCTCTATG 5599
QY 2011 TyrLeuLeuGlnProHis 2016
Db 5600 AACCCATCACACACACAC 5617

RESULT 11
US-11-251-465-8
; Sequence 8, Application US/11251465
; Publication NO. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 6371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-251-465-8

Alignment Scores:
Pred. No.: 2,19e-69 Length: 6371
Score: 1633.00 Matches: 546
Percent Similarity: 43.3% Conservative: 376
Best Local Similarity: 25.7% Mismatches: 773
Query Match: 13.6% Indels: 434
DB: Gaps: 74

US-09-611-257A-24 (1-2287) x US-11-251-465-8 (1-6371)
QY 35 ThrArgArgArgMetGlu-----ArgAlaProArgSerArgAsp----- 47
Db 150 ACCCAAGAAGAAAGAAAGATGATGATGAAGAGGCCCAAGCCCAAGCAGTACTGGA 209
QY 48 -----SerProValAlaSerArgSerSerThrThrCys 58
Db 210 AGCTGGCAACAACCTGCCCTTCATCTATGCGGACATTCCTCCGGCATGGTGTGCAGAGCC 269
QY 59 ProGlyProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSer 78
Db 270 CCTGGA---GGACTTGACCCCTACTACTGACAGACAAAAGACTTTCATAGTATTGACAA 326
QY 79 GluAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyr-LeuSerG1 98
Db 327 AGGAAACAAATCTTCCTGTTTCA-----TGCACACCTGCTTTATATATGCTTCTCC 380
QY 98 nAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgVa 118
Db 381 TTTCAGTCCTTAAGAAGAAATATCTATTAAAGATTTTAGTACACTCTCTATTTCAGCATGCT 440
QY 118 lSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgPro----- 135
Db 441 CATCATGTGCACATTTCTGACAAACTGCATATTTATGACCATGAATAACCCGCGGACTG 500
QY 136 -CysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPh 155
Db 501 GACCAAAATATGTC-----GAGTA 518

```

```

QY 155 eIlePhe---AlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIle-- 173
Db 519 CACTTTTACTGGAATATATACCTTTTGAATCACTTGTAAAAAATCTTGCAGAGGCTCTG 578
QY 174 -PheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI1 193
Db 579 TGTAGAGAAATTCACCTTTTCTCGTGACCCGTGGAACCTGGCTGGATTTTGTCTGTCATTGT 638
QY 193 eAlaGlyMetLeuGluTyr-SerLeuAspLeuGlnAsnValSerPheSerAlaValArgTh 213
Db 639 TTTTGGCTATTTAACAGAAATTTGTAAACCTAGGCAATGTT-----TCACCTCTTCGAAC 692
QY 213 rValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVa 233
Db 693 TTTTCAGATATTGAGAGCTTTGAAACTATTCTGTAATCCAGAGCCCTGAAGACAAATTGT 752
QY 233 lThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuLeuLeuLeu 253
Db 753 AGGGGCTTTGATCCAGTCAGTGAAGAGCTTCTGATGTCATGATCTCTGACTGTGTTCTG 812
QY 253 lPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCy 273
Db 813 TCTGAGTGTGTTTGCACATAATTGCACTACAGCTGTTTCATGCGAAACCTCGAAGCATAATG 872
QY 273 sPhe-----LeuProGluAsnPheSerLeuProLeuSerVal----- 285
Db 873 TTTTCGAAATTCACCTTGAATAATTAAGAAACATTGAAGACATAATGAATACCCCTAGAGAG 932
QY 286 -----AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCy 303
Db 933 TGAAGAAGACTTTTAGAAATAATTTTATTACTTGGAGAGATCCAAAGATGCTCTCCTTTTG 992
QY 303 sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyG1 323
Db 993 TGGTTTCAGACACATTCAGTTCAG----- 1017
QY 323 uGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerSerAsnTh 343
Db 1018 -----TGTCAGAGGGGTAC----- 1032
QY 343 rThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisSerProPh 363
Db 1033 -ACCTGTGTGAAATTTGGCAGA-----AACCTCTGA 1061
QY 363 eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValI1 383
Db 1062 TTATGCTACACAGCTTTGACACTTTCAGCTGGGCTTCTTAGCCTTGTTAGGCTAAT 1121
QY 383 eThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAs 403
Db 1122 GACCCCAAGATTACTGGGAAACCTTTTACCACACAGACGCTCGTCTGCGCAAAACCTA 1181
QY 403 nPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuCysLe 423
Db 1182 CATGATCTCTTTGTGCTAGTGAATTTCTGGGCTCTCTTTATCTATAAACTTGTATCCT 1241
QY 423 uValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgG1 443
Db 1242 GGCTGTGTTGCCATGCATATGAAGACAGACAGCAGGCAACACATTGAAGAGCTAAACA 1301
QY 443 uGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySe 463
Db 1302 GAAAGAAATTAGAATTTCAACAGATGTTAGACCGCTCTTAAAAAAAGACAGAAGAGCTGA 1361
QY 463 rCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLe 483
Db 1362 GGCAATTGACGGCGGCGCTGAAATATACAGTATTAGGAGAGCAGAAATATTGGGCTCT 1421
QY 483 uAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValAlaAr 503
Db 1422 CTCAGAGAGTCTCTCT-----GAAACATCCAACTGAGCTCTAAAGAGTGCTAA 1469
QY 503 g-----SerGlyGlnGluPr 508

```


Db 5300 ATTTAGTGTGCCACGAAGAGTACTGAACCTCTG-----AGTGAGAGTACT 5350
Qy 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP 1893
Db 5351 TTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCGATCCGACCCAGTTTATA--- 5406
Qy 1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913
Db 5406 ----- 5406
Qy 1913 laHisIleGlyAlaAlaSerGlyPhe-----SerLeuGluHisProThrMetValProH 1931
Db 5407 --GAGTCTCTAAACTCTCTGATTTTGACGTGCGCTGGATCTCTCTCTCATAGCAA 5464
Qy 1931 isProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyV 1951
Db 5465 AACCCAAACAAAGTCCAGTCTC---ATTGCCATGGATCTGCCCATGGTT-----AGTGGT- 5514
Qy 1951 alSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaG 1971
Db 5515 --GACCGATCCATGTCTT-----GACATCTTATT-----GCTTTTACAA 5554
Qy 1971 luArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuS 1991
Db 5555 AGCGTGTTTGGGT-----GAGAGTGGGAGATGGATT 5587
Qy 1991 erValHisSerGlnProAlaAspThr-SerCysIleLeuGlnLeuProLysAspValHis 2010
Db 5588 CTCTTCGTTACAGATGGAAGAAGTTTCATGTCTGCAAAATCCTTCCAAAGTGTCTTATG 5647
Qy 2011 TyrLeuLeuGlnProHis 2016
Db 5648 AACCCATCACAAACCAC 5665

RESULT 12

US-11-266-748A-56579
; Sequence 56579, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266.748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56579
; LENGTH: 6371
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56579

Alignment Scores:

Pred. No.: 2,19e-69 Length: 6371
Score: 1633.00 Matches: 546
Percent Similarity: 43.3% Conservative: 376
Best Local Similarity: 25.7% Mismatches: 773
Query Match: 13.6% Indels: 434
DB: 8 Gaps: 74
US-09-611-257A-24 (1-2287) x US-11-266-748A-56579 (1-6371)
Qy 35 ThrArgArgMetGlu-----ArgAlaProArgSerArgAsp----- 47
Db 150 ACCCAAGAAAGAAAGATGATGATGAAGAGCCCAAGCCCAAGCAGTACTTGGGA 209
Qy 48 -----SerProValAlaSerArgSerSerThrThrCys 58
Db 210 AGCTGGCAACAACCTGCTTCATCTATGGGGACATCTCCCGGCATGGTGTGAGAGCC 269
Qy 59 ProGlyProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSer 78
Db 270 CCTGGA---GGACTTGGACCCCTACTATGCAGACAAAGACATTTTCATAGTATTGAACAA 326
Qy 79 GluAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyr-LeuSerGl 98
Db 327 AGGAAACAAATCTCTCGCTTTCAA-----TGCCACACCTGCTTTATATATGCTTTCTCC 380
Qy 98 nAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTrpPheGluArgVa 118
Db 381 TTTTCAGTCTCTTAAGAAGAATATCTATTAAAGTTTATGATACATCTCTTTTTCAGCATGCT 440
Qy 118 lSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgPro----- 135
Db 441 CATCATGTGCATTTCTTGACAAATCATATTATGACCATGAATAACCGCGGACTG 500
Qy 136 -CysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPh 155
Db 501 GACCAAAATGTC-----GAGTA 518
Qy 155 ellePhe--AlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIle-- 173
Db 519 CACTTTTCTGGAATATATATCTTTTGAATCACTTGTAAATAATCTTCAAGAGAGCTTCTG 578
Qy 174 -PheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIl 193
Db 579 TGTAGGAGATTCTACTTTTCTCGTGAACCGTGAACCTGGCTGGATTTTGTCGCTATTGT 638
Qy 193 eAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgTh 213
Db 639 TTTTGGCTATTTAACAGAAATTTGTAAACCTAGGCAATGTT-----TCAGCTCTCGAAC 692
Qy 213 rValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVa 233
Db 693 TTTTCAGAGATTGAGAGCTTTGAAACATATTCTGTAAATCCAGGCTCGAAGACAAATTGT 752
Qy 233 lThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheVa 253
Db 753 AGGGGCTTTGATCCAGTCAGTGAAGAAGCTTCTGATGTCATGATCTCATGCTGCTGTTCTG 812
Qy 253 lPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCy 273
Db 813 TCTGAGTGTGTTTGCACTAATTGGACTACAGCTTTCATGATGTCATGATCTCATGCTGCTG 872
Qy 273 sPhe-----LeuProGluAsnPheSerLeuProLeuSerVal----- 285
Db 873 TTTTCGAAATTCACCTTGAAATAATGAACATTTAGAAAGCATATGATACCTTAGAGAG 932
Qy 286 -----AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCy 303
Db 933 TGAAGAAAGACTTTAGAAAAATATTTTATTACTTGAAGGATCCAAAGATGCTCTCCTTTG 992
Qy 303 sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGl 323
Db 993 TGGTTTCAGCACAGATTCAGGTCTAG----- 1017

323	uGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAsn	343
1018	-----TGTCCAGAGGGGTAC-----	1032
343	rThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPh	363
1033	-ACCTGTGTGAAATTTGGCAGA-----AACCTCTGA	1061
363	eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValI	383
1062	TTATGGCTACACGAGCTTTCACACTTCAGCTGGCCCTCTTAGCCCTGTTTAGGCTAAT	1121
383	eThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAs	403
1122	GACCAAGATTACTGGGAAAAACCTTTACCAACACAGACGCTCGTCTGGCAAAACCTA	1181
403	nPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuCysLe	423
1182	CATGATCTCTTGTGTAGTAGATTTTCCTGGGCTCTTTTATCTAATAAATTTGATCCT	1241
423	uValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgG	443
1242	GGCTGTGTGTCATATGAAGAACAGACACCGCAAAACATTGAAGAAGCTAAACA	1301
443	uGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySe	463
1302	GAAGAAGTAATGAATTTCAACAGATGTTAGACCGCTCTTAAAAAAGAGCAAGAAGCTGA	1361
463	rCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgL	483
1362	GGCAATTGACGGCGACGGCTGAATATACAAGTATTAGGAGAGCAAGAAATTATGGGCC	1421
483	uAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValAlaAr	503
1422	CTCAGAGATTCTTCT-----GAAACATCCAACCTGAGCTCTAAAAGTGCATA	1469
503	g-----SerGlyGlnGluPr	508
1470	AGAAAGAGAAACACAGAAAGAAAGAAAGAAATCAAAAGAGCTCTCCAGTCGAGAGGAAA	1529
508	oGlnProSerGlySerCysThrArgSerHis-----ArgArgLeuSerVa	523
1530	GGGAGATGCTGGAGAAATTTGCGAAATTCAGAAATCAGAGCAGCATCAGAGAAAAAGTTT	1589
523	lHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis	543
1590	CCACCTTGGTGTGCAAGGGCATAGGCAGCACATGAAAG-----AG	1631
543	rLeuArgValProArgAlaSerProGluIleGlnAspArgAspAla-----	558
1632	GTGTCTACCCCAATCAGTCACCA---CTCAGCATTCGTGGCTCTTGTTCCTGCAAG	1688
559	-AsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyPr	578
1689	GCGAAGCAGCAGAACCAAGTCTTTTAGTTTCAAAGGCAGAGAGAGATATAGATCTGA	1748
578	oProArgGlyAlaGluSerValHisSer-PheTyrHisAlaAspHisLeuLeuProV	598
1749	GACTGAATTTGGCCATGATGAGCACACATTT-----TTGGAGACAA	1790
598	alArgCysGlnAlaProProProArgCysProSerGlu--AlaSerGlyArgThrValG	617
1791	TGAGCAGAGAAGGGGCTCACTGTTTGTGCCCCACAGACCCAGGAGCGACGACAGTAA	1850
617	lySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspL	637
1851	CATCAGCCAAG-----	1861
637	ysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleP	657
1862	-----C	1862
657	roProGlyProPheSerSerMethHisLysLeuLeuGluThrGlnSerThrGlyAlaCysH	677

Db	1863		CATAGTCTCC-----	1874
Qy	677	isSerSerCysLysIleSerSerProCysSerLysAla---	AspSerGlyAlaCysGlyP	696
Db	1875	ACCAATCTGCCGTGNAACGGGAAATGCACACAGTCTGTGAGCTGCAACCGTGTGGTCTC	1934	
Qy	696	ro-----	AspSerCysProTyrcysAlaAargThrGlyAlaGlyGluProGluSerA	713
Db	1935	CCTGGTTGATGGACGCTCAGCCCTCATGTCTCCCC-AATGACACAGCTTCTGCCAGAGGCA	1993	
Qy	713	laAspHisValMetProAspSerAspSerCduLaValTyrgluPheThrGluAspAlaG	733	
Db	1994	CGACCAATCAAAATACACAAGAAAGGGTGTGTAGTCTCTATCTCTTTCAGAGGATATG-	2052	
Qy	733	lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753	
Db	2053	-----	CTGAATGATCCCAACCTCAGACAGAGCAATGAGT-----	2088
Qy	753	laGluProSerValLeuAla-	760	
Db	2089	-----	AGACCAAGCATATTAAACAACACACTGTGAAGAACTTTGAAGAGCTCCAGACAAAAT	2143
Qy	761	-----	PheTrpArgLeuIleCysAsp- 767	
Db	2144	GTCACCTGGTGGTACAGATTGGACACAAATTCCTTGATCTGGAAT-----	TGCTCTC 2197	
Qy	768	-----	ThrPheArgLys-----IleValAspSerLysTyrcPheGlyA 780	
Db	2198	CATATTGGATAAAATTCAAAAGTGATCTATTTATTGTAATGGATCCTTTTGTAGATC	2257	
Qy	780	rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrcHisGluG	800	
Db	2258	TTGCAATTACCATTTGTCATAGTTTAAACACATATTTATTATGGCTATGGAAACACCCACCA	2317	
Qy	800	lnProGluGluLeuThrAsnAlaIleuCluIleSerAsnIleValPheThrSerLeuPheA	820	
Db	2318	TGACTGAGGAATTCAAAATGTACTGCTATAGAAATTTGGTCTTTTACTTGGAAATCTTTG	2377	
Qy	820	laLeuGluMetLeuLeuLysLeuValTyrglyProPheGlyTyrcIleLysAsnProT	840	
Db	2378	CAGCTGAAATGGTATTAAACTGATGCCATGCATATGATGATATTCACAGTAGCT	2437	
Qy	840	yrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValIleGlyGlnGlnG	860	
Db	2438	GGAATATTTTGACAGCCTTATTGTGACTTTAAGTTTAGTGGAGCTCTTTCTAGCAGATG	2497	
Qy	860	lyGlyGlyLeuSerValLeuArgThrPheArgIleuMetArgValLeuLysLeuValArgP	880	
Db	2498	TGGAAGGAAATGTGAGTTCTCGCATCATTCAGACTGCTCCAGCTCTTCAAGTGTGGCAAAAT	2557	
Qy	880	heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaAt	900	
Db	2558	CCTGGCCAACTTGAACATCTGATTAAGATCATTTGGTACTCAGTAGGGGCTCTAGGTA	2617	
Qy	900	hrPheCysMetLeuLeuMetLeuPheIlePhePheSerIleLeuGlyMetHisLeuP	920	
Db	2618	ACCTCACCTTAGTTGGCCATCATCGTCTTCATTTTTTGTGTGGTGGCATGCGAGCTCT	2677	
Qy	920	heGly-----	CysLysPheAlaSerGluArgAspGlyAspThrIL 933	
Db	2678	TTGTTAGAGACTACAAGAAATGTCTGCAAGATC-----	AATGATGACTGTGACGC 2728	
Qy	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953	
Db	2729	TCCCA-----	CGTGGCACATGAACGACTTCTTCACCTCTTCCTGATTTGTTCGCGTGC 2785	
Qy	953	euThrGlnGluAspTrpAsnLysValLeuTyrcAsnGlyMet-----	AlaSerThrSerSerT 972	
Db	2786	TGTTGTGGAGAG--	TGGATAGACCATGTGGGAGCTGATGGAGTTCGCTGGTCAAGCTA 2842	
Qy	972	rpAlaAlaLeuTyrcPheIleAlaLeuMetThrPheGlyAsnTyrcValLeuPheAsnLeuL	992	

Db 2843 TGTGCTATTGTTTACATGATGTCATGTCATTTGGAACCTTGGTGGTCTCTAAACCTAT 2902
Qy 992 euValAlaIleLeuValIleGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerG 1012
Db 2903 TTCTGGGCTTATTATTGAGCTCATTTTATGTCAGAC--AATCTTACAGCAATTGAAGAAG 2959
Qy 1012 luProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgGluAlaL 1032
Db 2960 ACCCTGAT-----GCAACAACCTCAGATTGCAG 2989
Qy 1032 euValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleLeH 1052
Db 2990 TGACTAGAAATTAAGGAAGGAATAATTATGTAACAAACCTTACGTGAATTTATCTAA 3049
Qy 1052 isThrAlaAlaThrProMetSerHisProLysSerSerThrGlyValGlyGluAlaL 1072
Db 3050 AAGCA-----TTTTCAAAAGGCCAAGATTTCCAGGAGATTAAGACAAGCAG 3097
Qy 1072 euGlySerGlySerArgArg-----ThrSerSerGlySerAlaGluProGlyA 1089
Db 3098 AAGATCTGAATCTAAGAGAGAAACTATATTTCTAACCATACACTTGCTGAATGAGCA 3157
Qy 1089 laAlaHisGluMetLysCysProProSerAlaArgSerProHisSerProTrps 1109
Db 3158 AAGGTCACAATTTCTCTCAAG-----GAAAAAGATAAAATCA 3193
Qy 1109 erAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAla 1127
Db 3194 GTGTTTTGGAGCAGCGCTGACAAACACTTGATGGAGACAGTCAGTGGTCAATCATTTA 3253
Qy 1128 -----ProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuSerG 1145
Db 3254 TTCACATCCAGCTCACAGTCAGTGCCA-----ATTGCACCTG 3295
Qy 1145 lyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspArgAlaSerProA 1165
Db 3296 GGGAA-----TCCGATTTGGAAAAATATGAATGCTCAGGAACTTAGCAGTGTATT 3343
Qy 1165 laGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspL 1185
Db 3344 CGGATAGTGAATAC----- 3357
Qy 1185 euProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlas 1205
Db 3358 -----AGCAAGTCAGATTAAACCGGTCAAGCTCCT 3388
Qy 1205 erGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgT 1225
Db 3389 CAGAG-----TGCAGC-----A 3400
Qy 1225 hrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuSerLysGlyG 1245
Db 3401 CAGTTGTAAACCTTTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3460
Qy 1245 luArgIleGlnAlaTrpValArgSer-----ArgLeuProAlaCysCysArgGluA 1262
Db 3461 ATGACCCAGAGCCCTGTTTTCAGATGTTGTGTACGGAGGTCTCTCATGCTGCCAAGTTA 3520
Qy 1262 rg---AspSerTrpSerAlaTyrllePheProGlnSerArgPheArgLeuLeuCysH 1281
Db 3521 ACATAGAGTCAGGGAAGGAAAAATCTCG-----TGGAAACATCAGGAAAAACCTGCT 3571
Qy 1281 isArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnC 1301
Db 3572 ACAAGATTGTTGAACACAGATGGTTTGAAGAGCTTCATTGCTCTCATGATCTCTGCTCAGA 3631
Qy 1301 ysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheL 1321
Db 3632 GTGGGCCCCGCTTTTGAAGATATTTATATTGAAAGGAAAAAGACCATTAAAGATTATCC 3691
Qy 1321 euThrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGluMetThrValLysValV 1341
Db 3692 TGGAGTATGCAGACAAGATCTTCACTTACATCTTCACTTCACTTCACTTCACTTCACTT 3751

Qy 1341 alAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrlleuArgSerSerTrpAsnValLeuA 1361
Db 3752 TAGCA-----TATGGTTATAAAACATATTTACCAATGCCTGGTGTGGCTGG 3799
Qy 1361 spGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerG 1381
Db 3800 ATTTCTTAATTTGTATGTTTCTTGTGTTCTTCTAGTGGCAACACTCTT-----G 3850
Qy 1381 lyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuA 1401
Db 3851 GCTACTCAGATCTTGGCCCCCATTAATCCCTTCGGACACTGAGAGCTTTTAAGACCTCTAA 3910
Qy 1401 rgValIleSerArgAlaGlnGlyLysLeuValValGluThrLeuMetSerSerLeuL 1421
Db 3911 GAGCTTATCTAGATTTGAAGGAATGAGGGTCGTTGTGAATGCACCTCATAGGACCAATTC 3970
Qy 1421 ysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuG 1441
Db 3971 CTTCCATCATGAATGTCTACTTGTGTCTTATATTTCTGGCTGATATTCAGCATCATGG 4030
Qy 1441 lyValGlnLeuPheLysGlyLysPheValCys-----GlnGlyGlu--- 1455
Db 4031 GAGTAAATTTGTTGCTGGCAAGTTCTATGAGTGATTAACACCACAGATGGGTACGGT 4090
Qy 1456 --AspThrArgAsnIleThrAsnLysSerAspCys-----AlaGluAlas 1470
Db 4091 TTCTCTGCAAGTCAAGTTCCAAATCGTTCCGAATGTTTTGCTTATGCAATGTTAGTCAAA 4150
Qy 1470 erTyArgTrpValArgHisLysTyAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
Db 4151 ATGTGCGATGAAAAACCTGAAAGTGAACCTTGATAATGTGCGACTTGGTTTACCTATCTC 4210
Qy 1490 euPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrlleLeuAspAlav 1510
Db 4211 TGCTTCAAGTTGCAACTTTTAAAGGATGGAGATTATTTATGATGCGAGCAGTGATTCGT 4270
Qy 1510 alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrlleLes 1530
Db 4271 TTAATGTAGACAAGCACCACCAATATGAATATATGACCTCTACATGTATATTTTGTGCG 4330
Qy 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
Db 4331 TCTTTATCATCTTTGGGTCACTTCTTCACTTTTGAACCTTGTTCATCTGGTGTCTACATAGA 4390
Qy 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAla---ArgArgArgGluGluL 1569
Db 4391 ATTTCAACCAACACAGAAAGAGAGCTTGAGGTCAAGACATCTTTATGACAGAAGACAGA 4450
Qy 1569 ysArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaG 1589
Db 4451 AGAAATACTATATGCAATGAAAAGCTGGGGTCCAAGAGCCACAA----- 4497
Qy 1589 lnCysLysProTyTyTrpSerAspTyrllePheArgPheArgLeuLeuValHisLeuCysT 1609
Db 4498 -----AAGCCAAATTCCTCGACAGGAGCAAAAATCCAAAGGATGATATTTGACCTAGTGA 4552
Qy 1609 hrSerHisTyrlleAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetA 1629
Db 4553 CAATCAAGCCTTTGATATTAGTATCATGGTCTTCTTATCTGTCTCAACATGGTAACCATGA 4612
Qy 1629 laMetGluHisTyrlleGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrl 1649
Db 4613 TGGTAGAAAAGGAGGGGTCAAAAGTCAACATATGACTGAAGATTATATTTGGTATAAATGTGG 4672
Qy 1649 lePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgA 1669
Db 4673 TTTTATAATCCTTTTCTCAGAGAAATGTGTGCTAAACCTGATCTCCCTCACA---CACT 4729
Qy 1669 rgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG 1689
Db 4730 ACTACTTCACTGTAGGATGGAATATTTTGTGTTTGTGTTGTGATTTATCTCCATTTGTAG 4789

```
Qy 1689 lylerThrLeuGluGlu---ileGluValAsnLeuSerLeuProIleAsnProThrIleI 1708
Db 4790 GTATGTTTCTAGCTGATTTGATTGAAACGATATTT-----GTGTCCCTACCTGT 4840
Qy 1708 leArgIleMetArgValLeuArgValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 1728
Db 4841 TCCGAGTGATCCGCTCTTCCGAGGATGGCCGAATCCCTACGTCTAGTCAAAAGGACAAAG 4900
Qy 1728 lyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyL 1748
Db 4901 GGATCCGACGCTGCTCTTCTTGTATGATGTCCTCTCTCGCTGTTTAAACATCGGCC 4960
Qy 1748 euLeuPheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspL 1768
Db 4961 TCCTGCTCTTCTGCTCATGTTCTATCTACGCCATCTTTGGAATGTCCAACCTTTCCTATG 5020
Qy 1768 euGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsn 1788
Db 5021 TTAATAAGGAA-----GATGGAATTAATGACATGTTCAAATTTTGAGACCT 5065
Qy 1788 heGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleM 1808
Db 5066 TTGCAACAGTATGATTGCTGTTCCTCAATTAACACCTCTGCTGCTGGATGGATGTC 5125
Qy 1808 et-----LysAspProSerArgAspCysAspGln----- 1817
Db 5126 TAGCACCTATTCTTAACAGTAAGCACCC-----GACTGTGACCCAAAAAAGTTTCATC 5179
Qy 1818 -----GluSerThrCysTrpAsnThrValIleSerProIleThrPheValS 1833
Db 5180 CTGGAAGTTCAGTTGAAGGAGACTGTGTAACCATCTGTTGGAATATTTCTACTTTGTTA 5239
Qy 1833 erPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysH 1853
Db 5240 GTTATATCATCATATCTCTCTGTTGTGTGAACATGTACATTCAGATCATATCTGAGA 5299
Qy 1853 isLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluLeuGluL 1873
Db 5300 ATTTTAGTGTGCCACTGAAGAAAGTACTGAACCTCTG-----AGTGAGGATGACT 5350
Qy 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP 1893
Db 5351 TTGAGATGTTCTATGAGTTTGGGAGAAAGTTTGATCCCGATGCGACCCAGTTTATA---- 5406
Qy 1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrA 1913
Db 5406 ----- 5406
Qy 1913 laHisIleGlyAlaAlaSerGlyPhe-----SerLeuGluHisProThrMetValProH 1931
Db 5407 --GAGTTTCTAAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCTCTTCATAGCAA 5464
Qy 1931 isProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyV 1951
Db 5465 AACCCAAACAAAGTCCAGCTC---ATTGCCATGGATCTGCCCATGGTT-----AGTGGT- 5514
Qy 1951 alSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaG 1971
Db 5515 --GACCGGATCCATTGCTT-----GACATCTTATTT-----GCTTTTACAA 5554
Qy 1971 luArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuS 1991
Db 5555 AGCGTGTGTTGGGT-----GAGAGTGGGGAGATGGATT 5587
Qy 1991 erValHisSerGlnProAlaAspThr-SerCysIleLeuGlnLeuProLysAspValHis 2010
Db 5588 CTCTTCGTTCACATGGAAGAAAGGTTCATGTTCTGCAAAATCTTCCAAAAGTGCCTATG 5647
Qy 2011 TyrLeuLeuGlnProHis 2016
Db 5648 AACCCATCACACACACAC 5665
```

RESULT 13

```
US-11-263-326-98
; Sequence 98, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; TYPE: DNA
; LENGTH: 7008
; ORGANISM: Homo sapiens
US-11-263-326-98
```

```
Alignment Scores:
Pred. No.: 2,01e-67 Length: 7008
Score: 1593.00 Matches: 583
Percent Similarity: 40.5% Conservatives: 397
Best Local Similarity: 24.1% Mismatches: 816
Query Match: 13.2% Indels: 624
DB: Gaps: 88
```

US-09-611-257A-24 (1-2287) x US-11-263-326-98 (1-7008)

```
Qy 1 MeLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20
Db 13 ATGGCGCCCAACCCAGTCGCCGCCGCATCTCTCGCGCCTTTTGACGTCCGGC----- 66
Qy 21 ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgAlaMetGlu 40
Db 67 -----CGCGCCTCC 75
Qy 41 ArgAlaProArg-----SerArgAspSerProValAlaSerArgSerSerThrCys 58
Db 76 CGGGCCCCGGTTTAGGCGCGCCTGCTCTCCTCGCGCGCGCGCTGCCAGTCACCTGT 135
Qy 59 ProGly-----ProGlyAlaAlaGlyAla 66
Db 136 CTGGAGCGCAGCATAACTAACAAGCTGCTGCAGGATGAGAAGATGGCAGCGCGTGTCT 195
Qy 67 GlySerThr----- 69
Db 196 TGCACCAACAGGCCCTGATAGTTTCAAGCCTTTTCAACCCCTGAGTCACTGGCAACATTGA 255
Qy 69 ----- 69
Db 256 GAGCGCATTTGCTTGAGAGCAAGCTCAAGAAACCAACCAAGCCGATGGCAGTCATCGGA 315
Qy 70 -----GluLysAspProGlySerAlaAspSerGluAla 80
Db 316 GGACGATGAGGACAGCAAGCCCAAGCCAAACAGCGACCTCGAAGCAGGAGAGTTTGCC 375
Qy 81 GluGlyLeu-----ProTyrProAlaLeuAla-ProValValPhePhe----- 94
Db 376 TTTTCATCTACGGGACATCCCCCAAGCCTGTTGAGTTCCCTCTGGAGGACTTTGACCC 435
Qy 95 ----TyrLeuSerGln----- 98
Db 436 ATACTATTTGACGCAGAAACCTTTGTAGTATTAAACAGAGGAGAAACTCTCTTCAGATT 495
Qy 99 -AspSerArgPro-----ArgSerTrpCysLe 107
Db 99 ---- 107
```


Qy 752 -----AspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysA 767
Db 2364 CTTTCCTCATCTGGAGTGCACCCC-----TACTGGATAAAATGAAAG 2408
Qy 767 spThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleL 787
Db 2409 AGATTGTGAACCTTGTATGATAGTTATGGACCCCTTTTGTGGATTAGCCATCACCATCTGCATCG 2468
Qy 787 euValaenThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnA 807
Db 2469 TCCTGAATACACTGTTATGGCAATGGAGCACCATCTATGACACCAAAATTTTGAACATG 2528
Qy 807 laLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysL 827
Db 2529 TCITGGCTGTAGGAAATCTGGTTTTTCACTGGAATTTTTCACAGCGGAAATGTTCTCTGAAGC 2588
Qy 827 euLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValI 847
Db 2589 TCATAGCCATGGATCCCTACTATTATTCCAAAGAGGTTGGAACATTTTTCAGCGGATTTA 2648
Qy 847 leValValIleSerValTyrGluIleValGlyGlnGlyGlyGlyLeuSerValLeuA 867
Db 2649 TTGTCTCCCTCAGTTTAAATGAACTGAGCTAGCAGACGTGGAGGGCTTTTCAGTGTCTG 2708
Qy 867 rgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArg 887
Db 2709 GATCTTTCGATTGCTCGAGTCTCAAAATTTGGCCAAATCCTGGCCCCACCCTGAACATGC 2768
Qy 887 lnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetL 907
Db 2769 TAATCAAGATTATTGGAAATTCATGGGTGGTCCCTGGGCCAACCTGTGTCGGCCA 2828
Qy 907 euPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGly----- 921
Db 2829 TTATTGTCTTCATCTTTGGCCGTGGGGATGCACTCTTTGGAAAAAGCTACAAAGAGT 2888
Qy 922 -----CysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA 940
Db 2889 GTGTCTGCAAGATCAACAGGACTGTGAA-----CTCCCT---CGCTGGCATATGC 2936
Qy 940 spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL 960
Db 2937 ATGACTTTTTCATCTCCTCATCTCTTCTCGAGTGTGTGGGGGAG---TGGATTG 2993
Qy 960 ysValLeuTyrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleA 979
Db 2994 AGACCATGTGGAGTGCATGGAAGTGCAGCCAGGCCATGTGCTCTTTTAIGA 3053
Qy 979 laLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG 999
Db 3054 TGGTCATGGTGATTTGGCAACTTGGTGTGTGAACCTGTTCTGGCCCTTGTCTCTGAGCT 3113
Qy 999 lyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS 1019
Db 3114 CCTTCAGTGACAGACAACCTGGCT-----G 3137
Qy 1019 erValAspGlyAspGlyAspArg-----LysLysA 1029
Db 3138 CCACAGATGAGTGGGGAATGAAACACCTCCAGATCTCAGTGATCCGTATCAAGAAGG 3197
Qy 1029 rgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeu----- 1045
Db 3198 GTGTGGCTTGGACCAAACTAAAGGTGCAGCGCTTCATGAGGCCCACTTTTAAGCAGCGTG 3257
Qy 1046 -----LeuProProLeuIleIleHisThrAlaAlaThrProMetS 1059
Db 3258 AGGCTGATGAGGTGAAGCCTCTGGATGAGTTGTATGAAAGAGAGGCCAACTGTATCGCCA 3317
Qy 1059 erHis-ProLysSerSerSerThrGlyValGlyGlyAlaLeuGlySerGlySerArg 1078
Db 3318 ATCACACGTGCAGACATCCACCGGAATG----- 3347
Qy 1079 ThrSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProPro 1098

Db 3348 -----GTGACT 3353
Qy 1099 SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrp-----ThrSer 1116
Db 3354 TCACAGAATGATGCAACAGCGCGCTTGGCAGCGATGGAGGAGTACATCA 3413
Qy 1117 ArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSer 1136
Db 3414 TT-GATGAGGACCACATGCTCTTCATCAACAACCCCACTTGACTGTACGGGTACCC- 3469
Qy 1137 GlyGluArgArgSerLeuLeuSerGlyGluGly-----GlnGluSerGlnAspGluGlu 1154
Db 3470 -----ATTGCTGGCGAGTCTGACTTTTGAGAACCTTCAACACAGAGGAT 3514
Qy 1155 GluSerSerGluAlaArgAlaSerProAlaGlySerAspHisArgHisArgGlySer 1174
Db 3515 GTTAGCAGCGAGTCCGAT-----CCTGAAGCGACAAAGATAAATACTAGATGACACC 3565
Qy 1175 LeuGluArgGluAlaLysSerSerPheAspLeu---ProAspThrLeuGlnValProGly 1193
Db 3566 AGCTCCTCTGAAGGA---AGCACATTGATATCAAAACAGAGTAGAAGAGGTCCT- 3619
Qy 1194 LeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLys 1213
Db 3619 ----- 3619
Qy 1214 SerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAsp 1233
Db 3620 -----GTGGAACAGCCTGAGGAATACTTTGGATCCAGAT 3652
Qy 1234 AspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSer 1253
Db 3653 GCCTGCTTACACAGAGTTGTGTCCAGCGGTTCAAG----- 3688
Qy 1254 ArgLeuProAlaCysCysArgGluArg-----AspSerTrpSerAla 1267
Db 3689 -----TGCTGCCAGTCAACATCGAGGAAGGCTGAGCAAGTCTTGC- 3730
Qy 1268 TyrIlePheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLys 1287
Db 3731 TGGATC-----CTCGGAAAAACCTGCTTCTCATCTGGGACCAAC 3772
Qy 1288 MetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGlu 1307
Db 3773 TGGTTGAGACCTTCATCATCTTCATGATTTCTGCTGAGCAGTGGCGCCTTGGCTTCGAG 3832
Qy 1308 ArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIle 1327
Db 3833 GACATCTACATTGACGAGAGAAAGACCATCCGCACCATCTCTGGAATATGTGCAAAAGTC 3892
Qy 1328 PheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPhe 1347
Db 3893 TTCACCTATATCTTCATCTCGGAGATGTTGCTCAAGTGGAGCAGCTATGCTTCGTC- 3949
Qy 1348 GlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeu 1367
Db 3950 -----AAGTTCTTCCAAATGCCTGTTGGCTGGACTTCTCATTTGCTGCTGTC 4000
Qy 1368 SerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMet 1387
Db 4001 TCTTTAGTCAGCCTTAGTAATAGTCCCTG-----GGCTACTCGGAACATAGGTGCC 4051
Qy 1388 LeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGln 1407
Db 4052 ATAAAGTCCCTTAGACCCCTAAGAGCTTTGAGACCCCTTAAGAGCCTTATCAGCATTTGAA 4111
Qy 1408 GlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleVal 1427
Db 4112 GGGATGAGGTGTGGTGAATGCTTGTGGGGGCCATCCCTCCCATCATGAATGTGCTG 4171
Qy 1428 ValIleCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGly 1447
Db 1447 ----- 1447

QY 1046 -----LeuProProLeuIleIleHisThrAlaAlaThrProMets 1059
Db AGCTGATGAGGTGAAGCCCTCGATGATGTTGATGAAAGAGGCCAACTGATCGCCA 3317
QY 1059 erHis-ProlysSerSerThrGlyValGlyAlaLeuGlySerGlySerArgArg 1078
Db ATCACACCGGTGAGACATCCACCGGAATG----- 3347
QY 1079 ThrSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProPro 1098
Db -----GTGACT 3353
QY 1099 SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrp-----ThrSer 1116
Db TCCAGAAAGTGGCAATGGCACACACAGCGCATTTGGCAGCAGCGTGGAGAGTACATCA 3413
QY 1117 ArgArgSerSerArgAnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSer 1136
Db TT-GATGAGGACCACATGTCCTTCATCAACAACCCCAACTTGACTGTACGGGTACCC--- 3469
QY 1137 GlyGluArgArgSerLeuSerGlyGluGly-----GlnGluSerGlnAspGluGlu 1154
Db -----ATTGCTGGCGGAGTCTGACTTTGAGAACCTCAACACAGAGGAT 3514
QY 1155 GluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySer 1174
Db GTTAGCAGCGAGTCGGAT-----CCTGAAGGCAGCAAGAGATAAACTAGATGACACC 3565
QY 1175 LeuGluArgGluAlaLysSerSerPheAspLeu---ProAspThrLeuGlnValProGly 1193
Db AGCTCCTCTCAAGGA---AGCACCATTTGATATCAACCCAGAAAGTGAAGAGTCCCT--- 3619
QY 1194 LeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLys 1213
Db ----- 3619
QY 1214 SerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAsp 1233
Db -----GTGGAACAGCCTGAGGAATACTTTGGATCCAGAT 3652
QY 1234 AspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSer 1253
Db GCCTGCTTCAGAAAGTTGTGTCCAGCGTTCAAG----- 3688
QY 1254 ArgLeuProAlaCysArgGluArg-----AspSerTrpSerAla 1267
Db -----TGCTCCAGGTCACATCATCAGGAAGGGCTAGGCAAGTCTTGG--- 3730
QY 1268 TyrIlePheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLys 1287
Db TGGATC-----CTGCGGAAAAACCTGCTTCCTCATCGTGGAGCACAAAC 3772
QY 1288 MetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGlu 1307
Db PheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGlu 1307
QY 1307 TGGTTTGAGACCTTCATCATCTTCATGATTCGTGTGAGCAGTGGCGCCCTGGCCTTCGAG 3832
QY 1308 ArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIle 1327
Db GACATCTACATTTGAGCAGAGAAAGACCATCCGACCATCTTGGAAATATGTCGACAAAGTC 3892
QY 1328 PheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPhe 1347
Db TTCACCTATATCTTCATCCTGGAGATGTTGCTCAAGTGGACAGCCTATGGCTTCGTC--- 3949
QY 1348 GlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIle 1367
Db -----AAGTTCTTCACCAATGCCTGGTGTGGCTGGCATTCCTCATTTGGCTGTC 4000
QY 1368 SerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMet 1387
Db TCITTAGTCAGCCTTATAGCTAATGCCTG-----GGCTACTCGGAACCTAGGTGCC 4051
QY 1388 LeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGln 1407

Db ATAAAGTCCCTTAGGACCCCTTAAGAGCCTTAAGAGCCTTATCAGATTGGAA 4111
QY 1408 GlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleVal 1427
Db GGTATGAGGTGGTGGTGAATCCTTGGTGGCGCCATCCCTCCCATCATGATGTGCTG 4171
QY 1428 ValIleCysCysAlaPhePheIleIlePheGlyLeuGlyValGlnLeuPheLysGly 1447
Db CTGGTGTGCTCATCTTCTGGCTGATTTTCAGCATCATGGGAGTTAACTTTGTTGGCGGA 4231
QY 1448 LysPhePheValCysGlnGlyGlu-----AspThrArgAsnIleThr 1461
Db AAGTACCATCTACTGCTTTAATGAGACTTCTGAAATCCGATTTGAAATTTGAAGATGTCAAC 4291
QY 1462 AsnLysSerAspCysAlaGlu-----AlaSerTyrArgTTPValArg 1475
Db AATAAACTGAAATGTGAAAGCTTATGGAGGGAACAAATACAGAGATCAGATGGAAGAAC 4351
QY 1476 HisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSer 1495
Db GTCAAGATCAACTTTGACAATGTTGGGCAGGATACCTGCCCTTCTTCAAGTAGCAAC 4411
QY 1496 LysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGln 1515
Db TTCAAAGGCTGGATGGACATCATGTATGACAGCTGTAGATTCCCGGAAGCCTGTAGCAG 4471
QY 1516 ProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuVal 1535
Db CCTAAGTATGAGCAACAATATCTACATGTACATCTATTTGTCTATCTTCATCTTCGGC 4531
QY 1536 AlaPhePheValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArg 1555
Db TCCTTCTTCAACCTGAACTGTTTCAATGGTGTCTATTCATTAATCAATCAACAAAG 4591
QY 1556 GlnHisGlnGluGluGluAla---ArgArgArgGluGluLysArgLeuArgArgLeu 1574
Db AAAAAGTTCGAGCTCAGGACATCTTCATGACCCGAAGACAGAAAGTAGTACTACAATGCC 4651
QY 1575 GluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyr 1594
Db ATGAAAGAGCTGGCTCAAAGAACCCACAC-----AAACCCATTTCCC 4693
QY 1595 SerAspTyrSerArgPheArgLeuValHisHisLeuCysThrSerHisTyrLeuAsp 1614
Db CGCCCTTGAACAAATCCAAAGGAATCGTCTTTGATTTTGTCTCACTCAGCAAGCCTTTGAC 4753
QY 1615 LeuPheIleThrGlyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGln 1634
Db ATGTATCATGATGTCTCATCTGCTTAAACATGGTGAACAATGATGGTGGAGACAGACACT 4813
QY 1635 GlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePhe 1654
Db CAAAGCAGCAGATGGAGAACATCTCTACTGGATTAACCTGGTGTGTTTGTATCTTCTTC 4873
QY 1655 ValPheGluSerValPheLysLeuValAlaPheAlaPheArg---PhePheGlnAsp 1673
Db ACCTGTGAGTGTGTCTCAAAATG-----TTTGGCTTGGGCACACTACTACTTCAACATT 4927
QY 1674 ArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlu 1693
Db GGCTGGAACATCTTCGACTTCGTGGTAGTATCTCTCCATTTGGAATGTTCTTCTGGCA 4987
QY 1694 GluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgVal 1713
Db GATATATTCAGAAATACTTT-----GTTTCCCAACCTTATTCGAGTCATCCGATTG 5041
QY 1714 LeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeu 1733
Db GCCCGTATTGGCGCATCTTTGCGTCTGATCAAAAGGCCCAAGGGATTTCGTACCTGCTC 5101
QY 1734 HisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuPheMetLeuLeu 1753

```
Db 5102 TTTGCCTTAATGATGTCCTTGGCTGCTGTTCAACATCGGCTTCTGCTCTTCTCGTGC 5161
Qy 1754 PhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThr 1773
Db 5162 ATGTTTCATCTTCTCCATTTTGGGATGTCCTAAATTTTCATATGTAAGCAGCAG- 5215
Qy 1774 HisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu 1793
Db 5216 -----GCTGATTCGATGACATGTTCAACTTTTGAGACATTTGGCAACAGCATATC 5266
Qy 1794 ThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMet----- 1808
Db 5267 TGCCTGTTTCAATACACAACTCAGCTGTTGGATGCGCTGCTGCTGCCATCCTAAAC 5326
Qy 1809 LysAspProSerArgAspCysAspGlnGlu-----SerThrCys 1821
Db 5327 CGCCCCCTGACTGACGCTAGATAAGAAACACCCAGGGAGTGCTTTAAAGGAGATGTT 5386
Qy 1822 TyrAsnThrValIleSerProIleTyPheValSerPheValLeuThrAlaGlnPheVal 1841
Db 5387 GGGAAACCCCTCAGTGGGCATCTTCTTGTGAAGCTACATCATCATCTTTCTCTAATT 5446
Qy 1842 LeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAla 1861
Db 5447 GTCGTGAACATGTACATGCCATCATCTCGGAACTTCAGTGTAGCCACAGAGAAAGT 5506
Qy 1862 LysGlu-----GluAlaGluLeuGluAlaGluLeuGluMetLysThrLeu 1878
Db 5507 GCAGACCTCTGAGTGGAGTATGTTGAGACCTTCTATGAG----- 5548
Qy 1879 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyVal 1898
Db 5549 -----ATCTGGGAGAAGTTCGAC----- 5566
Qy 1899 AsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly----- 1916
Db 5567 -----CCCGATGCCACCCAGTTCATTGAGTACTGT 5596
Qy 1917 -----AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGlu 1934
Db 5597 AAGTGGCAGACTTTGCGAGATGCTTGGAGCATCTCTCCGAGTGGCCCAAGCCAAATACC 5656
Qy 1935 ValProValProLeuGlyProAspLeuThrValArgLysSerGlyValSerArgThr 1954
Db 5657 ATTGAGCTC---ATCGCTATGATCTGCCATGTG-----ACGGGG---GATCGCATC 5704
Qy 1955 HisSerLeuProAsnAspSerTyMetCysArgAsnGlySerThrAlaGluArgSerLeu 1974
Db 5705 CACTGCTTG-----GACATCTTTT-----GCCTTCACCAAGCGGCTCTG 5746
Qy 1975 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSer 1994
Db 5747 GGAGATAGCGGG-----GAGTTGGACATCCTCGGG 5776
Qy 1995 GlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyThrLeuGln 2014
Db 5777 CAGCAGATGGAGAGCGGTTCGTGGCATCCAACTCTCCCAAAGTGCTTAC----- 5827
Qy 2015 ProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgSerPro 2034
Db 5828 -----GAGCCA 5833
Qy 2035 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2054
Db 5834 ATCAACACCACACTGCTGCGAAGCAG----- 5860
Qy 2055 GlyLeuGlySerArgGluAspLeuSerGluValSerGlyPro-SerCysProLeuThr 2074
Db 5861 -----GAGGAGGTATCTGCAAGTGGTCTCGACGCTGCC 5893
Qy 2074 rArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleG 2094
Db 5894 T---ACCGGGGACATTTGGCAAGCGGGGCTTCATCTGCAAAAAGACAACTTCTAATAAG 5950
```

```
Qy 2094 nSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTr 2114
Db 5951 CTGGAGAATGAGGCACACACACCGGGAGAAAAAGAGAGACCCCATCTACAG----- 6002
Qy 2114 pAlaLysAspProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpI 2134
Db 6003 -----CCTCCCTCCGCTCTATGACAGTGTAACTAAACCTGAAAGAGGAGAAACAG 6052
Qy 2134 eSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuLys 2154
Db 6053 CAGCGGG-----CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6100
Qy 2154 sCysTySerValGluThrGlnSerCysArgArgGluProGlyPhe 2169
Db 6101 GTCA-----GAGAAATCCAAGTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6137

RESULT 15
US-10-473-173-94
; Sequence 94, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 6600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-94

Alignment Scores:
Pred. No.: 3.45e-67 Length: 6600
Score: 1587.50 Matches: 595
Percent Similarity: 38.7% Conservative: 336
Best Local Similarity: 24.7% Mismatches: 697
Query Match: 13.2% Indels: 780
DB: 6 Gaps: 81

US-09-611-257A-24 (1-2287) x US-10-473-173-94 (1-6600)
Qy 157 PheAlaPhe-----PheAlaValGluMetValValLysMetValAlaLeuGly--- 172
Db 22 TATGCCCTTCTCGATTATTTTACAGTCGAGACATTTTGAAGATTATAGCGTATGGATTA 81
Qy 173 IlePheGlyLysLysCysTyThrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 192
Db 82 TTGTCATCATCCTAATGCTTATGTAAGAAATGGATGGAAATTTACTGGATTTTGTATTAGTA 141
Qy 193 IleAlaGlyMetLeuGluTyThrSerLeuAspLeuGlnAsnValSer----- 207
Db 142 ATAGTAGATTG-----TTTAGTGTAAATTTTGGAAACAATTAACCAAGAAACAGAGAGGC 195
Qy 208 -----PheSerAlaValArgThrValArg 215
Db 196 GGGAAACCACTCAAGCGGCAAACTCTGGAGGCTTTGATGTCAAAGCCCTCCGTCCTTCGA 255
Qy 216 ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 235
Db 256 GTGTTGCGACCATTCAGCTAGTGTGAGGAGTCCCAAGTTTACAAAGTTGCTCCTGAATCC 315
Qy 236 LeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhePhe 255
Db 316 ATTATAAAGCCATGGTTCCTCCCTCCATACATACCCCTTTGGTATTATTGTATCATATA 375
Qy 256 IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu 275
```

Db 376 ATCTATGCTATTAGATTGGAATCTTTTATTGGAAAAATGCACAAACATGTTTTTT 435
Qy 276 ProGluasnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsn 295
Db 436 GCTGACTCA-----GATATC-----GTAGCTGAA 459
Qy 296 GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg 315
Db 460 GAGGACCACCTCCATGTCGTTCTCA----- 486
Qy 316 SerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGlu 335
Db 487 -----GGCAATGGACGCCAGTGT----- 504
Qy 336 ThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys 355
Db 505 ACTGCCAATGGC-----ACGGAATGT 525
Qy 356 SerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAla 375
Db 526 AGGAGTGGCTGGTGGCCCGACGGAGGCATCACCACCTTTGATAACTTTGCTTTGCC 585
Qy 376 TrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVal 395
Db 586 ATGCTTACTGTGTTTCACTGCATCACCATGAGGGCTGGACAGCGTGTCTACTGGGTA 645
Qy 396 MetAspAlaHisSerPhe---TyrAsnPheIleTyrPheIleLeuLeuIleValGly 414
Db 646 AATGATGCGATAGATGGGAATGCCATGGTGTATTTTGTAGTCATCATCCTTGGC 705
Qy 415 SerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLys 434
Db 706 TCATTTTCTCTTAACCTGGTCTTGGTGTCTTAGTCGAGAATTCACAAAGGAAGA 765
Qy 435 GlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThr 454
Db 766 GAGAAGGCAAAAGCACGGGAGATTTCCAGAAGCTCCGG----- 804
Qy 455 LeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyr 474
Db 805 -----GAGAAGCAGCAGCTGGAGGAGGATCTAAAGGGCTACTTGGATGG 849
Qy 475 Ile-----LeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVa 492
Db 850 ATACCCCAAGCTGAGGACATCGATCCGAGAAATGAGGAAGAGGAGGAGGAGG----- 901
Qy 492 lArgAlaGly---LeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSe 511
Db 902 -AAGGCAACGAAATACTAGCATGCCCCACGAGGAGACTGAGTCTGTGAACACAGAGAAC 960
Qy 511 rGlySerCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHi 531
Db 961 G---TCAGCGGTGAAGCGAGAACCGAGGTGCTGTG----- 994
Qy 531 sHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerPr 551
Db 994 ----- 994
Qy 551 oGluileGlnAspArgAlaAsnGlySerArgArgLeuMetLeuProProSerTh 571
Db 995 -GAAGTCTCTGCTGCTGGAGACGGAGGCGCG----- 1030
Qy 571 rProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAl 591
Db 1031 -----CCAAGCGGGGCGCT----- 1045
Qy 591 aAspCysHisLeuGluProValArgCysGlnAlaProProArgCysProSerGluAl 611
Db 1045 ----- 1045
Qy 611 aSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPr 631

Db 1046 -----CTGGGTGTCGGCGTGGG----- 1063
Qy 631 oGluileLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLe 651
Db 1064 -----GTCAAGCCCATCTCAAAATCCA----- 1084
Qy 651 uThrSerPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGl 671
Db 1084 ----- 1084
Qy 671 nSerThrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSe 691
Db 1085 -----AATCAGCCGACGC 1098
Qy 691 rGlyAlaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGl 711
Db 1099 TGGCGTGGTGGAAACCGATTCAAT----- 1122
Qy 711 uSerAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAs 731
Db 1122 ----- 1122
Qy 731 pAlaGlnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyPr 751
Db 1123 -----CCGAGAAGATGTAG----- 1137
Qy 751 oAspAlaGluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLy 771
Db 1138 -----GCCGCGTGAAGTCTGTACGTTTACTGGCTGGTTATC----- 1176
Qy 771 sIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLe 791
Db 1177 -----GTCCGTGGTGTTCGAACACCTT 1199
Qy 791 uSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSe 811
Db 1200 AACCATTTCTCTGAGCAGCTACAAATCAGCCAGATGGTTCACACAGATTCAGGATTCG 1259
Qy 811 rAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGl 831
Db 1260 CAACAAGTCTCTTGGCTCTGTTCACCTCGAGAGATGCTGGTAAATGTACAGCTTGGG 1319
Qy 831 yProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal----- 848
Db 1320 CTTCCAAAGCATATTCTGCTCTCTTTCAACCGGTTTGTATTGCTTCTGCTGTGTGGTGG 1379
Qy 849 -----ValIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSe 864
Db 1380 AATCAGTGGAGACGATCTTGGTGGAACTGGAAATCATGTCTCCCTG-----GGGATCTC 1433
Qy 864 rValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLe 884
Db 1434 TGTGTTTGGTGTGGCTCTTAGAATCTTCAAGTGCACCGACCTGGGACTTCCCT 1493
Qy 884 uGlnArgGlnLeuValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLe 904
Db 1494 GAGCAACTAGTGGCATCTTATTAACCTCATGAAGTCCATCGCTTCTGCTGTGTCTCT 1553
Qy 904 uLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPh 924
Db 1554 GCTTTTCTCTTCAATATCATCTTTCTTGGTGGATCGAGCTGTTTGGCGCAAGTT 1613
Qy 924 eAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr 944
Db 1614 TAATTTTGTAT-----GAAACGGCAACCAAGCGGACCTTTGACAAATTTCCCTCA 1664
Qy 944 pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAs 964
Db 1665 AGCATTCTCACAGTGTTCAGATCTCTGACAGCGGAAGACTGGAATGCTGTGATGTACGA 1724
Qy 964 nGlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyrPheIl 978
Db 1725 TGGCATCATGGCTTACGGGGGCCCTCTCTTTCAGGAATGATCGTCTGTCATCTACTTCAT 1784

Qy	978	eAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGl	998
Db	1785	CATCCTCTTCAATTTGCTAACTATATCTTACTGAATGCTTCTTGGCCATCGTGTAGA	1844
Qy	998	uGlyPhe-----GlnAlaGluGlyAspAlaThrLysSerGluSerGluProaspPh	1015
Db	1845	CAATTTGGCTGATGCTCAAAAGTCTGAACATGCTGCAGAAAGAGACGGAA-----	1896
Qy	1015	ePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLe	1035
Db	1897	-----GAAAGGAGAGAGAAAAG-----ATTGCCAG	1922
Qy	1035	uGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuLeuIleHisThrAlaAl	1055
Db	1923	AAAAGAGAGCCTAGAAAATAAAAGACAACAACACGAA-----	1962
Qy	1055	aThrProMetSerHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGl	1075
Db	1963	-----GTCAACCATGATGCCAACACGATGA	1985
Qy	1075	ySerArgArgThrSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLy	1095
Db	1986	CAACAAGGTTACAATTGATGACTATAGAGAAGAG-----	2019
Qy	1095	sCysProProSerAlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpTh	1115
Db	2020	-----CATGAAGACAAGGACCCCTATCCGCCTTGGCATGTG-----	2055
Qy	1115	rSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerPr	1135
Db	2056	-----CC	2057
Qy	1135	oSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGl	1155
Db	2058	AGTAGGGGAA-----CAGGAAGAGGA	2078
Qy	1155	uSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisargGlySerLe	1175
Db	2079	AGAGGAGAGGATGAACCTGAGGTTCCTGCGGACCCCGCTCGAAGGATCTCGGAGTT	2138
Qy	1175	uGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHi	1195
Db	2139	GAACATGAAGGAAAAATTGCC-----CCCATCCT	2169
Qy	1195	sArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAl	1215
Db	2169	-----	2169
Qy	1215	aSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAs	1235
Db	2169	-----	2169
Qy	1235	pAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLe	1255
Db	2170	-----GAAGGGAGC-----	2178
Qy	1255	uProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerAr	1275
Db	2179	-----GCTTTCTTCATTCTTAGCAAGACCAACC	2207
Qy	1275	gPheArgLeuLeuCysHisargIleIleThrHisLysMetPheAspHisValValLeuVa	1295
Db	2208	GATCCGGTAGGCTGCCACAAGTCATCAACCAACCATCTTCACCAACCTCATCTCTTGT	2267
Qy	1295	lIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe	1315
Db	2268	CTTCATCATGCTGAGACGCTGCCCTGGCGGAGAGACCCC-----ATCCGACGCACTC	2324
Qy	1315	rAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGl	1335
Db	2325	CTTCCGGAACACGATATCGGCTTACTTGTATGCTTATGCTTCACAGCCATCTTACTGTGA	2384

Qy	1335	uMetThrValIysValValalalaleuGlyTrpCysPheGlyGluAlaTyrIleuArgSe	1335
Db	2385	GATCCCTGTTGAAAGATGACAACTTTTGGAGCTTTCTCCCAAAAGGGGCTTTGCGAGAA	2444
Qy	1355	rSerTrpAsnValIeuAspGlyLeuLeuValIleuSerValIleAspIleLeuValSe	1375
Db	2445	CTACTTCAAATTGCTGGATATGCTGGTGTGGGTGCTCTCGTGTCAATTTGGGATTCA	2504
Qy	1375	rMetValSerAspSerGlyThrIysIleLeuGlyMetLeuArgValIleuArgLeuAr	1395
Db	2505	A-----TCCAGTGCATCTCCGTTGTGAAGATTCTGAGGTCTTTAAG	2546
Qy	1395	gThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuIysLeuValGluTh	1415
Db	2547	GGTCTCGTCCCTCAGGCCATCAACAGCAAAAGGACTTAGCACGTGTCCAGTG	2606
Qy	1415	rLeuMetSerSerIleuIysProIleGlyAsnIleValIleCysCysAlaPhePheIl	1435
Db	2607	CGTCTCGTGGCCATCCGGACCACGCAACATCATGATCGTACCACCCCTCCTCGAGTT	2666
Qy	1435	eIlePheGlyIleLeuGlyValGlnIleuPheIysGlyIysPhePheValCysGlnGlyGl	1455
Db	2667	CATGTTTGCCTGATCGGGTCCAGTTGTTCAAGGGAAGTTCTATCGCTGTACGGATGA	2726
Qy	1455	uAspThrArgAsn-----IleThrAsnIysSerAspCy	1466
Db	2727	AGCCAAAGTAAACCTTGAGAAATCCAGGGACTTTTCATCTCTACAAGGATGGGATGT	2786
Qy	1466	sAlaGluAlaSerTyrArg-----TrpValArgHisIysTyrAsnPheAspAsnLe	1483
Db	2787	TGACAGTCCCTGTGTGTCGTCGAACGGATCTGGCAAAACAGTGATTTCACATTCGACAACGT	2846
Qy	1483	uGlyGlnAlaIeuMetSerLeuPheValIleuAlaSerLysAspGlyTrpValAspIleMe	1503
Db	2847	CCTCTCTGCTATGATGGCGTCTTTCACAGTCTCCAGTTTGAGGGCTGGCTCGGTGCT	2906
Qy	1503	tTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTr	1523
Db	2907	GTATAAAGCCATCGACTCGAATCGAGAGAATCATCGGCCCAATCTACAACCCACCGCGTGA	2966
Qy	1523	pMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValIleuAsnMetPh	1543
Db	2967	GATCTCCATCTCTTCATCATCTACATCATCATTTAGCTTTCTTCATGATGAACATCTT	3026
Qy	1543	eValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluAl	1563
Db	3027	TGTGGCTTTGTCACTGTTACATTT-----CAGGAACAAGAGAAAAGAGTA	3074
Qy	1563	aArgArgArgGluIysArgIleuArgArgLeuGluLysLysArgArgSerIysGluLy	1583
Db	3075	TAAGAATCTGTGAG-----CTGGACAAAATCAGCGTCAGTGTGTGTGA	3116
Qy	1583	sGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLe	1603
Db	3117	ATACGCCCTTGAAAGCAGCTCCCTTGGGAGATACATCCCAAAAACCCCTACCAGTACAA	3176
Qy	1603	uValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLe	1623
Db	3177	GTTCTGTGTAGTGTGAACCTCTTCGCGCTTTCGAATACATGATGTTTGTCTCATCATGCT	3236
Qy	1623	uAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLe	1643
Db	3237	CAACACTCTGCTGTGCCATGACGACTACGACGACTCCAGATGTTCAATGATGCCAT	3296
Qy	1643	uLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheIysLeuVa	1663
Db	3297	GGACATTCTGAACATGCTCTCCCGGGGTGTTCCCGTCGAGATGGTTTGTGAAGATCAT	3356
Qy	1663	lAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspIleuAlaIleVa	1683
Db	3357	CGCATTTAAGCGCTAAGGGTATTTTAGTACGCGCTGGAAACAGCTTTGACTCCCTCATCGT	3416
Qy	1683	lLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu-----ValAsnLe	1699

Db 3417 AATCGGAGCATATAGACGTGGCCCTCAGCGAAGCAGACCACTGAAAGTGAATGT 3476
Qy 1699 uSerLeuProIle-:::||||::: ||| ||| :::
Db 3477 CCTGTCCCACTGCTACACTGGGAACCTCGAAGAGAGCAATAGAATCTCCATCACCTT 3536
Qy 1710 eMetArgValLeuArgIleAlaArgValLeuLysMetAlaValGlyMetAr 1730
Db 3537 TTTCCGTCCTTCCGAGTGATCGATTGGTGAAGCTTCTCAGCAGGGGGAGGCATCCG 3596
Qy 1730 gAlaLeuLeuHisThrValMet-----GlnAlaLeuProGlnValGlyAsnLeuG1 1747
Db 3597 GACATTGCTGGACTTTTATTAGTCTCTTACGGCGCTCCCGTATGTG-----GC 3647
Qy 1747 YLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValGluLeuPheGlyAs 1767
Db 3648 CCTCCTCATGCCATCGTGTCTTTCATCTATGCGGTTCATTGGCATGAGATGTTTGGAA 3707
Qy 1767 pLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAs 1787
Db 3708 AGTTGCCATGAGATTAACACACAG-----ATCAATAGGAACAATAACTTCCAGAC 3758
Qy 1787 nPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyI1 1807
Db 3759 GTTTCGCCAGCGGTGCTGCTCTTTCAGGTGTGCAACAGGTGAGGCTGGCAGGAGAT 3818
Qy 1807 eMetLysAsp-----ProSerArgAspCysAspGlnGluSer----- 1819
Db 3819 CATGCTGGCTGTCTCCAGGGAAGCTCTGTGACCCCTGAGTCAGATTACACCCCGGGGA 3878
Qy 1820 -----ThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuTh 1837
Db 3879 GGAGTATACATGT---GGGAGCAACTTGGCCATTGTCTATTTCATCAGTTTTCATGTCT 3935
Qy 1837 rAlaGlnPheValLeuValAsnValValIleAlaValLeuMet----- 1851
Db 3936 CTGTGCATTTCTGATCATCAATCTGTTGTGGTGTCTCATCTGATGATAATTTGCACTATCT 3995
Qy 1852 -----LysHisLeuGluGluSerAsnLysGluAlaLyl 1862
Db 3996 GACCCGGAGCTGCTATTTTGGGGCTCCACCATTTAGATGAATTC---AAAAAGATATG 4052
Qy 1862 sGluGluAlaGluLeuGluAlaGlu-----LeuGluLeuGluMetLysThrLeuSe 1879
Db 4053 GTCAGATATGACCTCAGGCAAGGGAAGGATAAACACCTTGATGTGCTCCTGCT 4112
Qy 1879 rProGlnProHisSerProLeuGlySerProPheLeuTrpPro----- 1893
Db 4113 TCAGCGCATCCAGCTCCCTGGGTTTGGGAAGTTATGTCCACACAGGGTAGCGTGCAA 4172
Qy 1894 -----GlyValGluGlyValAsnSerTh 1901
Db 4173 GAGATTAGTTGCCATGAACATGCTCTCAACAGTGCAGGACAGTCATGTTTAAATGCAAC 4232
Qy 1901 rAspSerProLysProGlyAlaProHisThrAlaHisIleGlyAlaAlaSerGlyPh 1921
Db 4233 C-----CTGTTTGTCTTGGTTCGAACGGCTCTTAAGAT 4265
Qy 1921 eSerLeuGlu----- 1924
Db 4266 CAAGACCGAAGGGAACCTGGAGCAAGCTAATGAAGAAGCTTCGGGCTGTGATAAAGAAAT 4325
Qy 1925 ----HisProThrMetValProHisProGluGluValProValProLeuGlyProAspLe 1943
Db 4326 TTGGAAGAAAACACAGCATGAATTAATTCTTGACCAAGTTGTCCCTCCAGCTGGTGAIGA 4385
Qy 1943 uLeuThrValArgLys----- 1948
Db 4386 GGTAAACGTGGGAAGTTCTATGCCACTTTCCTGATACAGGACTACTTTAGGAATTCAA 4445
Qy 1948 ----- 1948

Db 4446 GAAACGGAAGAAACAAGGACTGTGTGGGAAAGTAGTACCTCTCGAAGAACAACCAATTCGCCT 4505
Qy 1949 -----SerGlyValSerArgThrHisSerLeu----- 1957
Db 4506 ACAGCGGGGATTAAGGACACTGCATGACATTTGGGCCAGAAATCCGGGTGCTATATCGTG 4565
Qy 1958 -----ProAsnAspSerTyrMetCy 1964
Db 4566 TGATTTGCAAGATGACGAGCCTCGAGAAACAAAAACGAGAAGAAGATGATGTGTTCAA 4625
Qy 1964 sArgAsnGly----- 1967
Db 4626 AAGAAATGGTCCCTGCTTGGAAAAACCATGTCAATCATGTTAATAGTAGTAGGAGAGATTC 4685
Qy 1968 -----SerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLy 1983
Db 4686 CTTTACGACACCAATACCAACCCACCTCCCTTCATGTCTCAAGGCCCTTCAATTCACCC 4745
Qy 1983 sAlaGln-----SerGlySerIleLeuSerValHisSe 1994
Db 4746 TGCAAGTGATACTGAGAAACCGCTGTTTCTCCAGCAGGAAATTCGGTG--TGTCATAA 4802
Qy 1994 rGlnProAlaAspThrSerCysIleLeuGlnLeuProLyAspValHisTyrLeuLeuG1 2014
Db 4803 CCATATAACCAATAATTCCATAGGAAGCAAGTTTCCCACTCAACAAATCCCAATCTCAA 4862
Qy 2014 n-----ProHisGly-----AlaProThrTrpGlyAlaIleProLy 2026
Db 4863 TAATGCCAATATGTCCAAAGCTGCCATGGAAGGCCCCAGCATTTGGGAACCTTGAGCA 4922
Qy 2026 sLeuProProProGly-----ArgSerProLeuAlaGlnAr 2038
Db 4923 TGTGCTGTAATAATGGGCATCATTTCTCCCAACAGCATGACCGGAGCCTCAGAGAAGTC 4982
Qy 2038 gProLeuArgArg-----GlnAlaAlaIleArgThrAspSerLeuAspValG1 2054
Db 4983 CAGTGTGAAAAGAACCCCGCTATTATGAACCTTACATTAGTCCGACTCAGAGATGAACA 5042
Qy 2054 n---GlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLe 2073
Db 5043 GCTCCCAACTATTTCGGGGAAC-----CCAGAGATACATGGC-----TA 5084
Qy 2073 uThrArg-SerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI 2093
Db 5085 TTTTACGGACCCCACTGCTTGGGGAGCAGGAGTATTTTCAGTA----- 5128
Qy 2093 leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113
Db 5129 -----GTGAGGAATGTCTACGAGGATGACAGCTCCGCCCTGGAGCAGGCAAAA 5177
Qy 2113 eTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133
Db 5178 CTATGGCT-----ACTACAGCAGATACCCAGGCAACATCGA 5216
Qy 2133 rPileSerGly-AspLeuLeuProSerSerGlnGluGluProLeuPheProArg-AspLe 2152
Db 5217 CTCTGAGAGGCCCGAGGCTACCATCATCC---CCAAGGATTCTTGGAGGACGATGACTC 5273
Qy 2152 uLysLysCysTyrSerValGluThrGlnSerCysArgArg-----Pr 2167
Db 5274 GCCCGTTTGTATATGAT---TCACGGAGATCTCAAGGAGAGCGCTACTACTCCCAACCCC 5330
Qy 2167 oGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSerCysLeuAspSerG1 2187
Db 5331 AGCA-----TCCCACCGGAGATCCTCTTCAACTTTGAGTGCCTGCG-CCGGC 5377
Qy 2187 ySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyPr 2207
Db 5378 AGAGCAGCCAGGAAGAGGTCCCGTGTCTCCCATCTT-----CCCCCATCGCACGGCCC 5431
Qy 2207 oGlySer-----ArgProLysLysLysLeuSe 2216
Db 5432 TGCCTCTGTCATCTAATGTCAGCAACAGATCATGTCAGTTGCCGCGCTAGATTCAAGTAAAG 5491

```
Qy 2216 rProProSerIle-----SerIleAspProProGluSerGlnGlySerArgProProCy 2234
Db 5492 CCCAGAGTACTACCGAGTCACTCGACCCCGGTCGTGGGCCACCCCTCCAGCAACCCCTC 5551
Qy 2234 sSerProGlyValCysLeu-----ArgArgArgAlaPr 2245
Db 5552 CCTACCGGAGTGGACACCGTGCTACACCCCTGTATCCCAAGTGGAGAGTCAGAGGCC 5611
Qy 2245 oAlaSerAspSerLysAspProSerValSerPro---LeuAspSerThrAlaAlaSe 2264
Db 5612 TGGACCAAGTGAACGGCAGCCTGCCGTCCTCCCTGCACCCGAGCTCCT-GGTACACAGACGAG 5670
Qy 2264 rProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerSerAspProThrAspMe 2284
Db 5671 CCCGACA-----TCTCTACCGGACTTTTCACACCAGCCGCGCTGACT 5712
Qy 2284 tAspPro 2286
Db 5713 GTCCCCA 5719
```

Search completed: July 10, 2006, 20:37:56
Job time : 791.891 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 10, 2006, 06:41:34 ; Search time 814.741 Seconds
(without alignments)
7878.383 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRPRVRCVTPPLRGSR.....KKDTLSLSGLSSDPTDMPZ 2287

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Xgapop 10.0			
Xgapext 0.5			
Fgapop 6.0			
Delop 6.0			

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB_spool/US09611257/runat.10072006.064119.6880/app_query.fasta.1
-DB=Issued Patents NA -QMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs904 -USR=US09611257 @CGN 1.1 1140 @runat.10072006.064119.6880
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOPT=6
-FGAPEXT=7 -YGAPOPT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

	1:	2:	3:	4:	5:	6:	7:	8:	9:	10:
1:	/EMC_Celerra_SID33/ptodata/2/ina/1 COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/5 COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/6A COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/6B COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/7 COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/H COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/PCTUS COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/PP COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/RE COMB.seq.*	/EMC_Celerra_SID33/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11066.5	92.0	7741	3	US-09-426-998-4
2	10948.5	91.0	6822	3	US-09-426-998-3
3	10739	89.3	7405	3	US-09-949-016-3859
4	6241	51.9	7898	3	US-08-984-709A-49
5	6103	50.7	3993	3	US-09-398-522-51
6	5420	45.1	6816	3	US-09-404-650-1
7	5420	45.1	6816	3	US-09-935-541-1
8	5420	45.1	6816	3	US-10-425-800-1

9	5420	45.1	6855	3	US-09-404-650-3	Sequence 3, Appli
10	5420	45.1	6855	3	US-09-935-541-3	Sequence 3, Appli
11	5420	45.1	6855	3	US-10-425-800-3	Sequence 3, Appli
12	5407	45.0	6503	3	US-09-404-650-12	Sequence 12, Appl
13	5407	45.0	6503	3	US-09-935-541-12	Sequence 12, Appl
14	5407	45.0	6503	3	US-10-425-800-12	Sequence 12, Appl
15	2055	17.1	70308	3	US-09-949-016-15601	Sequence 15601, A
16	1974	16.4	1669	3	US-08-984-709A-51	Sequence 51, Appl
17	1745.5	14.5	7362	2	US-08-455-543A-7	Sequence 7, Appli
18	1745.5	14.5	7362	2	US-08-193-078B-7	Sequence 7, Appli
19	1745.5	14.5	7362	2	US-08-223-305C-7	Sequence 7, Appli
20	1745.5	14.5	7362	2	US-08-149-097D-7	Sequence 7, Appli
21	1745.5	14.5	7362	3	US-08-949-386-7	Sequence 7, Appli
22	1745.5	14.5	7362	3	US-08-450-562-7	Sequence 7, Appli
23	1745.5	14.5	7362	3	US-08-984-709A-7	Sequence 7, Appli
24	1745.5	14.5	7362	3	US-08-450-272-7	Sequence 7, Appli
25	1745.5	14.5	7362	3	US-08-450-273-7	Sequence 7, Appli
26	1743.5	14.5	7376	3	US-09-268-163-3	Sequence 3, Appli
27	1743.5	14.5	7376	5	US-10-033-026-3	Sequence 3, Appli
28	1740.5	14.5	7266	3	US-08-713-118-1	Sequence 1, Appli
29	1740.5	14.5	7266	3	US-09-452-007-1	Sequence 1, Appli
30	1739.5	14.5	7364	3	US-09-268-163-5	Sequence 5, Appli
31	1739.5	14.5	7364	5	US-10-033-026-5	Sequence 5, Appli
32	1727	14.4	7175	2	US-08-455-543A-8	Sequence 8, Appli
33	1727	14.4	7175	2	US-08-193-078B-8	Sequence 8, Appli
34	1727	14.4	7175	2	US-08-223-305C-8	Sequence 8, Appli
35	1727	14.4	7175	2	US-08-149-097D-8	Sequence 8, Appli
36	1727	14.4	7175	3	US-08-949-386-8	Sequence 8, Appli
37	1727	14.4	7175	3	US-08-450-562-8	Sequence 8, Appli
38	1727	14.4	7175	3	US-08-984-709A-8	Sequence 8, Appli
39	1727	14.4	7175	3	US-08-450-272-8	Sequence 8, Appli
40	1727	14.4	7175	3	US-08-450-273-8	Sequence 8, Appli
41	1721	14.3	7177	5	US-09-268-163-7	Sequence 7, Appli
42	1721	14.3	7177	5	US-10-033-026-7	Sequence 7, Appli
43	1703	14.2	5975	2	US-08-404-354B-1	Sequence 1, Appli
44	1703	14.2	5975	2	US-08-314-083B-1	Sequence 1, Appli
45	1703	14.2	5975	2	US-08-435-075B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-4

Alignment Scores:
Pred. No.: 0 Length: 7741
Score: 11066.50 Matches: 2134
Percent Similarity: 93.8% Conservative: 33
Best Local Similarity: 92.4% Mismatches: 112
Query Match: 92.0% Indels: 31
DB: 3 Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-426-998-4 (1-7741)

Db	2591	GCAGGCGAGTTTATGAGTTTACACAGAGATCCCGACGACGACCTTCGGGACCCCCACA	2650
Qy	742	erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaphet	762
Db	2651	GC---CGCGCGAACGGAGCGCTGGGCCAGATGCAGAGCCACAGCTCTGTGCTTCT	2707
Qy	762	rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTrpPheGlyArgGlyI	782
Db	2708	GGAGGCTAACTGTGCACACCTTCGAAAGATTGTGGACAGCAAGTAGCTTTGGCCGGGAA	2767
Qy	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTrpHisGluGlnProG	802
Db	2768	TCATGATCGCATCTCTGGTCAACACACTCAGCATGGGCATCGAATACACGACGACGCCG	2827
Qy	802	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2828	AGGAGCTTACCAAGCCCTAGAATACGAAACATCGTCTTACACAGCTCTTTGGCCCTGG	2887
Qy	822	luMetLeuLeuLysLeuLeuValTrpGlyProPheGlyTrpIleLysAsnProTrpAsnI	842
Db	2888	AGATGCTGCTGAAGCTGCTTGATGGTCCCTTTGGCTACATCAAGAAATCCCTACAACA	2947
Qy	842	lePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyG	862
Db	2948	TCCTTCGATGGTCAATTTGGTCAATCAGCGTGTGGAGATCGTGGGCCAGCAGGGGGCG	3007
Qy	862	lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	3008	GCCTGTCCGGTGTCCGGACCTTCGCCCTGATGGTGTGCTGAAGCTGGTGGCTTCTCGC	3067
Qy	882	roAlaLeuGlnArgGlnLeuValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	3068	CGCGCTGCAGCGCAGCTGGTGGTGCTCATGAAGACCATGGACCAACGTGGCCACTTCT	3127
Qy	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
Db	3128	GCATGCTGCTTATGCTCTTCATCTTCATCTTACGATCCTGGGCATGCATCTCTCGGCT	3187
Qy	922	ylsYsPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
Db	3188	GCAAGTTTGCTCTGACGGGGAATGGGACACCTTCGACAGCCGGAAGAAATTTTGACTCT	3247
Qy	942	euleuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL	962
Db	3248	TGCTCTGGGCATCGTCACTGTCTTTTCAGATCTGACCCAGGAGGACTGGAAACAAAGTCC	3307
Qy	962	euTrpAnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTrpPheIleAlaLeuMetT	982
Db	3308	TCTACAATGTATGGCTCCACGCTCGTCTCGGGCGGCCCTTTATTTATTTGCTTCATGA	3367
Qy	982	hrPheGlyAnTrpValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnA	1002
Db	3368	CCTTTCGGCAACTACGTGCTCTTCAATTTGCTGGTCCGCAATTCGTGGAGGGGCTTCCAGG	3427
Qy	1002	laGlu-----	1003
Db	3428	CGAGGAAATCAGCAAAACGGGAAGATCCGAGTGGACAGTTAAGCTGTTATTCAGCTGCCTG	3487
Qy	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPheSerProS	1019
Db	3488	TCGACTCCCGAGGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGAATTTCTTCTCACCCA	3547
Qy	1019	erValAspGlyAspGlyAspArgLysIysArgLeuAlaLeuValAlaLeuGlyGluHisA	1039
Db	3548	GCCTGGATGTGTATGGGGCAGGAAGAAGTGTCTTGGCTTGTGGTCTCCCTCGGAGAGCACC	3607
Qy	1039	laGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetS	1059
Db	3608	CGGAGCTTGGGAAGAGCTGCTGCGCGCTCTCATCTATCCACACGGCCGCCACACCCATGT	3667
Qy	1059	erHisProLysSerSerThrGlyValGluAlaLeuLeuGlySerGlySerArgArgT	1079

Db	3668	CGCTGCCAACAGAGCACAGCACCGGGCGCTGGCGAGCGCGCTGGCGCTCGCGCGCGCA	3712
Qy	1079	hrSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProS	1099
Db	3728	CCAGCAGCAGCGGTCGGCAGAGCCCTGGGCGGCC--CACGAGATGAAGTCACCGCCCA	3784
Qy	1099	erAlaArgSerSerProHisSerProTrpSerAlaSerSerTrpThrSerArgArgS	1119
Db	3785	CGCGCCGCAGCTCTTCGCA CAGCGCCCTGGAGCGCTGCAAGCAGCTGCACGAGCGCT	3844
Qy	1119	erSerArgAenSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyCluA	1139
Db	3845	CCAGCGGAACAGCTCGCGCGTGCAACCCAGCTGAAGCGGAGAGCCCAAGTGGAGAGC	3904
Qy	1139	rgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluG	1159
Db	3905	GGCGTCCCTGTGTGGGAGAGGCCAGAGAGCCAGGATGAAGAGGAGACTCAGAAG	3964
Qy	1159	luAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA	1179
Db	3965	AGGAGCGGCCAGCCCTCGGGCAGTGACCATCGCACAGGGGTCCCTGGAGCGGGAGG	4024
Qy	1179	lalySerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaAs	1199
Db	4025	CCAAGAGTTCCTTTGACCTGCCAGACACACTGAGGTGCCAGGGCTGCATCGCACATG	4084
Qy	1199	erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL	1219
Db	4085	GTGCCGAGGGTCTGCTTCTGAGCACAGGACTGCATGGCAAGTGGCTTCAGGGCGCC	4144
Qy	1219	euAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGluG	1239
Db	4145	TGGCCCGGCCCTGGCGCCTGATGACCCCCACTGGATGGGATGACGCCGATGACGAGG	4204
Qy	1239	lyAsnLeuSerLysGlyGluArgLleGlnAlaTrpValArgSerArgLeuProAlaCysC	1259
Db	4205	GCAACCTGACAAAGGGGAACGGGTCCGCGGTGGATCCGAGCCCACTCCCTGCCTGCT	4264
Qy	1259	ysArgGluArgAspSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeuL	1279
Db	4265	GCCTGAGCGAGACTCTGTGTAGCTACATCTTCCTCTCAGTCAGGTTCCGCGCTCC	4324
Qy	1279	euCysHisArgLlelleThrHisLysMetPheAspHisValValLeuValleIlePheL	1299
Db	4325	TGTTGCACCGGATCATCACCACAAGATGTCACCACAGTGTGCTTGTTCATCATCTTCC	4384
Qy	1299	euAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgI	1319
Db	4385	TTAACTGCATCACCATCGCATCGAGCGCCCCAAAATTGACCCCAACAGCGCTGAAACG	4444
Qy	1319	lePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValL	1339
Db	4445	TCITTCTGACCCCTCCAAATTACATCTTCACCGAGTCTTTCTGGCTGAAATGACAGTGA	4504
Qy	1339	ysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuArgSerSerTrpAsnV	1359
Db	4505	AGTGTGTGGCACCTGGGCTGTGCTTCGGGAGCAGCGCTACCTCGGAGCAGTTGGAACG	4564
Qy	1359	allLeuAspGlyLeuLeuValLeuIleSerValleIleAspIleLeuValSerMetValSerA	1379
Db	4565	TGCTGGACGGGCTGTGTGTCTCATCTCCGCTCATCGACATCTCTGGTGTCCATGGTCTCTG	4624
Qy	1379	spSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgP	1399
Db	4625	ACAGCGCACCAAGATCCTGGGCATGCTGAGGGTGTCTGGGCTGTCTGGGACCTCTGCCCC	4684
Qy	1399	roLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerS	1419
Db	4685	CGCTCAGGGTGATCAGCGCGGCAGGGGCTGAAGCTGGTGGTGGAGACGCTCATGTCTCT	4744
Qy	1419	erLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyI	1439
Db	4745	CACCTGAAACCATCGGAACATTTGATGTCATCTGCTGTGCTTCTTCATCATTTTCGGCA	4804

Qy 1439 leLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyValAspThrArgA 1459
Db 4805 TCCTGGGGGTGCAGCTCTTCAAGAGGAAGTTTTTCGTGTGCAGGGCAGGATACCAAGGA 4864
Qy 1459 snlleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrA 1479
Db 4865 ACATCACCAATAATCGGACTGTGCCGAGGCCAGTTACCGGTGGGTCCGGCACAAAGTACA 4924
Qy 1479 snPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyT 1499
Db 4925 ACTTTGACAACCTTGGCCAGGCCCTGTATGCTCCCTGTTCTGTTTGGCCCTCCCAAGATGGTT 4984
Qy 1499 rpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetA 1519
Db 4985 GGGTGGACATCATGTACCATGGGTGGATGCTGTGGGGCGTGACAGCAGGCCCATCATGGA 5044
Qy 1519 snHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV 1539
Db 5045 ACCACAACCCCTGGATGCTGTACTTCACTCGTTCTCTGCTCATTTGTGGCCCTCTTTG 5104
Qy 1539 alLeuAsnMetPheValGlyValValValGluAlaAsnPheHisLysCysArgGlnHisGlnG 1559
Db 5105 TCCTGAACATGTTTGGGTGTGGTGTGGAGAACTTCCACAAGTGTGGCAGCACCAAG 5164
Qy 1559 luGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgA 1579
Db 5165 AGGAAGAGAGGCCCGCGCGGGAGGAGAGCGCTACGAAGACTGGAGAAAGAGAA 5224
Qy 1579 rgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
Db 5225 GGAGTAAGGAGAAGCAGATGGCTGAAGCCAGTGCACAACTTACTACTCCGACTACTCCC 5284
Qy 1599 rgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrIleuAspLeuPheIleThrG 1619
Db 5285 GCTTCGGCTCTCTGCTCCACCACTTGTGCACAGCCACTACTCTGGACCTTTCATCACAG 5344
Qy 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
Db 5345 GTGTCTCGGGCTGAACGTGGTTCACATGGCCATGGACACTACACAGAGCCCCAGATTC 5404
Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
Db 5405 TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTATCTTGTCTTGGAGTCAG 5464
Qy 1659 alPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuA 1679
Db 5465 TTTTCAAACTTGTGGCCCTTGGTTTTCCGTGGTCTTCCAGACAGGTGGAAACCAAGCTGG 5524
Qy 1679 spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
Db 5525 ACCTGGCCATTGTGTGTGTCTCATCATGGGCATCACCTGGAGGAATCGAGGTCAACG 5584
Qy 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
Db 5585 CCTGCTGCCATCAACCCCAACCATCATCCGATCATGAGGTGTGGCATTTGCCGAG 5644
Qy 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaIleuLeuHisThrValMetGlnA 1739
Db 5645 TGCTGAAGCTGTGAAGATGGCTGTGGGCATGCGGGCGCTGTGGACACGGTGTATGTCAGG 5704
Qy 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaA 1759
Db 5705 CCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTGTGTTTTCATCTTTGCGAG 5764
Qy 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db 5765 CTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACAGACACACCCCTGTGAGGGCC 5824
Qy 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals 1799
Db 5825 TGGGCCGTGATGCCCACTTTCGGAACCTTGGCATGGCCCTTCTCAACCCCTTCTCCAGTCT 5884

Qy 1799 erThrGlyAspAsnTyrAsnGlyIleMetLysAspProSerArgAspCysAspGlnGlnS 1819
Db 5885 CCACAGGTGACAAATTGAATGGCATTATGAAGGACACCCCTCCGGAGACTGTGACCAAGAGT 5944
Qy 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5945 CCACCTGTCTACAACACACGGTCATCTCGCTATCTACTTGTGTCTCTGCTGTCAGGGCC 6004
Qy 1839 lnPheValLeuValAsnValIleAlaValLeuMetLysHisIleuGluGlnSerAsnL 1859
Db 6005 AGTTTCGTGCTAGTCAACGTGGTGTATCGCCGCTGTGATGAAGCACCTGGAGGAGACAACA 6064
Qy 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeus 1879
Db 6065 AGGAGGCCCAAGGAGGAGGCCGAGCTAGAGGTGAGCTGGAGCTGGAGATGAAGACCTCA 6124
Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyValA 1899
Db 6125 GCCCCAGCCCACTCGCCACTGGCGACGCCCTTCTCTGCGCTGGGTTCAGGGGCCCG 6184
Qy 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaS 1919
Db 6185 ACAGCCCGCAGAGCCCAAGCTTGGGCTTGCACCCAGCGGCCACCGAGATCAGGCT 6244
Qy 1919 erGlyPheSerLeuGluHisProMetValProHisProGluGluValProValProL 1939
Db 6245 CCCACTTTTCTCGAGCACCCCAAGATGCAGGCCACCCACCCACGAGCTGCCA----- 6297
Qy 1939 euGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA 1959
Db 6298 --GGACCAGACTTACTGACTGTGGGAAGTCTGGGTGAGCGGAGTGCAGCAACGACACTCTCTGCCCA 6355
Qy 1959 snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT 1979
Db 6356 ATGACAGCTCATGTGTGGCATGGGACACTGCCAGGGGCCCTGGGACACAGGGGCT 6415
Qy 1979 rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT 1999
Db 6416 GGGGGCTCCCCAAAGCTCAGTCAGCTCCGCTTGTCTGCTTCACTTCCAGCCAGCAGATA 6475
Qy 1999 hrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaP 2019
Db 6476 CCAGCTACATCTCGAGCTTCCCAAGATGACACTCATCTCTCTCCAGCCACACAGCGCC 6535
Qy 2019 roThrTrpGlyValAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgP 2039
Db 6536 CAACCTGGGGCACCATCCCCAACTGCCCCACACAGGACGCTCCCTTTGGCTCAGAGC 6595
Qy 2039 roLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerA 2059
Db 6596 CACTCAGCGCCGAGCAGCAATAAGACTGACTCTCTTGGACGTTTCCAGGTCTGGGCGAGC 6655
Qy 2059 rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerP 2079
Db 6656 GGGAGACCTCTGCGAGAGGTGATGGGCCCTTCCCGCCCTGCGCCCGGCTTACTCTT 6715
Qy 2079 heTTPxGlyLysSerIleGlnValGlnArgSerGlyIleGlnSerLysValSerL 2099
Db 6716 TCTGGGGCAGCTCAAGTACCCAGGCACAGCAGACTCCCGCAGCCACAGCAGATCTCCA 6775
Qy 2099 ysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProP 2119
Db 6776 AGCATGACCCCGCCAGCCCTTGGCCAGGCCCAAGAACCCCAACTGGGGCAAGGGCCCTC 6835
Qy 2119 roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL 2139
Db 6836 CAGACACAGAAAGCAGCTTAGAGTTGGACCGAGCTGAGCTGAGTTTTCAGGAGACCTCC 6895
Qy 2139 eu---ProSerSerGlnGluProLeuPhePheProArgAspLeuLysLysCysTyrSerV 2158
Db 6896 TGCCCCCTGGCGCCGAGGAGGAGCCCATCCCCACGGGACCTTGAAGAGTGTCTACAGCG 6955
Qy 2158 alGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgHisS 2178

Db 6956 TGGAGGCCAGAGCTGCCAGCGCGGCTACGTCCTGGCTGGATGAGCAGAGGAGACACT 7015
Qy 2178 erlleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerS 2198
Db 7016 CTATCGCCGCTGAGCTGCTGGACAGCGCTCCCAACCCACCTGGGGCAGACACCCCTCTA 7075
Qy 2198 erLeuGlyGlyGlnProLeuGlyProGlySerArgProLysLysLysLeuSerProp 2218
Db 7076 ACCTTGGGGGCCAGCCTCTTGGGGGGCCGGAGCGGCCCAAGAAAAAACTCAGCCCGC 7135
Qy 2218 roSerlleSerlleAspProGluSerGlnGlySerArgProProCysSerProGlyV 2238
Db 7136 CTAGTATCACCATAGACCCCGCCGAGAGCAAGGCTCTCGGACCCCGCCAGCCCTGGTA 7195
Qy 2238 alCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProL 2258
Db 7196 TCTGCCCTCCGAGAGGGCTCCGTCAGCGACTCCAAAGGATCCCTGGCCCTCTGGCCCC 7255
Qy 2258 euAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuS 2278
Db 7256 CTGACAGCATGGCTGCCTCGCCCTCCCAAGAAAGATGCTGAGTCTCTCCGGTTTAT 7315
Qy 2278 erSerAspProThrAspMetAspPro 2286
Db 7316 CCTCTGACCCAGCAGACCTGGACCCC 7341

RESULT 2

US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: GALINDO, JOSE E
; APPLICANT: ERLANDER, MARK G
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3

Alignment Scores:
Pred. No.: 0 Length: 6822
Score: 10948.50 Matches: 2111
Percent Similarity: 94.0% Conservative: 32
Best Local Similarity: 92.6% Mismatches: 105
Query Match: 91.0% Indels: 31
DB: 3 Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-426-998-3 (1-6822)

Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGTGGAGCGGCGCGGAGGAGTGGGACAGCCCGGAGCTTCATGC 61
Qy 54 SerSerThrThrCysProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
Db 62 GGCTCAACGACCTCTCGGGGGCGGGGCGCGCGGGGTCAGCAAGAAAGGACC 121
Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValp 93
Db 122 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGCCCGGGTGT 181
Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113

Db 182 TCTTCTACTTGGCCAGGACAGCGCGCGGAGCTGGTGTCTCCGACCGCTCTGTAAAC 241
Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGGTTTGGCCGATCAGCATGTGGTTCATCTCTTCAAACTGGCTGACCTGGGCATGT 301
Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATCGAGGACATCGCTGTGACTCCCGAGCGCTGCCGATCTCTGAGGCCCTTG 361
Qy 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTTCATCTTGGCTTCTTTCGCTGGAGATGGTGGTGAAGATGGTGGCTTGGGCA 421
Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTGACTTTTTCATCGTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGATGTGGAGTACTCGCTGGACCTGCAGAACGTCAGCTTCTAGCTCTCAGGA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGCTGTCTGCGACCGCTCAGGGCCATTAAACCGGGTCCCGAGCATCGCATCTCTG 601
Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGCTGGATACGCTGCCCATGTGGGCAACGTCCTGCTGCTCTGCTTCTTCG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTTCATCTTTCGCGCATCGTCGGCGTCCAGCTGTGGGCGAGGCTCTCTCGGAACCGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCTCTACCTGAGATTTTCAGCCTCCCGCTGAGCGTGGACCTGGAGCGCTATTACCAGA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCTTTCATCTGCTCCCGAGCCAGCGAGAACGGCATCGGT 841
Qy 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAACGCTGCCACCGCTGCGGGGACGCGGGCGGTGGCCACCTTTCGGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCTTACACAGCTCCAGCAACACCTGTGTCACTGGAACCCAGTACTACA 961
Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGCGCATCACTTTTGACAAACATTG 1021
Qy 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
Db 1022 GCTATGCTGATCGCCATCTTCCAGGTATCCAGCTGGAGGCTGGGTGACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleV 413
Db 1082 ACTTTGTGATGGATGCTCATCTCTTACAAATTTTCATCTACTTCTCTCATCTCATCG 1141
Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCTCTTTCATGATCAACTGTGCTGGTGGTGGTATTCGCCACCGAGTTCTCAGAGA 1201
Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas 453
Db 1202 CCAAGCAGCGGGAAAGCCAGCTGATGGGGGAGCAGCGTGTGGGTCTCTGTCCAACGCCA 1261
Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473

Db 1262 GCACCTCGGTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
Qy 473 alTyrIleLeuArglyValalaArgArgLeuAlaGlnValSerArgAlaIleGlyVala 493
Db 1322 TGTACATCTTCTGAAGCAGCCCGCAGCTGGCTCAGTCTCTCGGCACGACGAGTGTGC 1381
Qy 493 rGAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCAGCACCCTCGGGGGCCAGAGACCAGCCCGCAGCAGA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCACCGCGCTTATCGTCCACCACTGGTGCAACCAACCAACCA 1501
Qy 533 isHisHisHisGlyHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCACCACTACCACCTGGGCAATGGGAGCGCTCAGGGCCCGCCGCGCCGAGGA 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGGACAGGATGCCAATGGTCCCCGAGCTCATGCTGCCACCCCTCGACGCCCTG 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCTCTCGGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGCTTCTTACCATGCCGACT 1681
Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGGCGCCCCCTCCAGAGTCCCCATCTGAGGCATCCG 1741
Qy 613 lYAtqThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
Db 1742 GCAGAGCTGTGGGCAGCGGAGGTGTATCCACCGTGCACACCAAGCCCTCCACCGGAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTCAAGGAGAGGACACTAGTAGAGGTGGCTGCCAGCTCTGGGGCCCCCAACCTCACCA 1861
Qy 653 erPheAsnIleProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCGGGCCCTACAGCTCCATGCACCAAGCTGCTGGAGACACAGATA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCTCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGTGTAAGACACACAGTGGAG 1981
Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGGTCCAGACAGCTGCCCTACTGTGCCGGCGCGGCGAGGGAGGTGGAGCTCG 2041
Qy 713 laAspHisValMetProAspSerAppSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAAATGCTGACTCAGACACGAGGCGAGTTATGAGTTACACAGGATGCC 2101
Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGAGGACCTCCGGACACCCCAAGC ---CGCGCGCAACCGAGCTTGGGCCCAGATG 2158
Qy 753 laGluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCCAAGCTCTGTGCTGGCTTCTGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGCACAGCAAGTACTTTGGCGGGGAATCATATGCGCATCTGTTGTAACACACTCAGCA 2278
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCAATCGAATACCAACGAGCAGCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProP 833
Db 2339 TCGTCTTCACCAAGCTCTTTGGCCCTGGAGATGCTGTAAGCTGCTTGTGTATGTTCCCT 2398

Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValT 853
Db 2399 TTGGCTACATCAAGAAATCCCTTACCAATCTTTCGATGGTGTGTCATTCAGCGTGT 2458
Qy 853 rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCCAGCAGGGGGCGCTGTGGTGTCTCGGACCTTCCGCTGATGC 2518
Qy 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGTGCTTCTGCGCGCTGTCAGCGCAGCTGGTGTGTCTCATGA 2578
Qy 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2579 AGACCATGGACACAGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCA 2638
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2639 GCATCTGGGCATGCATCTCTTCGCTGCAAGTTTGCCTCTGAGCGGATGGGACACCC 2698
Qy 933 euProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGAAATTTGACTCTTGTCTTGGGCCATCGTCACTGCTTTTTCAGATCC 2758
Qy 953 euThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrA 973
Db 2759 TGACCCAGGAGGACTGGAAACAAAGTCTCTACAATGGTATGGCTTCCACGTCTGCTGGG 2818
Qy 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2819 CGGCCCTTTATTTTCATTTGCTCATGACTTCGGCAACTACGTGCTCTTCAATTTGCTGG 2878
Qy 993 alAlaIleLeuValGluGlyPheGlnAlaGlu ----- 1003
Db 2879 TCGCATTTCTGTGGAGGGCTTCCAGCGGAGGAAATCAGCAACCGGAAGATGCGAGTG 2938
Qy 1004 -----GlyAspAlaThrLysSerG 1010
Db 2939 GACAGTTAAGCTGTATTTCAGCTGCTGCTGACTCCAGGGGGGAGATGCCAACAGTCCG 2998
Qy 1010 luSerGluProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgL 1030
Db 2999 AATCAGAGCCCGATTTCTTCTCACCCAGCTGGATGGTGTATGGGCACAGGAAGATGCT 3058
Qy 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuI 1050
Db 3059 TGGCTTTGGTGTCTGGAGAGCACCCGGAGCTGCGGAAGAGCTGCTGCGGCTCTCA 3118
Qy 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
Db 3119 TCATCCACAGCGCGCCACACCATGCTGCTGCCCAAGAGCACACGAGCGGCTGGGCG 3178
Qy 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGGCGCTGGGCCCTGCGTCCGCGCCACACAGCAGCGCGGTGCGGACAGACCTGGGGCGG 3238
Qy 1090 laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTyrSerA 1110
Db 3239 CC---CAGCAGATGAAGTCAACCGCCAGCGCGAGCTCTCCGACACAGCCCTGGAGCG 3295
Qy 1110 laAlaSerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130
Db 3296 GTCCAGCAGCTGGACAGCAGCGCTCCAGCGGAACAGCTCGGCGCTGCACCCAGCC 3355
Qy 1130 euLysArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluS 1150
Db 3356 TGAAGCGGAGAAGCCCAAGTGGAGAGCGCGCTCCCTGTTGTCGGGAGAGGCGCAGGAGA 3415
Qy 1150 erGlnAspGluGluLysSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3416 GCCAGGATGAAGAGGAGAGCTCAGAAGAGGAGCGGCGCCCTCGGGCAGTGTGACCATC 3475

QY 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
DB 3476 GCCACAGGGGTCTCTGGAGCGGAGGCCAAGAGTTCCTTTGACCTGCCAGACACATGC 3535
QY 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
DB 3536 AGGTGCCAGGGCTGCATCGCAGTGCAGTGGCGAGGGTCTGCTTCTGAGCACAGGACT 3595
QY 1210 ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
DB 3596 GCAATGGCAAGTCCGGTTCAGGGCGCTTGGCCGGGCGCTTGGCGCTGATGACCCCCAC 3655
QY 1230 euAspGlyAspAspAspAspGluGlyAsnLeuSerLysGlyArgIleGlnAlaT 1250
DB 3656 TGGATGGGATGACCGCCGATGACGAGGCAACCTGAGCAAGGGGAAACGGGTCCGCGCT 3715
QY 1250 rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
DB 3716 GGATCCGAGCCGACTCCCTGCTGCTCGCTCGAGCGAGACTCTCTGCTCAGCCTTACATCT 3775
QY 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
DB 3776 TCCCTCTCTAGTCAGGTTCCGCTCTCTGTGTACCGGATCATCACCAAGATGTTCTG 3835
QY 1290 spHisValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
DB 3836 ACCACGTGGTCTTGTTCATCATCTTCTTAACATGCATCAGCATCGCCATGGAGCGCCCA 3895
QY 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330
DB 3896 AAATTGACCCCCACAGCGCTGAACGCATCTTCTTGACCCCTCTCCAAATTATCATCTTCA 3955
QY 1330 laValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluG 1350
DB 3956 CAGTCTTCTGGCTGAATGACAGTGAAGTGGTGACCTGGGCTGTGTCTCGGGAGC 4015
QY 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
DB 4016 AGCGCTACCTCGGAGCAGTTGGAACGTGTGGACGGGCTGTTGGTCTCATCTCCCGTCA 4075
QY 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
DB 4076 TCGACATTTCTGGTGTCTCTGACAGCGCACCAAGATCCTGGGATGCTGAGGG 4135
QY 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
DB 4136 TGCTGGGCTGTGCGGACCTTGGCCCGCTCAGGCTGATCAGCGGGCGGAGGGGTGA 4195
QY 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
DB 4196 AGCTGGTGGTGGAGACGCTGATGTCTCTCACTGAAACCCATCGGCAACATTTAGTCTATCT 4255
QY 1430 ysCysAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
DB 4256 GCTGTGCTCTTCTCATATTTTCGGCATCTTGGGGGTGCGAGCTCTTCAAGGGGAAGTTT 4315
QY 1450 heValCysGlnGlyAlaSpThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
DB 4316 TCGTGTCCAGGGCGAGATACAGAGAACATCACCAATTAATTCGACTGTGCGGAGGCCA 4375
QY 1470 erTyrArgGtrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
DB 4376 GTTACCGGTGGTCCGGCACAAAGTACAACCTTTGACAACCTTGGCGAGGCCCTGATGTCCC 4435
QY 1490 euPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaV 1510
DB 4436 TGTTCGTTTTGGCTTCCAAGGATGGTTGGTGGACATCATGTACGATGGGCTGATGCTG 4495
QY 1510 alGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS 1530
DB 4496 TGGCGGTGGACAGACCCCATCATGAACCAACCCCTCGATGCTGCTACTTCTATCT 4555
QY 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550

DB 4556 CGTTCTCTGCTCATTTGTGGCCCTTCTTGTCTGAAACATGTTTGTGGGTGTGGTGTGAGA 4615
QY 1550 snPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysA 1570
DB 4616 ACTTCCACAAGTGTGGCAGCACACGAGGAGAAAGGAGGCCCGCGCGGAGGAGAAC 4675
QY 1570 rgLeuArgArgLeuGluLysLysArgSerLysGluLysGlnMetAlaGluAlaGlnC 1590
DB 4676 GCCTACGAAGACTGGAGAAAAAGAGAGAGTAAGGAGAAAGCAGATGCCTGAAGCCCACT 4735
QY 1590 ysLysProTyrTyrSerAspTyrSerArgPheArgIleuValHisHisIleuCythrS 1610
DB 4736 GCAAAACCTTACTACTCCGACTCTCCGCTTCCGGCTCTCGGCTCCCTCCACCATTTGCA 4795
QY 1610 erHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaM 1630
DB 4796 GCACACTACCTGGACCTTCTCATCAGGTGTCTATCGGGCTGAACGTGTGCCATGGCCA 4855
QY 1630 etGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIleP 1650
DB 4856 TGGAGCACTACCAAGCAGCCCGAGATCTGGATGAGGCTCTGAAGATCTGCAACTTACATCT 4915
QY 1650 heThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgP 1670
DB 4916 TCACTGTCTATCTTGTCTTGGAGTCAAGTTTCAAACTTGTGGCTTGTGGTTCGTCGCT 4975
QY 1670 hePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyI 1690
DB 4976 TCTTCAGGACAGGTGGACACAGCTGGACCTGGCCATTGTGCTGTCTCCATCATGGCCA 5035
QY 1690 leThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgI 1710
DB 5036 TCACGCTGGAGGAAATCGAGGTCAACGCTCGCTGCTGCCATCAACCCCACTCATCA 5095
QY 1710 leMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetA 1730
DB 5096 TCATGAGGGTGTGCGCATTTGCCGAGTGTCTGAAGTGTCTGAAGATGGCTGGGCGATGC 5155
QY 1730 rgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyValAsnLeuGlyLeuLeuP 1750
DB 5156 GGGCGCTGTGGACACCGGTGATGCGAGCCCTTGGCCAGGTGGGGAACCTGGGACTTCTCT 5215
QY 1750 heMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluC 1770
DB 5216 TCATGTTGTTGTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGT 5275
QY 1770 ysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyM 1790
DB 5276 GTGACGAGACACCCCTGTGAGGGCTTGGGCGCTCATGCCACCTTTTCGGAACCTTTGGCA 5335
QY 1790 etAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysA 1810
DB 5336 TGGCTTCTCAACCTCTTCCGAGTCTCCACAGGTGACATTTGGAATGGCATTTATGAAGG 5395
QY 1810 spProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleT 1830
DB 5396 ACACCTCCGGGACTGTGACAGAGTCCACCTGCTACAACACCGGTCTATCTCGCCTATCT 5455
QY 1830 yrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValL 1850
DB 5456 ACTTTGTCTCTTGTCTGACGGCCAGTTCTGCTAGTGTAGTCAACGTGGTGTATCCCGTGC 5515
QY 1850 euMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaG 1870
DB 5516 TGATGAAGCACTTGGAGGAGCAACAAGGAGGCCAAGAGGAGGCCGAGCTAGAGGCTG 5575
QY 1870 luLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProp 1890
DB 5576 AGCTGGAGCTGGAGATGAAGACCCCTCAGCCCCCAGCCCCCACTCGCCACTGGGCGAGCCCT 5635
QY 1890 heLeuTrpProGlyValGluGlyValAsnSerThrAspSerProGlyAlaProH 1910

```
Db 5636 TCCTCTGGCTGGGGTCGAGGGCCCCGACAGCCCGCCGACAGCCCTGGGGCTCTGC 5695
Qy 1910 isThrThrAlaHisIleGlyAlaIaSerGlyPheSerLeuGluHisProThrMetValP 1930
Db 5696 ACCGAGCGGCCACCGCAGATCAGCCTCCCACTTTTCCCTGGAGCACCACCCACGATGCAGC 5755
Qy 1930 roHisProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerG 1950
Db 5756 CCCACCCACGAGCTGCCA-----GGACCACCTTACTGCTACTGTCGGCATGGGAGCTG 5806
Qy 1950 lyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrA 1970
Db 5807 GGGTCAGCCGAACGCACTCTCTGCCAATGACAGCTACATGTGTGCGCATGGGAGCACTG 5866
Qy 1970 laGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleL 1990
Db 5867 CCGAGGGGCCCTGGGACACAGGGGCTGGGGCTCCCCAAAGCTCAGTCAGGCTCCGGTCT 5926
Qy 1990 euSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValH 2010
Db 5927 TGTCCGTTCATCCAGCCAGCAGATACAGCTACATCTCTGAGCTTCCCAAGATGCAC 5986
Qy 2010 isTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProp 2030
Db 5987 CTCATCTCTCCAGCCCCACAGCGGCCCAACCTGGGGCACCATCCCCAAACTGCCCCAC 6046
Qy 2030 roGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAsps 2050
Db 6047 CAGGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGCAGCAATAAGGACTGACT 6106
Qy 2050 erLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProS 2070
Db 6107 CTTGGAGCTTCAGGGTCTGGGACCCGGGAAGACTCTCTGGCAGAGGTGAGTGGGCCCT 6166
Qy 2070 erCysProLeuThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnA 2090
Db 6167 CCCC GCCCTGGCCGGGCCCTACTCTTTCTGGGCCAGTCAAGTACCCAGGCACAGCAGC 6226
Qy 2090 rgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyL 2110
Db 6227 ACTCCCGCAGCCACAGCAAGATCTCCAAGCAGCATGACCCCGCCAGCCCTTGGCCAGGCC 6286
Qy 2110 euGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrG 2130
Db 6287 CAGAAACCAACTGGGCAAGGCCCTCCAGAGACCAGAAAGCAGCTTAGAGTTGGACACGG 6346
Qy 2130 luLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluProLeuPheP 2149
Db 6347 AGCTGAGCTGGATTTTCAGGAGACCTCTCTGCCCTTGGCGGCCAGGAGGCCCCATCCC 6406
Qy 2149 roArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyP 2169
Db 6407 CACGGGACCTGAAGAAGTGCTACAGCTGGAGGCCCAGAGCTGCCAGCGCCGGCCCTACGT 6466
Qy 2169 heTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerG 2189
Db 6467 CTGGCTGGATGAGCAGAGGAGACACTCTATCGCCGCTCAGCTGCTTGACAGCGGCTCC 6526
Qy 2189 lnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlys 2209
Db 6527 AACCCACCTGGGCACAGACCCCTCTAACTTGGGGGCCAGGCCTCTTGGGGGGCCCGGA 6586
Qy 2209 erArgProLysLysLysLeuSerProProSerIleSerIleAspProGluSerGlnG 2229
Db 6587 GCCGCCCCAAAGAAAAAATCAGCCCGCCCTAGTATCACCATAGACCCCCCGAGAGCCCAAG 6646
Qy 2229 lySerArgProProCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAsps 2249
Db 6647 GTCTCTGGACCCCGCCAGCCCTGTATCTGCTCCGGAGGAGGCTCCGTCCACGACT 6706
Qy 2249 erLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysL 2269
Db 6707 CCAAGGATCCCTTGGCCCTCTGGCCGCCCTGACAGCATGGCTGCCTCGCCCTCCCCAAAGA 6766
```

```
Qy 2269 ysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6767 AAGATGTGCTGAGTCTCTCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 6819
```

RESULT 3

```
US-09-949-016-3859
; Sequence 3859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3859
```

```
Alignment Scores:
Pred. No.: 0 Length: 7405
Score: 10739.00 Matches: 2077
Percent Similarity: 92.1% Conservatives: 29
Best Local Similarity: 90.8% Mismatches: 95
Query Match: 89.3% Indels: 86
DB: 3 Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-949-016-3859 (1-7405)
```

```
Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 281 CCGCGCGGGCCCCCGGGTTGCGTGAGGACACCTCTCTGAGGGCGCGCTTGCCTCT 340
Qy 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAla 42
Db 341 CCGATGCCCGGGGGCCCCGGCTGCCAGAGATGGACGAGGAGGATGGAGCGGGCG 400
Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
Db 401 CCGAGGAGTCGGACAGCCCCCGGAGCTTCATCGCGCTCAACGACCTGTCGGGGCGGGG 460
Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82
Db 461 GCCGCGCGGGCGCGGGGTTCAGCAGAAAAAGGACCCCGGCGAGCGGACTCCGAGGCGGAGG 520
Qy 82 lyLeuProTrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
Db 521 GGCTGCCGTATACCCGGCGCTGGCCCCGGTGGTTTCTTCTACTTTGAGCCAGGACACCGCC 580
Qy 102 roArgSerTrpCysLeuArgThrValCysAsnPro---TrpPheGluArgValSerMetL 121
Db 581 CGCGGAGCTGGTGTCTCCGCGACGGTCTGTAAACCTACCTGTTTTCAGCGCATCAGCATGT 640
Qy 121 euValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaC 141
Db 641 TGGTCATCTCTCAACTCGGTGACCTCCGGCATGTTCCGGCCATCGCAGGACATCGCT 700
Qy 141 ysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheA 161
Db 701 GTGACTCCACGCGCTGCCGGATCCCTGCGAGGCTTTGATGACTTCATCTTTGCTTTT 760
Qy 161 laValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuG 181
```


Db 761 |||||CCGTGGAGATGGTGGTGAAGATGGTGGCTTTGGGCATCTTTGGGAAAAAGTGTACCTGG 820
Qy 181 lyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerL 201
Db 821 GAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCAATCGAGGATCGTGGAGTACTCGC 880
Qy 201 euAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuA 221
Db 881 TGGACCTGCAAGACGTTCAGCTTCTCAGCTGTGAGGACAGTCCGTGTGCTCGACCGCTCA 940
Qy 221 rgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuP 241
Db 941 GGGCCATTAACCGGGTCCCGAGCATGGCGATCCCTTGTGTCAGTGTCTGCTGCTGATACGCTGC 1000
Qy 241 roMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValG 261
Db 1001 CCATGCTGGGCAAGCTCTGCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1060
Qy 261 lyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerL 281
Db 1061 GCGTCCAGCTGTGGGCAAGGCTGCTTCGGAACCGATGCTTCTTACCTAGAAATTCAGCC 1120
Qy 281 euProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProp 301
Db 1121 TCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAGACAGAGAACGAGGATGAGAGCCCT 1180
Qy 301 heIleCysSerGlnProArgGluAsnGlyMetArgSerCysAtgSerValProThrLeuA 321
Db 1181 TCATCTGCTCTCCAGCCACGAGAACGGCATGCGGTCTTCGAGAAAGCGTGCCACGCTGC 1240
Qy 321 rgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerS 341
Db 1241 GCGGGGACGGGGCGGTGGCCACCTTTCGGCTCTGGACTATGAGCGCTTACAACAGCTCCA 1300
Qy 341 erAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisA 361
Db 1301 GCAACACCACTGTGTCAACTGGAAACCACTACTACACCAACTGTCTCAGCGGGGAGACCA 1360
Qy 361 snProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheG 381
Db 1361 ACCCTTCAAGGGCGCCATCAACTTTGACAACTGGCTATGCTTGGCTGATGCCATCTTCC 1420
Qy 381 lnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerP 401
Db 1421 AGGTCAATCAGCTGGAGGGCTGGTTCGACATCATGTACTTTGTGATGGATGCTCATTCCT 1480
Qy 401 heTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnL 421
Db 1481 TCTACAAATTTTCATCTACTTTCATCTCTCATCTCATCTGTTGGGCTCCTTCTTCATGATCAACC 1540
Qy 421 euCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuM 441
Db 1541 TGTGCTTGGTGGTATGTCACCGAGTCTTCAGAGACCAAGCAGCGGGAAGCCAGCTGA 1600
Qy 441 etArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluP 461
Db 1601 TGGGGGAGCAGCGTGTGCGGTTCCTGTCCAAGCCAGCACCCCTGGCTAGCTTCTCTCAGC 1660
Qy 461 roGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaA 481
Db 1661 CCGGCAGCTGTATGAGGAGCTGTCAAGTACCTTGGTGTATCATCTTCTCGTAAGGACGCC 1720
Qy 481 rgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProv 501
Db 1721 GCAGGCTGGCTCAGGCTCTCTCGGGCAGCAGGTGTGGGGTGGGCTGCTCAGCAGCCAG 1780
Qy 501 alAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgL 521
Db 1781 CACCCCTCGGGGCGCAGGAGACCAGCCAGCAGCAGCTGCTCTCGCTCCACCGCGCC 1840
Qy 521 euSerValHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis 541

Db 1841 TATCCGCTCCACCACCTGGTGCCACCAACCAACCATCACCACCATCACCACCTACCACTGGGCA 1900
Qy 541 snGlyThrLeuAlaGlyValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlyS 561
Db 1901 ATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGAGTGCCTAATGGT 1960
Qy 561 erArgArgLeuMetLeuProProSerThrProThrProThrProSerGlyGlyProProArg 581
Db 1961 CCGCGCGGCTCATGCTGCCACCACTCCGAGCGCTGCCCTCTCCGGGGGCCCCCGCTGGTG 2020
Qy 581 lyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysG 601
Db 2021 GCCAGAGTCTGTGCACAGCTTTTACCATCCGACTGCCACTTAGAGCCAGTCCGCTGCC 2080
Qy 601 lnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysV 621
Db 2081 AGCGGCCCTCCAGGTCCTCCATCTGAGGCATCCGCGAGGACTGTGGGCGAGCGGAAGG 2140
Qy 621 alTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValG 641
Db 2141 TGTATCCACCGTGCACACCACTCCACCGAGCGCTGAGGAGGAGGACCTAGTAG 2200
Qy 641 luValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProp 661
Db 2201 AGTGGCTGCCAGCTCTGGGGCCCCCAACCTCACCAGCCTCAACATCCCACCGGGCCCT 2260
Qy 661 heSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysL 681
Db 2261 ACAGCTCCATGCACNAGCTGCTGGAGACACAGAGTACAGGTGCTGCAAGCTCTTGCA 2320
Qy 681 ysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProT 701
Db 2321 AGATCTCCAGCCCTTGTCTGAAAGCAGACAGTAGTGAGCTGTGGTCCAGACAGCTGCCCT 2380
Qy 701 yrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerA 721
Db 2381 ACTGTGCCCCGGGGCGGGAGGGAGGTGGAGCTGCGCCGACCTGGAATGCTGACTCAG 2440
Qy 721 spSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH 741
Db 2441 ACAGCGAGGAGTTTATGAGTTTACACAGGATGCCAGCAGCAGCAGCTCCGGGACCCCC 2500
Qy 741 isSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaP 761
Db 2501 ACAGC---CGGCGGCAACGAGGCTGGGCCCAGATGTCAGAGCCAGCTCTGTGCTGCCCT 2557
Qy 761 heTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgG 781
Db 2558 TCTGGAGGCTTAATCTGTGACACCTTCCGAAAGATTGTGGACAGCAAGTACTTTTGGCCGG 2617
Qy 781 lyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnP 801
Db 2618 GAATCATGATCGCATCTCTGTTCAACACACTCAGCATGGGCATCGAATACCACGAGCAGC 2677
Qy 801 roGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaL 821
Db 2678 CCGAGGAGCTTACCAACGCGCTTGAATTCAGCAACATCGTCTTCCAGCAGCTCTTTGCC 2737
Qy 821 euGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrA 841
Db 2738 TGGAGATGCTGCTGAAGCTGCTTGTGTATGGTCTCTTGGCTACATCAAGAAATCCCTTACA 2797
Qy 841 snIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyG 861
Db 2798 ACATCTCGATGGTGTTCATTTGGTCATCAGCGTGTGGAGATCGTGGCCAGCAGGGG 2857
Qy 861 lyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheL 881
Db 2858 GCGGCTGTGCGTGTGCGGACCTTCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2917
Qy 881 euProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrP 901
Db 2918 TGCCGGCGCTGCAGCGGCGAGCTGGTGTGCTCATGAAAGACCATGGACAACTGGTCCACCT 2977

Qy 901 heCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheG 921
Db 2978 TCTGATGCTGCTATGCTCTTCATCTTCATCTTCAGCATCTGGCATGCTCTTCG 3037
Qy 921 lyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAsps 941
Db 3038 GCTGCAAGTTTGCCTCTGAGCGGATGGGACACCCCTGCCAGACCGGAAGAAATTTGACT 3097
Qy 941 erLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysV 961
Db 3098 CTTGCTGTGGCCATCGTCTGTTTTCAGATCCTGACCCAGGAGACTGGAAACAAAG 3157
Qy 961 alLeuTrpAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTrpPheIleAlaLeuM 981
Db 3158 TCCTCTACAATGGATGGCCCTCCAGTCGTCTGGCGGGCCCTTATTTCAATTCGCTTCA 3217
Qy 981 etThrPheGlyAsnTrpValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheG 1001
Db 3218 TGACCTTCGGCAACTACGCTCTTCATATTTGCTGGTGCCTATCTGGTGGAGGCTTCC 3277
Qy 1001 lnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValA 1021
Db 3278 AGGCGGAGGAGATGCCAACAAAGTCCGAATCAGAGCCGATTTCTTCTCACCCAGCCTGG 3337
Qy 1021 spGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluL 1041
Db 3338 ATGGTGATGGGACAGGAAGAAGTCTTGGCTTGGTGTCTTGGGAGAGCACCCGGAGC 3397
Qy 1041 euArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetSerHisP 1061
Db 3398 TGCGGAAGAGCTGTGCGGCTCTCATCATCCACACGCGGCCACACCCATGTGCTGC 3457
Qy 1061 roLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerS 1081
Db 3458 CCAAGACACCAAGCAGCGGCTGGCGAGGCGCTGGGCGCTCGGTCGCGCGCCGACCAACA 3517
Qy 1081 erSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProSerAlaA 1101
Db 3518 GCAGCGGTTCGCAGAGCTGGGCGGCC---CACGATGAATCAACGCCCGCCAGCGGCC 3574
Qy 1101 rgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgSerSerA 1121
Db 3575 GCAGCTCTCCGCACACGCCCTGGAGCGCTGCAAGCAGCTGGACACGAGCGCTCCAGCC 3634
Qy 1121 rgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArgS 1141
Db 3635 GGAAACAGGCTCGGCCGTGCACCCAGCTGAAGCGGAGAGGCCAAAGTGAGAGCGCGGT 3694
Qy 1141 erLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAspA 1161
Db 3695 CCCTGTTTGGGAGAGCCAGGAGAGCCAGGATGAAGAGAGAGCTCAGNAGAGGAGC 3754
Qy 1161 rgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysS 1181
Db 3755 GGGCCAGCCCTGCGGCGAGTACCATCGCACAGGGGTTCCTGGAGCGGAGGCCAAGA 3814
Qy 1181 erSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyA 1201
Db 3815 GTTCTTTGACCTGCACACACATCGCAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCC 3874
Qy 1201 rgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaA 1221
Db 3875 GAGGCTGTGCTTCTGAGCACCCAGGACTGCAATGGCAAGTCGGCTTCAGGGCGCTTGGGCC 3934
Qy 1221 rgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyAsnL 1241
Db 3935 GGGCCCTGCGGCTGATACCCCCCTGATGGGATGACGCCGATGACAGGGGCAACC 3994
Qy 1241 euSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgG 1261
Db 3995 TGAGCAAGGGGAAAGGGTCCGCGGTGGATCCGAGCGCGACTCCCTGCTGCTGCTGCTG 4054

Qy 1261 luArgSpSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeuLeuCysH 1281
Db 4055 AGCGAGACTCTGTGTCAGCTACATCTTCCCTCCTCAGTCAGGTTCCGCTCCTGTGTC 4114
Qy 1281 isArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnC 1301
Db 4115 ACCGGATCATCACCAAGATGTTGCACCAAGTGTTCGACCAAGTGTGCTTGTGTCATCATCTTCTTA 4174
Qy 1301 ysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheL 1321
Db 4175 GCATCACCATCGCATGGAGCGCCCAAAATGACCCCAAGCGCTGAACGCATCTTCC 4234
Qy 1321 euThrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLysValV 1341
Db 4235 TGACCCCTCTCAATTAATCATCTTACCGCAGTCTTTTGGCTGAAATGACAGTGAAGGTGG 4294
Qy 1341 alAlaLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuArgSerSerTrpAsnValLeuA 1361
Db 4295 TGGCACTGGGCTGTTCGGGAGCAGGCGTACCTGCGGAGCAGTGTGGAAACGTGCTGG 4354
Qy 1361 spGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerG 1381
Db 4355 ACGGGCTGTGGTGCTCATCTCCGTATCGACATTCGTGGTGTCATGGTCTCTGACAGCG 4414
Qy 1381 lyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuA 1401
Db 4415 GCACCAAGATCTGGGCATGCTGAGGGTGTGCGGCTGCTGCGGACCCCTGCGCCGCTCA 4474
Qy 1401 rgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuL 1421
Db 4475 GGGTGATCAGCGCGCGCAGGGCTGAAGCTGTGGTGGAGACGCTGATGCTCTCACTGA 4534
Qy 1421 ysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuG 1441
Db 4535 AACCCATCGGCAACATTTAGTCATCTGTCTGCTCTTTCATCATTTTCGGCATCTTGG 4594
Qy 1441 lyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsnIleT 1461
Db 4595 GGGTGACAGCTCTTCAAGGGAAGTTTTTGTGTGCCAGGCGAGGATACCAAGGAACATCA 4654
Qy 1461 hrAsnLysSerAspCysAlaGluAlaSerTrpArgTrpValArgHisLysTrpAsnPheA 1481
Db 4655 CCAATAAATCGGACTGTGCGAGGCCAGTTTACCCTGGGTCCGCGCACAAAGTACAACTTTG 4714
Qy 1481 spAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValA 1501
Db 4715 ACAACCTTGGCCAGCCCTGATGTCCTGTTTGGTTCCTCCAGGATGGTGGGTGG 4774
Qy 1501 spIleMetTrpAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisA 1521
Db 4775 ACATCATGTACGATGGGCTGGATGCTGTGGCGTGGACACGAGCCCATCATGAACCACA 4834
Qy 1521 snProTrpMetLeuLeuTrpPheIleSerPheLeuLeuIleValAlaPhePheValLeuA 1541
Db 4835 ACCCTGTGATGCTGCTGACTTTCATCTGTTCTGCTCATTTGGGCTTCTTTGTCCTGA 4894
Qy 1541 snMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG 1561
Db 4895 ACATGTTTGTGGGTGTGGTGGAGAACTTCCACAAGTGTGGGAGCACCAAGAGGAGAG 4954
Qy 1561 luGluAlaArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgSerL 1581
Db 4955 AGGAGCCCGCGCGGAGGAGGAGCGCTACGAAGACTGGAGAAAAAGAGAGAGTA 5014
Qy 1581 ysGluLysGlnMetAlaGluAlaGlnCysLysProTrpTrpTrpSerAspTrpSerArgPheA 1601
Db 5015 AGGAGAACCATGGCTGAAGCCCAAGTGCAAACCTTACTTCCAGCTACTCCCCCTCC 5074
Qy 1601 rgLeuLeuValHisHisLeuCysThrSerHisTrpLeuAspLeuPheIleThrGlyValI 1621
Db 5075 GGCTCTCTCCACCACTTGTGCACCGCACTACTTGCACCTTTCATCACAGGTGTCA 5134
Qy 1621 leGlyLeuAsnValValThrMetAlaMetGluHisTrpGlnGlnProGlnIleLeuAspG 1641

Db 5135 TCGGGCTGAACGTTGGTCCACCATGGCCATGGAGCACTACCCAGCAGCCCAAGTTCGGATG 5194
Qy llaLaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheL 1661
Db 5195 AGGCTCTGAAGAATCTGCAACTACATCTCTCACTGTCATCTTGTGCTTGGATCAGTTTCA 5254
Qy 1661 ysLeuValAlaPheAlaPheArgPhePheGlnAspArgTTPAsnGlnLeuAspLeuA 1681
Db 5255 AACTGTGGCTTTGGTTCCTCGTGGTTCCTCCAGGACAGGTGGAACACAGCTGGACCTGG 5314
Qy 1681 laileValLeuSerIleMetGlyIleThrLeuGluIleGluValAsnLeuSerL 1701
Db 5315 CCATTGTGCTGTCTCATATGGGCATCATCGCTGGAGGAATCGAGGTCAACGCCCTCGC 5374
Qy 1701 euProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuL 1721
Db 5375 TGCCCATCAACCCACCATCATCCGCATCATAGGGTGTGCGCATTTGCCGAGTGTCTGA 5434
Qy 1721 ysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuP 1741
Db 5435 AGCTGTCTGAAGATGGCTGTGGGCATCGGGCGCTGTCTGGACACCGTGTATGCAGGCCCTGC 5494
Qy 1741 roGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuG 1761
Db 5495 CCCAGGTGGGGAACCTGGGACTTCTCTCATGTGTGTGTTTTCATCTTTGCAGCTCTGG 5554
Qy 1761 lyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyA 1781
Db 5555 CGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGGCC 5614
Qy 1781 rgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrG 1801
Db 5615 GTCATGCCACTTTTCGGAACCTTTGGCATGGCTTCTTAAACCTCTTCCGAGTCTCCACAG 5674
Qy 1801 lyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrC 1821
Db 5675 GTGACAAATTGGAAATGGCATATTGAAGACACCCCTCCGGGACTGTGACCGAGGTCCACCT 5734
Qy 1821 ysTrpAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheV 1841
Db 5735 GCTACAAACAGGTCATCTCGCTACTACTTGTGTCTTGTCTGTGCTGACGGCCAGTTCG 5794
Qy 1841 alLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluA 1861
Db 5795 TGCTAGTCAACGTGTGATCGCGTGTGTATGAAGCACCTGGAGGAGAGCAACAAGGAGG 5854
Qy 1861 lalyGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProG 1881
Db 5855 CCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTCAGCCCCC 5914
Qy 1881 lnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerT 1901
Db 5915 AGCCCACTCGCACTGGGAGCCCTTCTCTGGCTGGGTGAGGGCCCGACAGACC 5974
Qy 1901 hrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyP 1921
Db 5975 CCGACAGCCCCAAGCTGGGGCTCTGCACCCAGCGGCCCGACGCGAGATCAGCTCCCACT 6034
Qy 1921 heSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyP 1941
Db 6035 TTTCCCTGGAGCACCCCAAGTGGAGCCCAACCCCGAGGAGCTGCCA-----GGAC 6085
Qy 1941 roAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAsps 1961
Db 6086 CAGACTTACTGACTGTGGGAAGTCTGGGGTACCCGACCCCACTCTCTGCCCCAATGACA 6145
Qy 1961 ertyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyL 1981
Db 6146 GCTACATGTGTGGCATGGGAGCATGCTCCGAGGGGGCCCCCTGGGACACAGGGGCTGGGGC 6205
Qy 1981 euProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerC 2001

Db 6206 TCCCCAAAGCTCAGTCAGGCTCCGTCTTGTTCGTTACTCCAGCAGCAGATACCAGCT 6265
Qy 2001 ysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrT 2021
Db 6266 ACATCTGTCAGCTTCCCAAAGATGCACCTCATCTGTCTCCAGCCCCACAGCGCCCAACCT 6325
Qy 2021 rpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuA 2041
Db 6326 GGGGCACCATCCCAAACTGCCCCACAGGAGCTCCCTTTGGCTCAGAGGGCACTCA 6385
Qy 2041 rgArgGlnAlaIleAtqThrAspSerLeuAspValGlnGlyLeuGlySerArgGluA 2061
Db 6386 GGGCCAGGAGGAGCAATAAGACTGACTCTTGGACGTTTACAGGTCTGGGACGCGGAG 6445
Qy 2061 spLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTrpG 2081
Db 6446 ACCTGCTGGCAGAG----- 6459
Qy 2081 lyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisI 2101
Db 6459 ----- 6459
Qy 2101 leArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProGluT 2121
Db 6459 ----- 6459
Qy 2121 hrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro 2141
Db 6459 ----- 6459
Qy 2141 erSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrG 2161
Db 6460 -----GAGGAGGCCCTTCCACCGGACCTGGAAGAAAGTGTACAGCGTGGAGGCC 6511
Qy 2161 lnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlav 2181
Db 6512 AGAGCTGCCAGCGCGGCCCCACGCTCTGGCTGGATGAGCAGAGAGACACTCTATCGCG 6571
Qy 2181 alSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyG 2201
Db 6572 TCAGCTGCCTGGACAGCGGCTCCCAACCCACCTGGGACAGACCCCTCTAACCTTGGGG 6631
Qy 2201 lyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIleS 2221
Db 6632 GCCAGCCTCTTGGGGGCTGGGAGCGCGCCCAAGAAAAAATCAGCCCGCTAGTATCA 6691
Qy 2221 erIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeuA 2241
Db 6692 CCATAGACCCCGAGAGCAAGGTCTCTCGACCCCGCCAGCCCTGTGTATCTGCTCTCC 6751
Qy 2241 rgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspSerT 2261
Db 6752 GGAGGAGGCTCGTCCAGCGACTCCAAGGATCCCTTGGCTCTGGGCCCTCCACAGCA 6811
Qy 2261 hrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspP 2281
Db 6812 TGGCTGCTCTCGCTCCCAAAAGAAAGATGTGTGAGTCTCTCCGGTTTATCTCTCTGACC 6871
Qy 2281 roThrAspMetAspPro 2286
Db 6872 CAGCAGACCTGGACCCC 6888

RESULT 4

US-08-984-709A-49
; Sequence 49, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 52

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7898 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 249..7307
; OTHER INFORMATION:
;
; US-08-984-709A-49
;
; Alignment Scores:
; Pred. No.: 0 Length: 7898
; Score: 6241.00 Matches: 1385
; Percent Similarity: 65.0% Conservative: 209
; Best Local Similarity: 56.4% Mismatches: 537
; Query Match: 51.9% Indels: 325
; DB: 3 Gaps: 64
;
; US-09-611-257A-24 (1-2287) x US-08-984-709A-49 (1-7898)
;
; QY 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
; DB 188 CCCGGCGATGCCCCGGGGAGCGCCCGCCGAGCAGAGCGAGGTGCTGC-CGGCCG--- 243
;
; QY 23 SerAspProProGlyProArgLeuAlaArgGly-----Trp 34
; DB 244 -----CCACCATGACCGAGG---CGCACGGGGCGCCGACGAGGTCCGGGTGCCCTGG 294
;
; QY 35 ThrArgArg-----ArgMetGluArgAlaProArgSer 45
; DB 295 GCGCGCCGCCCTGGCCCTCGCGCGTGTGGGGGCGTCCCGGAGAGAGCCCCGGGGCGC 354
;
; QY 46 ArgAspSerProValAlaSerArgSerThrThrCysProGlyProGlyAlaAlaGly 65
; DB 355 CCGGACGCGAGCGGAGGGGGTCCGAGCTCGCGGTGTACCCCTCCGAGAGCCCG-CGG 413
;
; QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
; DB 414 GCC-----GAGCGCGCGCGAGCTGGGTGGTCCGACGAGGAGCGCGTCCCGTAC 464
;
; QY 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
; DB 465 CCGGCTTTGGCGGCCACCGTCTTCTTCTGCTCGGTCTAGACCACCGCGCGCGAGCTGG 524
```

```
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
; DB 525 TGCCTCCGGCTGGTCTGCAACCCATGGTTCCAGCACGTGAGCATGCTGGTAAATCATGCTC 584
;
; QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
; DB 585 AACTGCGTGACCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGGCGCTCCGAGCGC 644
;
; QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaValGluMetVal 165
; DB 645 TGCAACATCCTGGAGGCTTTGACGCCCTTCATTTTCGCCCTTTTGGCGTGGAGATGCTC 704
;
; QY 166 VallysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
; DB 705 ATCAAGATGGTGGCTTTGGGGCTGTTCGGGCAGAGTGTACCTGGGTGACACGTGGAGC 764
;
; QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
; DB 765 AGGCTGGATTCTTTCATCGTCGTCGGCGGCATGATGGAGTACTCGTTGGACGGACACAAC 824
;
; QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
; DB 825 GTGAGCCTCTCGGCTATCAGGACGTCGGGTGCTGGCGCCCTCCGCGCCATCAACCGC 884
;
; QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
; DB 885 GTGCTAGATGCGGATCCTGGTCACTCTGCTGTGGATACGCTGCCCATGCTCGGGAGC 944
;
; QY 246 ValLeuLeuLeuCysPhePheValPhePheIleValGlyIleValGlyValGlnLeuTrp 265
; DB 945 GTCCTTCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1004
;
; QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
; DB 1005 GCTGGCCTCTCGCGAAACCGCTGCTTCTGACAGTGCCTTTGTGAGAAACAACACCTG 1064
;
; QY 286 Asp---LeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSer 304
; DB 1065 ACCTTCTCTGCGCGCGTACTACACAGGAGGAGGCGGAGAGAGAGAGAGAGAGAGAGAG 1124
;
; QY 305 GlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 324
; DB 1125 TCAGCGCGAGACAACGCGCATGAGAAAGTCTCGCACATCCTCC---GGCGCGCGC 1175
;
; QY 325 GlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsn----- 338
; DB 1176 GAGCTGCGCATGCCCCCTGCACCTGGGTGGGAGGCGCTACACGCGCCCGAGCGCGAGGG 1235
;
; QY 339 ---SerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
; DB 1236 GTGGGCGCTGCACGCAACCGCTGCATCAACTGGAACAGTACTACAACGCTGTGCCGCTCG 1295
;
; QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
; DB 1296 GGTGACTCAACCCCAACGCGTGCATCAACTTCGACAAATCGCATCGCTCGCTCGCTGATT 1355
;
; QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
; DB 1356 GCCATCTTCCAGGTGATCACCCTGGAAGCTGGGTGGAGATCATGTACTACTCATGTCATG 1415
;
; QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValIleGlySerPhePhe 417
; DB 1416 GCCCACTCATTTCTACAACCTTCATCTATTTCTCTGCTCATCATCTGGGCTCTCTTCT 1475
;
; QY 418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
; DB 1476 ATGATCAACCTGTGCTGTGTGATTCGCCAGCAGTGTCTCGAGAGCAAGCAGCGGGAG 1535
;
; QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
; DB 1536 AGTCAGCTGATGCGGAGCAGCGGCGACGCCACCTGTCCAACGACGACGACGCTGGCCAGC 1595
```

QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
DB 1596 TTCTCCGAGCTGGCAGCTGCTACGAGAGCTGCTGAAGTACGTGGGCCACATATTCCGC 1655
QY 478 LysAlaIleArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
DB 1656 AAGGTCAAGCGGCGAGCTTGCCTCTACGCCCGCTGGCAGAGCCGCTGGCCAAAGAAG 1715
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
DB 1716 GTGACCCCAAGTGTGTGCAAGCCAGGCTCC-----GGG 1751
QY 518 HisArgArg-----LeuSerValHisIleVal-----HisHis 529
DB 1752 CACGCCAGCCGCGGCGAGCAGCAGCAGCAGCAGCTCGGTGCACACCTGGTCTACCAACAC 1811
QY 530 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAla 549
DB 1812 CATCACCAACCAACCACTACCAATTTCAGCCATGGCAGCCCGCCGCGCGGCC 1871
QY 550 SerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu-----Pro 567
DB 1872 GAGCAGCGCCTGCGAC-----ACCAGGCTGGTCCGAGCTGGCGCG 1913
QY 568 ProProSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSer 587
DB 1914 CCCCCCTCGCACCTTCCCGCAGCGCGGAGCCCC-----GACGACAGTGTGTGCACAGC 1970
QY 588 PheTyrHisAlaAspCysHisLeuGlu-----ProValArgCysGlnAlaProProPro 605
DB 1971 ATCTACCATCCGACTCCCATAGAGGGCGCAGGAGGGCGCGGCGTGGCACATGCC 2030
QY 606 ArgCysProSerGluAlaSerGlyArg---ThrValGlySerGlyLysVal---TyrPro 623
DB 2031 GCAGCCACTCGCGTGCAGCCTCAGCGTGCACAGGCTGGCCACCATCACTACCC 2090
QY 624 ThrVal-----HisThrSerProProProGluIle 633
DB 2091 ACATCTGCTCCAGGGTGGCGAGCGCAAGGACGAGCAGCCCCCGGACCAAG--- 2147
QY 634 LeuLysAspLysAlaLeuValGluValAlaProSerPro-----Gly 647
DB 2148 -----GGGAAGTGGCGCGTGGACCGCCAGCAGCAGCAGCGCGGCGCACCGC 2189
QY 648 ProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHisLysLeu 667
DB 2190 CCGTGAAGTTGAACAC-----CCTGATCCCTACGAGAAGATCCCGCATGTG 2237
QY 668 LeuGluThrGlnSerThrGlyAlaCys-----HisSerSer-----Cys 680
DB 2238 GTCGGGAGCATGAGCTGGGCGAGGCCCTCGCCATCTGTGGGCTCAGTGTGCCCTGC 2297
QY 681 LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro 700
DB 2298 CCGCTGCCAGCC-----CCAGCGGGCACACTGACCTGTGAGCTGAAGAGCTGCCCG 2351
QY 701 TyrCysAlaArgThr---GlyAlaGlyProGluSerAlaAspHisValMetProAsp 719
DB 2352 TACTGCACCCGTGCCCTGGAGGACCCGAGGGTGAGCTACGGCTCGGAAGTGGAGAC 2411
QY 720 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 739
DB 2412 TCAGATGGCGTGGCGTCTATGAATTTCAGCGAGACGTCGCGCACGCTGACCGCTGGGAC 2471
QY 740 Pro-----HisSerArg 743
DB 2472 CCCAGCGACACACCCCGTGGCAGCGACACACAGCGCCCGAGCGCCCGCCAGCGG 2531
QY 744 ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheThrArg 763
DB 2532 CGGCACAGCAGAGGGCAGCCCG-----GGCAGCGCAGCTGGATGGCGCGCTCTGGGT 2588
QY 764 LeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMet 783

DB 2589 ACCTTCAGCGGCAAGCTGCGCCGCTCGTGAGCAAGTACTTCAGCCGTGGCATCATG 2648
QY 784 IleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGlu 803
DB 2649 ATGGCCATCTTGTCAACACGCTGAGATGGGTGGATACCATGAGACGCCGAGAG 2708
QY 804 LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet 823
DB 2709 CTGACTAATGCTCTGGAGATCAGCAACATCGTTTCAACAGCATGTTTGCCTGGAGATG 2768
QY 824 LeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe 843
DB 2769 CTGCTGAAGTGTGCGCTCGGCCCTCTGGGTGTACATCCGGAACCCGTCACCATCTTC 2828
QY 844 AspGlyValIleValValIleSerValTyrGluIleValGlyGlnGlnGlyGlyGlyLeu 863
DB 2829 GACGGCATCTGTTGTCATCAGCTGTGGAGATCGTGGGCGAGCGGTGGGTG 2888
QY 864 SerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAla 883
DB 2889 TCTGTGCTGCGCACTTCCGGCTGCTGCGTGTGCTGAAGCTGGTGCCTTCTGCCAGCC 2948
QY 884 LeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMet 903
DB 2949 CTGCGGCGCCAGCTCGTGTGCTGTGAAGACCATGGAACCGTGGCTTCTCTGCACG 3008
QY 904 LeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLys 923
DB 3009 CTGCTCATGTCTTTCATCTTCAGCATCTGGGCATGACCTTTTCGGCTGCAAG 3088
QY 924 PheAlaSerGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeu 942
DB 3069 TTCAGCTGAAGACAGACACCGGAGACACCGCTCTGACAGGAAGAACTTCGACTCCCTG 3128
QY 943 LeuThrAlaIleValThrValPheGlnIleLeuThrGlnGluAspThrAsnLysValLeu 962
DB 3129 CTGTGGGCCATCGTCAACGCTTCCAGATCTCTGAGGAGGACTCGAAGCTGCTCTG 3188
QY 963 TyrAsnGlyMetAlaSerThrSerTyrAlaAlaLeuTyrPheIleAlaLeuMetThr 982
DB 3189 TACAACGGCATGGCTCCACTCTCTGGGCGCCCTTACTTCGTGGCCCTCATGACC 3248
QY 983 PheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnAla 1002
DB 3249 TTCGCAACTATGTGCTCTTCAACCTGCTGGTGGCCATCTCTCGTGGAGGGCTTCAGGCG 3308
QY 1003 GluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspGly 1022
DB 3309 GAGGCGCATCCCAACAGATCCGACCGAGGAGCAAGACGTCGCTCCACTTCGAGGAG 3368
QY 1023 AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeu----- 1035
DB 3369 GACTTCCCAAGCTCAGAGAACTCCAGACCCAGAGCTGAAGATGTTTCCCTGGCCGTG 3428
QY 1036 -----GlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisThr 1053
DB 3429 ACCCCCAACGGCACCTGGAGGAGCAGGACGCTGCTCCCTCCCTCATCATGTGCACA 3488
QY 1054 AlaAlaThrProMetSerHisProLysSerSerSer---ThrGlyValGlyGluAlaLeu 1072
DB 3489 GCTGCCACGCGCATGCTTACCCCAAGAGCTCAACATTCCTTGGATGACGCCCCCAGCGCTC 3548
QY 1073 GlySerGlySerArgThrSerSerGlySerAlaGluProGlyAlaAlaHisHis 1092
DB 3549 CCAGACTCTCGGCTGTCAGCAGCAGCTCCGGGACCCCGCCACTGGGA----- 3596
QY 1093 GluMetLysCysProProSerAlaArgSerSerProHisSerProTyrSerAlaAlaSer 1112
DB 3597 GACCAGAAGCTCCGGCCAGCCTCCGAAGTTCTCCCTGTGCCCCCTGGGGCCCGAGTGGC 3656
QY 1113 SerThrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArg 1132

Db 3657 GCCTGGAGCACC GCGCGCTCCAGCTGGAGCAGCCTGGCGCTGCCCCAGCCTCAAGCGC 3716
Qy 1133 ArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluSerGlnAsp 1152
Db 3717 CGCGGCCAGTGTGGGAACGTGAGTCCCTGCTGTGGCGAGGCAAGGCGAGCAGCCGAC 3776
Qy 1153 GluGluGluSerGluGluAspArgAlaSerProAla-----GlySerAspHisArg 1170
Db 3777 GACGAA-----GCTGAGGACGGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3830
Qy 1171 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu--- 1189
Db 3831 CGSGCCGAGTCCCTGGACCCACGCGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3890
Qy 1190 -----GlnValProGlyLeuHis-----ArgThrAlaSer 1199
Db 3891 CGCGATCGCGACGGCAGGTGGTCCCTGCCACGCGACTTCTTCCTGCGCATCGACAGC 3950
Qy 1200 GlyArgSerSerAlaSerGluHisGlnAspCysAenGlyLysSerAlaSerGlyArgLeu 1219
Db 3951 CACGCTGAGGATGACGCCAGCTTGACAGCACTCGGAGGACAGCTGCTGCTCGCGCTG 4010
Qy 1220 AlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGluGly 1239
Db 4011 CATAAAGTGTGGAGCCCTACAAGCCCGAG----- 4040
Qy 1240 AsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCys 1259
Db 4041 -----TGC 4046
Qy 1260 ArgGluArgAspSerTrpSerAlaTrpIlePheProProGlnSerArgPheArgLeuLeu 1279
Db 4047 CGGAGCCCGAGGCTGGGCCCTTACCTCTTCCCCACAGAACCGGTTCCGGGTCTCC 4106
Qy 1280 CysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIlePheLeu 1299
Db 4107 TGCCAGAAGGTCAACACACAGATGTTGATCACGTGGTCTCGTCTTCATCTTCCTC 4166
Qy 1300 AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1319
Db 4167 AACTGCGTCACATCGCCCTGGAGGCGCTGACATTGACCCCGGAGCAGCGAGCGGTC 4226
Qy 1320 PheLeuThrLeuSerAsnTyriIlePheThrAlaValPheLeuAlaGluMetThrValLys 1339
Db 4227 TTCTCAGCGCTCAAAATACATCTTCAGGCCATCTTCGTGGCGAGATGATGGTGAAG 4286
Qy 1340 ValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyLeuArgSerSerTrpAsnVal 1359
Db 4287 GTGGTGGCCCTGGGCTGCTGTCGGCGAGCAGCGCTACCTGCAGAGCAGCTGGAACCTG 4346
Qy 1360 LeuAspGlyLeuLeuValIleSerValIleAspIleLeuValSerMetValSerAsp 1379
Db 4347 CTGGATGGGCTGCTGGTGTGCTGCTGGTGGACATTGCTGGCCATGGCCCTCGGCT 4406
Qy 1380 SerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPro 1399
Db 4407 GGTGGCGCAGATCCTGGGTGCTTCGCGCTGCTGCTGCTGCGGACCTCGGGCT 4466
Qy 1400 LeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSer 1419
Db 4467 CTAGGGGTCAACAGCGGGCCCGGCGCTCAAGCTGGTGGTGGAGACGCTGATATCGTCG 4526
Qy 1420 LeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIle 1439
Db 4527 CTCAGGCCATTGGGAACATGCTCTCATCTGCTCGGCTTCTTCATCATTTTGGCATC 4586
Qy 1440 LeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyAspThrArgAsn 1459
Db 4587 TTGGGTGTGAGCTCTCTCAAAGGGAAGTTCTACTACTCGAGGGCGCCGACACAGGAAC 4646
Qy 1460 IleThrAsnLysSerAspCysAlaGluAlaSerTyArgTrpValArgHisLysTyArg 1479
Db 4647 ATCTCCACCAAGGCACAGTGGCGGGCGGCCACTACCGCTGGGTGCGAGCAAGTACAAC 4706

Qy 1480 PheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrp 1499
Db 4707 TTCACAACTTGGGCCAGGCCCTGATGTGCTGTGCTGTGCTCATCCAAGATGGATGG 4766
Qy 1500 ValAspIleMetTyAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsn 1519
Db 4767 GTGAACATCATGTACGACGGCTGATGCGGTGTCGACCAAGCAGCCTGTGCAGAAC 4826
Qy 1520 HisAsnProTrpMetLeuLeuTyPheIleSerPheLeuLeuIleValAlaPhePheVal 1539
Db 4827 CACAACCCCTGGATGCTGTACTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4886
Qy 1540 LeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGlu 1559
Db 4887 CTCAACATGTTCTGGGCGTCTGTTGAGAACCTTCACAAGTCCGCGCAGCAGCAGAG 4946
Qy 1560 GluGluAlaArgArgGluGluLysArgLeuArgArgGluGluLysLysArgArg 1579
Db 4947 GCGGAGGAGCGCGCGCGAGAGAGAGCGGCTGCGGCGCTAGAGAGAGCGCGCAGG 5006
Qy 1580 SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyTrpSerAspTySerArg 1599
Db 5007 AGCACTTTCCCGCAGC-----CCAGAGCGCCAGCGCGGCTTACTATGCGGACTCTCGCCC 5063
Qy 1600 PheArgLeuLeuValHisHisLeuCysThrSerHisTyTrpLeuAspLeuPheIleThrGly 1619
Db 5064 ACGCGCGCTCCATTCCTGCTGTGCACGACCACTATCTCGACCTCTTCATCACCTTC 5123
Qy 1620 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyTrpGlnGlnProGlnIleLeu 1639
Db 5124 ATCATCTGTGTCAACGTCACTCACCATGTCTCATGAGCACTATAACCAACCAAGCGCTG 5183
Qy 1640 AspGluAlaLeuLysIleCysAsnTyriIlePheThrValIlePheValPheGluSerVal 1659
Db 5184 GACGAGCGCCCTCAAGTACTGCAACTAGCTTTCACCATCGTGTGTGTCTTCGAGGCTGCA 5243
Qy 1660 PheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAsp 1679
Db 5244 CTGAAGCTGTGATGATTTGGGTTCCGTCGGTCTTCAAGGACAGGTGGAAACAGCTGGAC 5303
Qy 1680 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu 1699
Db 5304 CTGGCCATCGTGTCTGTCTACTCATGGGCATCAGCTGGAGGAGATAGAGATGAGCGCC 5363
Qy 1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719
Db 5364 GCGTGGCCCATCAACCCCAACCATCATCGCATCATGCGCGCTTCGTCATTTGCCGCTGTG 5423
Qy 1720 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739
Db 5424 CTGAAGCTGTGAAGATGGCTACGGGCATGCGCGCTGCTGGACACTGTGGTGAAGCT 5483
Qy 1740 LeuProGlnValGlyAsnLeuLeuPheMetLeuLeuPhePheIlePheAlaAla 1759
Db 5484 CTCCCCCAGGTGGGAACCTGGGCGCTCTTTTTCATGCTCTCTCTCTCTCTCTCTCT 5543
Qy 1760 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1779
Db 5544 CTGGAGTGGAGCTGTTCCGGAGGCTGGAGTGCAGTGAAGACCAACCCCTCGAGGGCGCTG 5603
Qy 1780 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1799
Db 5604 AGCAGGCAGCCACTTCAGCACTTCGGCATGGCTTCCTCACGCTGTTCGCGCTGTCC 5663
Qy 1800 ThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys-----Asp 1816
Db 5664 ACGGGGGCAACTGGAACGGGATCATGAAGGACACGCTGCGCGAGTGTCCCGTGAAGAC 5723
Qy 1817 GlnGluSerThrCysTyAsnThrValIleSerProIleTyPheValSerPheValLeu 1836
Db 5724 AAGCACTCCCTGAGCTACTCGCGGCCCTGTCGCCCGCTTACTTCTGCTGACCTTCTGTGTG 5783

Qy 43 ProArgSerArgAspSerProValAlaSerArgSerThrThrCysProGlyProGly 62
Db 401 CCGAGGAGTCGGGACAGCCCCGGAGCTTCATGCGGCTCAAGACCTGTCGGGGGCGGGG 460
Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82
Db 461 CCGGCGGGGCGGGGTTCAGCAGAAAAGGACCCGGGCGAGCGGACTCCGAGGGGAGG 520
Qy 82 LysLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgp 102
Db 521 GGCTGCCGTACCCGGCGCTGGCCCGGTGGTTCCTTCTACTTGAGCCAGACAGCGGCC 580
Qy 102 roArgSerTrpCysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuV 122
Db 591 CCGGAGCTGGTGTCTCCGCACGGTCTGTAAACCTCTGGTTTGGAGCGCATCAGCATTTGG 640
Qy 122 alIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
Db 641 TCATCCTTCTCAACTGCGTGACCTTGGGCATGTTCCGGCCCATGCGAGGACATCGCTGTG 700
Qy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlav 162
Db 701 ACTCCAGCGTGGCGGATCTCTGAGGCTTTGATGACTTTCATCTTTGCCCTTCTTTGCCG 760
Qy 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA 182
Db 761 TGGAGATGGTGTGAAGATGGTGGCTTGGGCATCTTTGGGAAAAGTGTACCTGGGAG 820
Qy 182 spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA 202
Db 821 ACATTTGAACCGGCTTGCATTTTTTCATCGTCATCGCAGGGATGTCGAGTACTCGCTGG 880
Qy 202 spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
Db 881 ACCTGCAGACGTCAGCTTCTCAGCTGTTCAGACAGTCCGTGTGTCGACCGCTCAGGG 940
Qy 222 laIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM 242
Db 941 CCAITTAACGGGTGCCCCAGCATGCCATCCTTGTTCACCTGCTGCTGGATAGCTGCCCA 1000
Qy 242 etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIleValGlyV 262
Db 1001 TGCTGGGCAACGTCCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1060
Qy 262 alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP 282
Db 1061 TCCAGCTGTGGCAGGGCTGCTTCGGAAACCGATGCTTCTACCTGAGAAATTCAGCCTCC 1120
Qy 282 roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI 302
Db 1121 CCCTGAGCGTGGACCTTGGAGCGCTATTACACAGACAGAGAACGAGGATGAGAGCCCCITCA 1180
Qy 302 leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG 322
Db 1181 TCTGTCTCCAGCACCGCAGAACGCGCATCGGTCTTCGAGAAGCGTGCCACGCTCGCGCG 1240
Qy 322 lylGluGlyGlyGlyProProCysSerLeuAspTyrGluThrThrAsnSerSerSera 342
Db 1241 GGGAGGGGGGGGTGGCCACCTTCGGGTCTGGACTATGAGGCGCTACAAACAGCTCCAGCA 1300
Qy 342 snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP 362
Db 1301 ACACACCTGTGTCAACTGGACACCACTACTACACCACTGTCTACGCGGGGGAGCACACCC 1360
Qy 362 roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV 382
Db 1361 CCTTCAAGGGCGCCATCAACTTGAACAATGGCTATGCCCTGGATCGCCATCTTCCAGG 1420
Qy 382 alIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT 402
Db 1421 TCATCACGCTGGAGGGCTGGGTCGACATCATGATCTTTGTGATGATGCTCATTCCTTCT 1480
Qy 402 yrAsnPheIleTyrPheIleLeuLeuIleValIleValGlySerPhePheMetIleAsnLeuC 422

Db 1481 ACATTTTCATCTACTTCT 1540
Qy 422 ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA 442
Db 1541 GCCTGGTGGTGATTCGCCACGCGAGTTCCTCAGAGACCAAGCAGCGGAAAGCAGCTGATGC 1600
Qy 442 xgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG 462
Db 1601 GGGAGCAGCGGTGCGGTTCCTGTCCAAGCGCACCCCTGGGTAGCTTCTCTGAGCCCG 1660
Qy 462 lysSerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA 482
Db 1661 GCACCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTATACCTCTTCGTAAGSCAGCCGCA 1720
Qy 482 rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA 502
Db 1721 GGCTGGCTCAGGTCTCTCGGCAGCAGGTGTGCGGGTGGGCTGCTCAGCAGCCAGCAC 1780
Qy 502 laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS 522
Db 1781 CCCTGGGGGCGAGAGACCCAGCCAGCAGCAGCTGCTCTCGCTCCACCGCGCCTAT 1840
Qy 522 erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis 542
Db 1841 CCGTCCACCACTGTCGCCACCAACCACCACTACCACTACCACTACCACTACCACTACCACT 1900
Qy 542 lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA 562
Db 1901 GGACGCTCAGGGCCCCCGGGCCAGCCGGAGATCCAGGACAGGAGATGCCAATGGGTCCC 1960
Qy 562 xgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA 582
Db 1961 GCCGCTCATGCTGCCACCACTCTGAGCGCTGCCCTCTCCGGGGCCCCCTTGGTGGCG 2020
Qy 582 laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA 602
Db 2021 CAGAGTCTGTGCACAGCTTCTACCATCGCAGCTGCCACTTAGAGCCAGTGCCTGCCAGG 2080
Qy 602 laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT 622
Db 2081 CGCCCCCTCCAGGTCCCATCTCAGGCATCCGCGAGACTGTGGGACAGCGGAGGTGT 2140
Qy 622 yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV 642
Db 2141 ATCCACCGTGCACACAGCCCTCCACCGGAGACGCTGAAGGAGAGAGCCTAGTAGAGG 2200
Qy 642 alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS 662
Db 2201 TGGCTGCCAGCTCTGGGCCCCCAACCTCTCACAGCCTCAACATCCACCGCGGCCCTACA 2260
Qy 662 erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI 682
Db 2261 GCTCCATGTCACAAGCTGCTGGAGACACAGAGTACAGGTGCGCTGCCAAAGCTCTTCAAGA 2320
Qy 682 leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC 702
Db 2321 TCTCCAGCCCTTGTGTGAACACAGACAGTGGAGCTGTGGTCCAGACAGTGCCTCTACT 2380
Qy 702 ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspS 722
Db 2381 GTGCCGCGGCGGGCAGGGGAGGTGGAGCTCGCGCAGCCGTGAAATGCTGACTCAGACA 2440
Qy 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS 742
Db 2441 GCGAGGCAAGTTTATGAGTTCACAGGATGCCAGCAGCAGCAGGACCTCCGGGACCCCCACA 2500
Qy 742 erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db 2501 GC---CGCGGCAACGAGGACCTGGGCCAGATGCAGAGCCCGAGCTCTGTGCTGGCCTTCT 2557
Qy 762 rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782

```
Db 2558 GGAGGCTAATCTGTGACACCTTCGGAAGAGATTGGGACAGCAAGTACTTTGGCGGGGAA 2617
Qy 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyHisGluGlnProG 802
Db 2618 TCATGATCGCATCTCTGTCAACACACTCAGCATGGCGCATCGAATACACAGAGAGCCG 2677
Qy 802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
Db 2678 AGGAGCTTACCAAGCCCTAGAAATCAGCAACATCGTCTTCCACGAGCTCTTTGGCCCTGG 2737
Qy 822 luMetLeuLeuLysLeuValTyGlyProPheGlyTyIleLysAsnProTyAsnI 842
Db 2738 AGATGCTGCTGAAGCTCTTGTATGCTCCCTTTGGCTACATCAAGAATCCCTACAA 2797
Qy 842 lePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyG 862
Db 2798 TCITCGATGTGTCATTTGGTCATCAGCGTGTGGGAGATCGTGGGCGCAGAGGGGGCG 2857
Qy 862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
Db 2858 GCCTGTGCGTGTGCGGACCTTCGCGCTGATGCGTGTGTGCTGAAGCTGGTGGCTTCCCTGC 2917
Qy 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db 2918 CGCGCTGCAGCGGACGCTGGTGTCTCATGAAGACCATGGACACGCTGGCCACCTTCT 2977
Qy 902 ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db 2978 GCATGCTGCTATGCTCTTCTCATCTTTCATCTTCCAGCATCTGGCGCATCATCTTCCGCT 3037
Qy 922 yslsPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
Db 3038 GCAAGTTTGGCTCTGAGCGGATGGGACACCTTCCAGACCCGGAAGAAATTTGACTCCT 3097
Qy 942 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysVal 962
Db 3098 TGCTCTGGGCGATCGTCACCTGCTTTTCAGATCTTCCAGCCAGGAGACTGGAAACAAAGTCC 3157
Qy 962 euTyAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyTrpPheIleAlaLeuMet 982
Db 3158 TCTACATGATGTGGCTTCCAGCTGCTGCTGGGCGGCTTTATTTCTATTTGCCCTCATGA 3217
Qy 982 hrPheGlyAsnTyValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db 3218 CCTTCGGCAACTACGCTCTCTCAATTTGCTGTGCTGCCCATCTTGTGGAGGCTTCCAGG 3277
Qy 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
Db 3278 CGGAGGAGATGCCAACAGTCGGAATCAGAGCCCGATTTCTTCTACCCAGGCTGGATG 3337
Qy 1022 lyAspGlyAspArgLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
Db 3338 GTGATGGGACAGGAAGATGCTTGGCTTGGTGTCTCTGGGAGAGACACCCGAGGTGC 3397
Qy 1042 rglYsSerLeuLeuProProLeuIleHisThrAlaAlaThrProMetSerHisProL 1062
Db 3398 GGAAGAGCTGCTGCGCCCTCTCATCTCCACAGCGCGCACACCCATGCTGCGTGCCCA 3457
Qy 1062 ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSers 1082
Db 3458 AGAGCACACAGCGGCTGGCGGCGCTGGGCGCTGGCGCTGGCGCGGACACAGCAGCA 3517
Qy 1082 erGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSerAlaArgS 1102
Db 3518 CGGGGTGGGACAGCTTGGGGGCGCC--CACGAGATGAAGTCAACCCCGCAGCGCCGCA 3574
Qy 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArg 1122
Db 3575 GCTCTCCGCAAGCCCTGAGCGCTGCAAGCAGCTGGAACAGAGCGCTCCAGCCGGA 3634
Qy 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL 1142
Db 3635 ACAGCTCGGCGGTGCAACCCAGCTGAAGCGGAGAGCCCAAGTGGAGAGCGCGGTCCC 3694
```

```
Qy 1142 euLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAspArgA 1162
Db 3695 TGTGTGCGGAGAAGGCCAGGAGCCAGGATCAAGAGGAGAGCTCAGAAAGAGAGCGGG 3754
Qy 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers 1182
Db 3755 CCAGCCCTGCGGCGAGTGACCATCGCCACAGGGGGTCCCTGGAGCGGGAGGCCAAGATT 3814
Qy 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202
Db 3815 CCTTTGACCTGCCAGACACACTCGAGGTGCAGGGCTGCATCGCACTGCCAGTGGCCGAG 3874
Qy 1202 erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
Db 3875 GGTCTGCTTCTGAGCACAGGACTGCAATGCAAGTCGGCTTCAGGGCGCTGCCCCGGG 3934
Qy 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeu 1241
Db 3935 CCCTGGCGCTGATGATGACCCCCCACTGGATGGGATGACCGCATGACGAGGGCAACCTG 3993

RESULT 6
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: McGivern, Paul S.
; APPLICANT: Dietrich, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Alignment Scores:
Pred. No.: 3 46e-314 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.7% Conservative: 234
Best Local Similarity: 51.8% Mismatches: 494
Query Match: 45.1% Indels: 413
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-1 (1-6816)
Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCTCTCTCATCTGCAGCAGCCCGCCAGCGCTGAGCGAGGAGTCAACACGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCCGAGCCCCCG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCTCTGGAGAGCTCTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTy 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValValPhePheTyLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACTGCGCGCTATTGCTTCTTCTGCTCGCAGACACCACCGCCCCCGGAACTGG 404
```

Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGAACCGGTGTTGAATGTGTACATGCTGGTATCCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGGGTGACATTTGGCATGTACACGCGGTGCGACGACATGGAGTCTGCTCCGACCGC 524
Qy 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaValGluMetVal 165
Db 525 TGCAGATCTTCAGGCTCTTTCATGACTTCATCTTTATCTTTTGGCATGGAGATGGTG 584
Qy 166 ValIysMetValAlaLeuGlyIlePheGlyIysIysCysTyrLeuGlyAspThrTrpAsn 185
Db 585 CTCAGATGGTGGCCCTGGGATTTTGGCAAGAGTGTCTACCTCGGGGACACATGGAAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCCTGGATTCTTCATCGTCATGCGAGGGATGGTGCAGTACTCCTTGGACCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTGAGCCATCCGACCGTGGCGTCTCTGAGGCCCTCAAAAGCCATCAACCGC 764
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuLeuLeuLeuLeuLeuLeu 245
Db 765 GTGCCAGATGCGGATCCTGGTAACTGCTCTGGACACACTGCCCATCTGGGGAAT 824
Qy 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCCGTGCTGCTGCTCTTGTCTTCTTCATCTTTTGGCATCATAGGTGTGCAGCTCTGG 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGCGCTGCTGCGTAACCGTCTCTCTGAGGAGAACTTCACCATACAAGGGGATGTG 944
Qy 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGGCCCCATATACAGCGGAGGAGATGATGATGATGCCCTTCATCTGCTCCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGCGCAATGGATAATGGCTGCCATGATGATCCCCCGCTCAAGGAGCAG----- 1058
Qy 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCCGTGAGTGTGCTGTGTCCAAGGACGACGTCTACGACTTTTGGGCGGGCGCCAG 1115
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCCGACG 1175
Qy 358 GlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCAACCCCAAGGGTGCCATCAACTTTTGACAACATCGTTATGCTTGGATT 1235
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCACTCTCCAGGTGATCACTCGGAAGGCTGGGTGGAGATCATGTACTGTATGGAT 1295
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTACTCTCTTACAACTTCATCTACTTCATCTCTGCTTATCATAGTGGCTCTCTCTC 1355
Qy 418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrIysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGCTGTGTCATAGCACCCAGTCTCTCGAGACCAAGCAACGGGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGTGGAGCAGCGGCGCTACCTGTGCC---TCCAGCACGCTGGCCAGC 1472

Qy 458 PheSerGluProGlySerCysTyrGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TAGCCGAGCTGGGACTGCTACGAGAGATCTTCAGTATGTCTCCACATCTCTGCGC 1532
Qy 478 LysAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGCCCAAGGCG-----CGGCCCTGGGCTCTACCAAGCCCTCGAG 1574
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
Qy 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537
Db 1578 ---CGGCCGAGGCCCTG----- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGGCCCGCCCAACCTGGGCC----- 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CACGCCAAG-----GAGCCC 1643
Qy 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACCAAGTGTGCCCGCAACATAGCCCCCTGGATGCG----- 1685
Qy 618 SerGlyLysValTyrProThrValHisSerProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCAAC----- 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGGTGCAG-----CCCATCCCCCGCCAGCTGGCTTC----- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCAGCTGCCCTTGTGTGCCAG 1757
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGNAGCGCGCGGCTCGGGCTGGGACACCGACTCGGGCAGGAGGCTCG 1817
Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCCGCTGGTGGCGAGGACGAGCG----- 1853
Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACGCGGCC-----CGGAGCAGCGAGGACGAGCTCTCCAGAA 1898
Qy 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGAAGGAGGAGGAGGAGGAGGAG-----GCGATCGGGCG 1940
Qy 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCTGGCTGTGCGGGGATGTGTGGCGGAGACGCGAGCAAGCTCGCGGCATCTGTGGAC 2000
Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGATCATGATGGCCATCTCTGGTCAACACCGTACGATGGC 2060
Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCGAGCACCGAGCAGCGGAGGAGTGCACCAACATCTCTGGAGATCTGCAATGTGTC 2120
Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPheGly 834


```

Db 6119 CGCGGAGCGCTCGAGACACCGCTCGAGGACAGCGCTGACCCCTGAGCGACAGCCCCCGCGC 6178
Qy 2220 IleserileAspProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
Db 6179 -----TGGCCCTGGGGCGCCCGCGCGCTGCTCCAGGACCCCGGGC 6217
Qy 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCCTGTCGCCCGCGCTCGCGCGCTGAGCGCTCGCGCGCGGGCGCTCTTCAGCCT 6277
Qy 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuGlyLeu 2277
Db 6278 GCGGGGCTGGCGCGCATCAGCGACCGACGAGCGGGGCTCCACCAGCCCGGGCTG 6337

RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: McGivern, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 3,46e-314 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.7% Conservative: 234
Best Local Similarity: 51.8% Mismatches: 494
Query Match: 45.1% Indels: 413
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)
Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCCCTCCTCATCTGAGCAGCCCGCCGCTGAGCCAGGAGTCAACAGGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCCAGCGCTGGAGAGCCTCGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCCTTCTTCGCTGCGACAGACACACCGCCCGGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCCGTGGTTTGAATGTGTGTCAGCATGCTGGTGATCCTGCTG 464

```

```

Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACCAGCGTGCAGACATGCATGCCTGTCGACCGC 524
Qy 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TGAAGATCCTGCAAGTCTTTGATGACTTTCATCTTTATCTTCTTGCATGGAGATGGTG 584
Qy 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn 185
Db 585 CTCAGATGTGGCCCTGGGATTTTGGCAAGAGTGTACTCTCGGGGACACATGGAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCCTGGATTCTTCATCGTCGTCAGGAGGATGTCGAGTACTCCCTGGACCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTGACCCATCCGACCGCTGCGCGCTCTGAGGCCCTCAAGGCCATCAACCGC 764
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGATATGGGATCTCTGTGAACCTGCTCTTGACACACATGCCCATGCTGGGAAT 824
Qy 246 ValLeuLeuLeuCysPhePheValPhePheIleValGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCTGCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGGGCTGCTGGGTAAACCGCTCTCTCGAGGAGAACTTCAACATACAAAGGGATGTG 944
Qy 286 AspLeuGluProTyrTrpGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGGCCCATCTACTACAGCCGAGGAGATGATGAGATGCCCTTCACTGCTCCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGGGACAAATGGGATAATGGGCTGCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
Qy 326 GlyGlyProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCGTGAGTGTCTGCTCCAAAGACGAGCGTCTACGACTTTGGGGGGGGCGGCAG 1115
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTrpThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGCTCTGTGTCAACTGGACCGTTACTACATGTGTGCCGACG 1175
Qy 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCCCAACCCCAAGGAGTGCATCAACTTTGACAACATCGGTATGCTTGGATT 1235
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCAGGTGATCACTCTGGAGGCTGGGTGGAGATCATGTACTAGTATGAT 1295
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTCACTCTTCTACAACTTCACTTCACTCTGCTTATCATAGTGGGCTCTCTTCTTC 1355
Qy 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTCTGTGTATGATGAGCGACCCAGTCTCTGGAGACCAAGCAACGGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGTGGAGCGAGCGAGCTACCTGTCC---TCCAGACCGGTGGCGCAGC 1472
Qy 458 PheSerGluProGlySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TAGCCGAGCGCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTCCCATCTCTGGC 1532

```


3216	CCCATCTGGCGCACCCGCCACCGCCACCACCGCGGAGCGTGTCTCCTGACAACAGGGAC	3275
1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201
3276	TGGTGACCTTGGCCGAGCTGGTCGCCCGGTGGCGCCCCACCCCGGGCGCGCTGGAGG	3335
1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
3336	GCGCAGCGCCGGCCCCCGGCATGAGACTGCAATGGCAGGATGCCACAGC-----ATC	3389
1220	AlaArgThrLeuArgThrAsp--AspProGlnLeuAspGlyAspAspAspAsnAspGlu	1238
3390	GCCAAAGACGCTTCCACAAGATGGCGACCGCGGGATCGCGGGAGGATGAGGAGGAA	3449
1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
3450	ATCGACTACACCTGTGCTTCCGGTCCGCAAGATGATCGACGCTCTATAAGCCCGACTGG	3509
1259	CysArgGluArgAspSerTrpSerAlaTyrllePheProProGlnSerArgPheArgLeu	1278
3510	TGCAGGTCGCGAAGACTGCTGTCTACTCTCTCTCTCCGAGAACAGGTTCCGGGTC	3569
1279	LeuCysHisArgIlelleThrHisLysMetPheAspHisValValLeuValIlellePhe	1298
3570	CTGTGTGAGACCATATTGCCCCAAAATCTTTCGACTACGTGCTCTGGCCTTCATCTTT	3629
1299	LeuAsnCysilleThrIleAlaMetGluArgProLysileAspProHisSerAlaGluArg	1318
3630	CTCAACTGCATCACATCGCCTGGAGGGGCTCAGATCGAGGCCGCGCAGCACCGAACGC	3689
1319	IlePheLeuThrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGluMetThrVal	1338
3690	ATCTTTCTACCGTGTCCAATCATCTTACGGCCATCTTCGTGGCGCAGATGACATTG	3749
1339	LysValValAlaLeuGlyTrpCysPheGlyGlnIleAlaTyrlleuArgSerSerTrpAsn	1358
3750	AAGTAGTCTCGCTGGGCGCTGTACTTCGGCGAGCAGCGTACCTTACGACGAGCTGAAC	3809
1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspileLeuValSerMetValiser	1378
3810	GTGCTGATGGCTTCTTGCTTCGTGTCAATCATCGACATCGTGGTGTCTCTGGCCTCA	3869
1379	AspSerGlyThryllysilleLeuGlyMetLeuArgValLeuArgLeuLeuArggThrLeuArg	1398
3870	GCCGGGGAGGCCAAGACTTGGGGGTCTTCGAGTCTTGGCGTCTCTGCGCACCCCTACGC	3929
1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
3930	CCCCCTGGCTGTCACTCAGCGGGCGCCGGGCGCTGAAGCTGGTGGTGGAGACATCATCTCC	3989
1419	SerLeuLysProIleGlyAsnIleValIleCysValPhePheIlellellePheGly	1438
3990	TCCCTCAAGCCCATCGGCACATCGTGTCTCATCTGCTGTGCGCTTCTTCATCATCTTTGGC	4049
1439	IleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlnGlyGiuAspThrArg	1458
4050	ATCTCGGAGTGCAGCTCTTCAAGGGCAAGTTCTTACCACITGCTCGGGCGTGCACCCCGC	4109
1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrrArgTrpValArgHisLysTyrr	1478
4110	AACATCACCAACCGCTCGACTGTCATGGCCGCCCACTACCGCTGGGTCCCATCACAATAAC	4169
1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
4170	AAC TTCGAACACCTGGGCGCAGGCTCTGTATGTCCTTGTTCCTGGGCATCCAGAAGTGGT	4229
1499	TrpValAspileMetTyrrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
4230	TGGGTGAACATCATGTACAATGGACTGGATGCTGTCTGCTGGGACGACGACCTGTGACC	4289
1519	AsnHisAsnProtrpMetLeuLeutyrrPheIleserPheLeuLeuilleValAlaphPhe	1538
4290	AACCAACACCTGATGCTGCTGACTTATCTCTTCTCTGCTCATCTCTCTGCTCATCGTCAGTCTCTTT	4349

Qy	1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln	1558
Db	4350	GTGCTCAACATGTTTGTGGGTGTCGTGGTGGAGAACTTCACAAAGTGC CGCGAGCACCCAG	4409
Qy	1559	GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArg	1578
Db	4410	GAGCTGAAGAGGACCGCGCGGTGAGGAGAGCGGCTGCGGCGCCTGGAGAGAGAGCGC	4469
Qy	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598
Db	4470	CGG-----AAGCCGACGCGCTGCCTTACTATGCACCTATTGT	4508
Qy	1599	ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1618
Db	4509	CACACCCGGCTGCTCATCTCACTCATGTGCACGACCCACTTACCTGGACATCTTCATCACC	4568
Qy	1619	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1638
Db	4569	TTCATCATCTGCCTCAACGTTGTCACCATGTCTCTGGAGCACTACAATCAGCCACGCTCC	4628
Qy	1639	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer	1658
Db	4629	CTGAGACAGCCCTCAAGTACTGCACATATATGTTCACCACTGTCTTTGTGCTGGAGGCT	4688
Qy	1659	ValPheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTyrTpAsnGlnLeu	1678
Db	4689	GTGCTGAAGCTGTGGCATTTGGTCTCAGAGGGCTTCTTCAAGGACCGATGGAACCACTG	4748
Qy	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
Db	4749	GACCTGGCCATTTGTCTACTGTCTCAGTTCATGGGCATCACCTGGAGGAGATCGAGATCAAT	4808
Qy	1699	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1718
Db	4809	GCGGCCCTGCCCATCAATCCACCATCATCCGATCATAGGGTTCTTGCAGATTGCCCGA	4868
Qy	1719	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln	1738
Db	4869	GTGCTGAAGCTGTTGAAGATGGCCACAGGAATGCGGCGCCTGCTGGACACGGTGTGCA	4928
Qy	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuPhePheIlePheAla	1758
Db	4929	GCATTGCCCGAGTGGCAACCTGGGCTCTCTTTCATGTGTCTTCTTTCATCTATGCT	4988
Qy	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
Db	4989	GCTCTCGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTGCGAGGGC	5048
Qy	1779	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATGAGCCGGATGCCACTTTCGAACTTCGGGATGCGCTTCTCTCACACTCTTCCAGGTC	5108
Qy	1799	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln	1817
Db	5109	TCCACGGGTGACAACTGGAACGGGATCATGAAGGACACGCTGCGGAGTGCACCCACGAC	5168
Qy	1818	GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1835
Db	5169	GAGCGCAGCTGCCTGAGCAGCCTGCAGTTTGTGTGTCGCGGTGTACTTCGTGAGCTTCGT	5228
Qy	1836	LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu	1855
Db	5229	CTCACCGCGCAGTTTGTGCTCATCAACGTTGGTGTGTGTGCTGTGCTCATGAAGACACCTG	5288
Qy	1856	GluSerAsnLysGluAlaLysGluGluGluAlaGluLeuGluAlaGluLeuGluMet	1875
Db	5289	GACAGCAACAAGGAGGCGCAGGAGGACGCCGAGATGATGCCGAGCTCGAGCTGGAGATG	5348
Qy	1876	---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly	1894
Db	5349	GCCCATGGCTGGGCCCTGGCGCCGAGGCTGCTTACCGGCTCC-----	5390

```
Qy 1895 ValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHis 1914
Db 5391 -----CGGGCGCCCTTGGCCGAGGCGG--- 5414
Qy 1915 IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro----- 1930
Db 5415 --GGAGGGCGGGCGGGG--GGGCGACACGAGGGGGCTGTGGCGGCGCTGCTACTC 5470
Qy 1931 -----HisProGluGluValProValPro 1938
Db 5471 GCCTGCCCGAGACTCTTTGGAGGGGAGCTGACCATCATCGACCACTGTCCGGCTCCAT 5530
Qy 1939 LeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
Db 5531 CTTCCACCACCTACTCTCTCCCTGCGGCTGCAAGAGTGTC-----CCA 5575
Qy 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
Db 5576 CGACAA-----GCAAGAGGTGCAGCTGGCTGGAGCGGA 5608
Qy 1979 TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp 1998
Db 5609 GGCCTTCTCCCTGAACTCAGACAGGTCTCTCCATCTCTGGGTGACGACCTGAGTCT 5668
Qy 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
Db 5669 CGAGGA-----CCCCACAGCCTG 5686
Qy 2019 ProThrTrpGlyAlaIleProLys----- 2026
Db 5687 CCCACCTGG-----CCGCAAGCAGCAAGGGTGCAGCTGGACCCACCTGAGCCCAT 5737
Qy 2027 ---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla 2045
Db 5738 GCGTGTGGGAGACCTTGGCGAATGCTTCTTCCCTTGT-CCTCTACGGCCCTGCGCGG 5796
Qy 2046 IleArgThrAspSerLeuAspValGlnGlySerArgGluAspLeuSerGlu 2065
Db 5797 ATCCAGAACTTCTGT---GTGAGTGGAGGAGATCCCAT-----TCAACC 5841
Qy 2066 ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyLysSerIle 2085
Db 5842 CTGTCCGGTCTCTGGCTGAACATGACA----- 5868
Qy 2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
Db 5869 -----GCAGTCAAGCATCCCAAGTCCCTTCT 5895
Qy 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125
Db 5986 CCC-----CGGATGCCTCCAGCC----- 5913
Qy 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2145
Db 5914 -----CTCTCTGCCCATGCCAGCCAGTCTTCCACCCCTG 5949
Qy 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163
Db 5950 CAGTGTCTGCCAGCCAGAAAGCCCGAGGAGGCACTGGCATCGAACCCTCCCAAGA 6009
Qy 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
Db 6010 TTGCCCTG-CAGGGTCTCTGGCATCT-----CTGCGGTCCACCAAGGTCAACTGT 6059
Qy 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
Db 6060 ACCCTCTCCCGCAGCGCCACCGGAGCGACACGTCTGCGTGGACGCGCCGCCAGCAG-CTC 6118
Qy 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProProSer 2219
Db 6119 CCGGGGAGCCTGACACACCTCGAGCAGCTGACCTGAGCGACGACGCCCCCGGG 6178
Qy 2220 IleSerIleAspProGluSerGlnGlySerArgProCysSer-----ProGly 2237
```

```
Db 6179 -----TGCCCTGGGCGCCCGCGCTCTCCAGGACCCCGGC 6217
Qy 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCTCTGCCCGCGCTCGCGCGCTGAGCTCGCGCGCGGCGCTTTCAGCCT 6277
Qy 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTGGGCGGCATCAGCCAGCACGAGCGGGGCTCCACCACCGGGCTG 6337

RESULT 8
US-10-425-800-1
; Sequence 1, Application US/10425800
; Patent No. 6893842
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-RSG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-10-425-800-1

Alignment Scores:
Pred. No.: 3,46e-314 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.7% Conservative: 234
Best Local Similarity: 51.8% Mismatches: 494
Query Match: 45.1% Indels: 413
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-10-425-800-1 (1-6816)
Qy 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCCCTCTCATCTGCGACAGCCCGCCGCTGAGCCAGGAGTCACCACGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCGCGCTGGAGGAGCTCTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCTCTTCTGCTCGACAGACACCAGCCCGCGGAAGTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCGGTGTTGAATGTGTGAGCATCTGTGTATCTGTCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACCGCGCTGCGAGCATGGAGTCTGTCTCCAGCC 524
```

146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValGluMetVal 165
147 : : : : :
525 TGCAAGATCTGCGAGGCTTTGATGACTTCATCTTTATCTTTGCGCATGGAGATGGTG 584
166 ValIysMetValAlaLeuGlyIlePheGlyIysCysTyrLeuGlyAspThrTrpAsn 185
167 : : : : :
585 CTCGAAGTGGTGGCCCTGGGGATTTTGGCAAGAAGTGTACCTCGGGGACACATGGGAAC 644
186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
187 : : : : :
645 GCGCTGGATTCTTCATCGTCATGCGAGGATGGTCGAGTACTCCCTGGACCTTCAGAAC 704
206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
207 : : : : :
705 ATCAACCTGTGCGGATCTGTCGACCGCTGCGGCTGCTGAGGCCCTCAAAAGCCATCAACCGC 764
226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
227 : : : : :
765 GTGCCAGTATGCGGATCTGTCGTAACCTGTCCTCGGACACACTGCGCCATGCTGGGAAT 824
246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
247 : : : : :
825 GTCTGCTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGCTG 884
266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
267 : : : : :
885 GCGGCGCTGTGCGTACCGCTGCTTCTGAGGAGAACTTCACCATACAGGGGATGTG 944
286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
287 : : : : :
945 GCCTTGCCCCCATACTACACGCGGAGGAGATGATGAGATGCGCTTTCATCTGCTCCCTG 1004
306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
307 : : : : :
1005 TCGGGCCAAATGGGATTAATGGGCTGCATGAGATCCCCCGCTCAAGGAGCAG- 1058
326 GlyGlyProProCysSerLeu- 1115
1059 --GGCCGTGAGTGTCTGCTTCCAAAGCAGCAGCTACTGACCTTTGGGGGGGCGCCAG 1115
340 SerSerAsnThrThr- 1175
1116 GACCTCAATCGACGGCGCTGTGTCAACTGGAAACCGTTACTACAAATGTGTGCGCAGC 1175
358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
377 : : : : :
1176 GGCAGCCCAACCCCAAGGGTGCCATCAACTTTGACAACTCGGTATGCTTGGATT 1235
378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
397 : : : : :
1236 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTATGGAT 1295
398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
399 : : : : :
1296 GCTCACTCTTCTACAACTTCATCTACTTCTGCTTATCATAGTGGGCTCTCTTCTC 1355
418 MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
437 : : : : :
1356 ATGATCAACCTGTGCTGCTGTGTCATGCGACCCAGTTCTCGGAGACCAAGCAACGGGAG 1415
438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
457 : : : : :
1416 CACCGGTGATGCTGGAGACGCGGAGCGCTACCTGTCC- -TCCAGCAGCGGTGGCCAGC 1472
458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
477 : : : : :
1473 TACCGGAGCTGGCGACTGTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCTGCGC 1532
478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
497 : : : : :
1533 AAGGCCAAGCCG- - - - -CGCGCCCTTGGGCCCTTACGAGGCCCTCTGAC 1574

498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
517 : : : : :
1575 AGC- - - - - 1577
518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537
537 : : : : :
1578 --CGGCGCCAGGCCCTG- - - - - 1592
538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
557 : : : : :
1593 -- - - - -CGCCCGGAG- - - - - 1601
558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
577 : : : : :
1602 -- - - - -GCCCGCGCCCGCCCAACCTGGGCC- - - - - 1628
578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
597 : : : : :
1629 -- - - - -CACGCCAAG- - - - -GAGCCC 1643
598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
617 : : : : :
1644 CGGCACTACGAGTGTGCGCGCAACATAGCCCTGATGCG- - - - - 1685
618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
637 : : : : :
1686 -- - - - -ACGCCCCACACC- - - - - 1697
638 AlaLeuValGluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIlePro 657
657 : : : : :
1698 --CTGGTGAG- - - - -CCATCCCGCCACGCTGGCTTCC- - - - - 1730
658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys- - - 676
676 : : : : :
1731 -- - - - -GATCCCGCCAGCTCCCTTGTCTGCCAG 1757
677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
696 : : : : :
1758 CATGAGCAGCGCGCGCGCTCGGGCTGGGAGCAGCACCGACTCGGCGCAGGAGGCTCG 1817
697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
716 : : : : :
1818 GGCTCC- - - - -GGGAGCTCGCTGGTGGCGGAGCAGGAGCG- - - - - 1853
717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
736 : : : : :
1854 -- - - - -GATCGGCGCGGGCC- - - - -CGGAGCAGCGGAGCAGGCGCTCTCAGAA 1898
737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
756 : : : : :
1899 CTGGGAAGGAGGAGGAGGAGGAGGAGCAG- - - - -GCGGATGGGCGC 1940
757 SerValLeuAla- - - - -PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
774 : : : : :
1941 GTCTGGCTGTGCGGGGATGTGCGGGGAGACGCGAGCCAAAGCTGCGCGCATCTGGAC 2000
775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
794 : : : : :
2001 AGCAAGTACTTCAACCGGCGCATCATGATGCCATCTCTGGTCAACACCGTCAGCATGGC 2060
795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
814 : : : : :
2061 ATCGAGCACCGAGCAGCGGAGGAGGAGTCAACCAATCTCTGGAGATCTGCAATGTGGTC 2120
815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGly 834
834 : : : : :
2121 TTCACAGCATGTTCCTCGGAGATCATCTCTGAAGCTGGCTGCATTTGGGCTCTTCAC 2180
835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGlu 854
854 : : : : :
2181 TACTGGTAAACCCCTACACATCTTCGACAGCATCATTTGTCATCATCAGCATCTGGAG 2240
855 IleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874

Db 2241 ATCTGGGGCAGCGGACGGTGGGCTGTCGGTCTCGGACCTTCGGGCTCTGGCGTG 2300
Qy LeuLysLeuValAlaArgPheLeuProAlaLeuGlnArgGlnLeuValLeuMetLysThr 894
Db CTGAACTGGTGGCTTCATGCTGCCCTGGCGGCCAGCTCGTGGTCTCATGAAGACC 2360
Qy MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db ATGGACAACGGTGGCCACTTCGTGATGCTGTCTATGCTTCATCTTCAGCATC 2420
Qy LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db CTGGGATGATATTTTGGCTGCAAGTTACGCTCCGACGACACTGGAGACACGGTG 2480
Qy ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db CCCGACAGGAAGAACTTCGACTCCCTGCTGGGCGCATCGTCACTGTTCAGATCCTC 2540
Qy ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 973
Db ACCGAGGAGGACTGGAAAGCTGCTTCTACAAATGGCATGGGCTCCACTTCTCCCTGGGCC 2600
Qy AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db TCCCTCTACTTGTGCGCCTCATGACCTTCGGCAACTATGTGCTCTTCAACTGCTGGTG 2660
Qy AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
Db GCCATCTCTGGTGGAGGGTTCCAGCGGAGGGTGACGCGCAATCGCTCCTACTCGGACGAG 2720
Qy AspPhePheSerProSerVal-----AspGlyAsp 1023
Db GACCAAGACTATCCAAATAGAGAGTTTGATAGCTCCAGGAAGGCTCGACAGCAGC 2780
Qy GlyAspArgLysLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043
Db GGAGATCCCAAG-----CTCTGCCCAATCCCATGACCCCCCAATGGGCACTTGGACCCC 2834
Qy SerLeuLeuProProLeuIleHisThr-----AlaAlaThrProMetSer 1059
Db AGTCTC-----CCACTGGGGGGACCTAGGTCTCTGGGGCTCGCGGACCTGCC--- 2885
Qy HisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db ---CCCCGACTCTACTGAGCGGACCCCATGCTGGTGGCCCTGGGCTCCGAAAGAGC 2942
Qy SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db AGTGTATGCTCTA-----GGGAGGATGAGCTATGACCGCGCTCCCTGTGCCAGC 2993
Qy AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db TCCCGAGCTCTACTAGCGGCATGGGCGCGCAGCGGCGCTGGGCGAGCGCTCGCTCC 3053
Qy SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
Db AGCTGGAAC-----AGCTCAAGCACAAGCCCGCTGGCGGAGGAT 3095
Qy ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158
Db GAGTCCCTGCTCTCTCGGAGCGGCGGCGCGCGCGCTGCTGGAGTTCGCGCGGAC 3155
Qy Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db GAGGGGCG 3215
Qy ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db CCCCATCTGGCGCACCGCCACCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3275
Qy SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201

Db 3276 TCGGTGACCTGGCGGACGTGGTCCCGCGGTGGCGCGCCACCCCGCGCGCTGGAGG 3335
Qy SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db CGCGCAGCG 3389
Qy AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu 1238
Db GCCAAAACAGCTCTTCAACAAGATGGCGGGGATCGCGGGGAGGATGAGGAGAA 3449
Qy GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys 1258
Db ATCGACTACACCTGCTGCTCCCGCTCGCAAGATGATCGACGTCTATAAGCCGACTGG 3509
Qy CysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeu 1278
Db TCGAGGTCCGCGAAGACTGGTCTGTACTCTTCTCCCGAGAACAGGTTCGCGGTC 3569
Qy LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIlePhe 1298
Db CTGTGTGAGACCATATTGCCCAAACTCTTCGACTACGTCTGCTGGCCTTCATCTTT 3629
Qy LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
Db CTCAACTGCATCACCATCGCCTGGAGCGGCTCAGATCGAGCGCGGAGCAGCAACGC 3689
Qy IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal 1338
Db ATCTTCTCAGGTGTCCACTATCTTACGGCCATCTTCGACTACGTCTGCTGGCGAGATGACATG 3749
Qy LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1358
Db AAGTAGTCTCGCTGGGCTGTACTTCGGCGAGCAGCGGTACTACGCGAGCTGGAAAC 3809
Qy ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1378
Db GTGTGGATGCTTCTGTCTGTGTCTATCATCGACATCGTGGTGTCTCTGGCGCTCA 3869
Qy AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398
Db GCGGGGAGCCAGATCTTGGGGTCTCTCGAGTCTTGGGCTCTCGCGCACCTACGC 3929
Qy ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1418
Db CCCCTGCGTGTATCAGCGCGCGCGCGCTGAAGCTGGTGGTGGAGACACTCATCTCC 3989
Qy SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly 1438
Db TCCCTCAAGCCCATCGGCAACATGCTGTCTGTGTCTCTTCTCATCATCTTTGGC 4049
Qy IleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArg 1458
Db ATCTGGAGTGCAGCTCTTCAAGGGCAAGTTTACCACCTGTCTGGGCTGGACACCGC 4109
Qy AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr 1478
Db AACATCAACCAACCGCTCGACTGTCATGCCGCCAACTACCGCTGGTCCATCACAATAC 4169
Qy AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 1498
Db AACTTCGACAACCTGGCGGAGCTGTGATGTCCTCTTGTCTGGCATCAAGAGATGGT 4229
Qy TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet 1518
Db TGGGTGAACATCATGTACATGGACTGGATGCTGTGTGTGGACGACGCTGTGACC 4289
Qy AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db AACCAACACCCCTGGATGCTGTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4349
Qy ValLeuAsnMetPheValGlyValValGlnAsnPheHisLysCysArgGlnHisGln 1558
Db GTGCTCAACATGTTTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4409


```
Db 6218 CGGCTGTCCTCCCGCGCTGCGCGCTGAGCCTGCGCGCGCGGCGCTTTCAGCCT 6277
Qy 2258 LeuAspSerThrAlaAspSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 CGGGGGCTGGGGGCGATCAGCGCAGCAGCGGGGGCTCCACCGCGGGGCTG 6337

RESULT 9
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGiven, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3

Alignment Scores:
Pred. No.: 3,49e-314 Length: 6855
Scores: 5420.00 Matches: 1228
Percent Similarity: 62.0% Conservative: 235
Best Local Similarity: 52.0% Mismatches: 500
Query Match: 45.1% Indels: 402
DB: 3 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-404-650-3 (1-6855)
Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCTCCTCATCTGCGAGCAGCCGCGCTGAGCCAGGAGTCCACCACGGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgProArgSer 45
Db 267 CCGGACCCCG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCGCAGCGCTGGAGGAGCTCTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValValPheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTTATTGCTTCTCTGCTGCGACAGACACCCAGCCCGCGGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValileLeuLeu 125
Db 405 TGCATCAAGATGCTGCAACCCGTTTGAATGTGTGTCAGCATCTGGTATCTCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTCGGTGACACTTGGCATGTACAGCGCTGCGACGACATGGACTGCTGTCCAGCCG 524
Qy 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TCACAGATCCTCAGGTCTTTGATGACTTCATCTTTATCTCTTTGCCATGGAGATGGTG 584
Qy 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn 185
```

```
Db 585 CTCAAGATGTGGCCCTGGGGATTTTGGCAAGAAGTGTCTACCTCGGGGACACATGGAAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCTGGATTTCTTTCATCGTCATGGCAGGATGTCGAGTACTCCCTCGGACCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTGAGCATCCGACCGCTGGCGTCTCTGAGGCCCTCAAAGCCATCAACCGC 764
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTAGTATCGGATCTGCTGAACCTGCTCTCGACACACATCGCCCATCTGGGAAT 824
Qy 246 ValLeuLeuLeuCysPhePheValPhePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCTGTGCTGCTCTCTTTGCTCTTTCATCTTTGGCATCATAGGTGTGCAGCTCTGG 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGCGCTGTGCTGCTAACCCTGCTTCTGGAGGAGAACTTCACCATACAAGGGATGTG 944
Qy 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGGCCCATACTACAGCGGAGGAGATGATGAGATGCGCTTTCATCTGCTCCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGGCGACAATGGGTAATGGGCTGGCATGCCCGCCCGCTCAAGAGGACAG----- 1058
Qy 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCGTGAGTGTCTGCTGTCCAAGGACAGCTCTACGACTTTGGGGCGGGCGCCAG 1115
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAAACCGTTACTACAAATGTGTGGCGACG 1175
Qy 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGCAACCCCGCCAGGGTGCCATCAACTTTGACAACTCGGTATGCTTGGATT 1235
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCAGGTGATCACTCTGGAAGCTGGGTGGAGATCATGTACTACGTGATGAT 1295
Qy 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1296 GCTCACTCTCTTCAACTTCACTTCACTCTGCTTATCTGCTTATCATAGTGGGTCTCTTC 1355
Qy 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGCTGTGTATGCGACCCAGCTTCTCGGAGACCAACGACGGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGCTGTATGTGGAGCAGCGCGCTACCTGTCC---TCCAGCACGGTGGCCAGC 1472
Qy 458 PheSerGluProGlySerCysTyrGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TACGCCAGCGCTGGCGACTGTCTAGGAGAGATCTTCCAGTATGTCTGCACATCTCTGCGC 1532
Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCCG-----CGCGCCCTGGGCGCTCTACCGCCCTGGCAG 1574
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
Qy 518 HisArgArgLeuSerValHisHisHisHisHisHisHisHisHisHisHisTyr 537
```

Db 1578 ----CGGCCCGCAGGCCCTG----- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 ----CGGCCCGCAG----- 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577
Db 1602 ----GCCCCGGCCCCCGCAACCTGGGGCC----- 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 ----CACGCCAAG-----GAGCCC 1643
Qy 598 ValArgCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACCTACGAGTGTGCCCGCAACATAGCCCCCTGGATGG----- 1685
Qy 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Db 1686 ----ACGCCCCACACC----- 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ----CTGGTGCGAG-----CCCATCCCGCCACGCTGGCTTCC----- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys-- 676
Db 1731 ----GATCCCGCCAGCTGCCCTTGTGCGAG 1757
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGACGGCGCGCGCCCTCGGGCTGGGCGAGCACCGACTCGGGCCAGGAGGCTCG 1817
Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCGCTGGTGGCGAGCAGAGCGC----- 1853
Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 ----GATGGGACGGGGC-----CGGAGCAGCGAGGAGCGAGCCTCTCAGAA 1898
Qy 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGAAGGAGGAGGAGGAGGAGCAG-----CGGATGGGGCG 1940
Qy 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCTGGCTGTGCGGGGATGTGTGGCGGAGACGCGAGCCCAAGCTGCGCGCATCGTGGAC 2000
Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGCATCATGATGGCCATCTGTCTCAACACCGTCAGATGGGC 2060
Qy 795 IleGluTyrHisGluGlnProGluGluThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCAGCACACGAGCAGCGGAGAGCTGACCAACATCTCGGAGATCTGCAATGTGGTC 2120
Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPheGly 834
Db 2121 TTCACGAGCATGTTTGGCTGGAGATGATCTGAAGCTGGCTGCAATTTGGGCTCTTCGAC 2180
Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGlu 854
Db 2181 TACTTGGTAACCTTACAACATCTTTCAGACGATCATTTGTCATCATCAGCATCTGGAG 2240
Qy 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCTGGGGCAGCGGAGCGGTGGCTGTCTGGTGTGGGACTTCTCGGCTGCTCGCGGTG 2300
Qy 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAACCTGGTGTGCTTTCATGCTGCCCTGCGGCGCCAGCTCGTGGTGTCTCATGAAGACC 2360

Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db 2361 ATGGAACAAGTGGCCACCTTTCATGCTCATGCTCATGCTTTCATCTTTCAGCATC 2420
Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db 2421 CTTGGGATGATATTTTGGCTGCAAGTTTCAGCTCCGACGAGACACTGGAGACACGGT 2480
Qy 934 ProAspArgLysAsnPheAspSerLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCTGCTACTGTTCAGATCTCTC 2540
Qy 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCCAGGAGGACTGGAACGCTTCTCTACAATGGCATGGCTCCACTTCTCCCTGGGCC 2600
Qy 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2601 TCCCTCTACTTTTTCGCCCTCATGACTTCGGAACCTATGTGCTTTCACACCTGCTGGT 2660
Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTGTGTGAGGGCTTCCAGGCGGAGGGTACGCCAATCGCTCTACTCGGACGAG 2720
Qy 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGAGCTCATCCAACATAGAAGAGTTTGATAAGCTCCAGGAAGGCGCTGGACAGCAGC 2780
Qy 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043
Db 2781 GAGATCCCAAG-----CTCTGCCCAATCCCCATGACCCCCCAATGGGCGACCTGGACCCC 2834
Qy 1044 SerLeuLeuProProLeuIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGTGGGACCTAGGTCTCTCTGGGCTCGGGACCTGCC--- 2885
Qy 1060 HisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ---CCCCGACTCTCACTGCGAGCGGACCCCATGCTGGTGGCCCTCGGAGAGCAGC 2942
Qy 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCTATGTCTCTA-----GGAGGATGAGCTATACACGAGCTCCCTGTCGAGC 2993
Qy 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCGAGAGCTCTTACTACGGGCCATGGGGCGGAGCGCGGCGCTGGGCGACCGCTCGCTCC 3053
Qy 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
Db 3054 AGCTGGAAC-----AGCCTCAAGCACAAGCGCGCTCGCGGAGGAT 3095
Qy 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGTCTCTCGGAGCGCGGCGGCGGCGGCTGCGAGGTTCGCGGAGC 3155
Qy 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGCGCGCGGGCGGCGGCGGCGGCGGCGGCTGCGAGGTTCGCGGAGC 3215
Qy 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCATCTGCGCGCACCCGCGCACACCGCGGAGCGTGTCTCTCGACACAGGAGC 3275
Qy 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGAGCTGCGCGAGCTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3335
Qy 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 GCGGAGCGCGCGCGCGCGCGGCGATGAGACTGCAATGGCAGGATGCCCAGC-----ATC 3389

Db 5525 CTTGGAGGG---GGAGCTGACCAT-----CATCGACAACTGTGGGCTC 5566
Qy 1938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957
Db 5567 CATCTTCCACCACTACTCTCTGGCTGGCGCTGCAAGAGTGTC----- 5611
Qy 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5612 CCACGACAA-----GCAAGAGGTGCAGCTGGTGAGAC 5644
Qy 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db 5645 GGAGCGCTTCTCCCTGAACCTCAGACAGCTCTGCTCATCTCTGGTGGACACCTGAG 5704
Qy 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db 5705 TCTCGAGGA-----CCCCACAGC 5722
Qy 2018 AlaProThrTrpGlyAlaIleProLysLeuPro----- 2029
Db 5723 CTGCCCACTGG-----CCGCAAGACAGCAAGGTGAGCTGGACCCACCTGAGCC 5773
Qy 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db 5774 CATCGGTGTGGAGACCTGGCGCAATGCTTCTCCCTTGT-CTCTACCGCCGCTTCGC 5832
Qy 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSer 2064
Db 5833 CGGATCCAGAGAACTTCTGT--GTGATGGAGGAGATCCCAT-----TCA 5877
Qy 2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySer 2084
Db 5878 ACCGTGCTCGGTCTGCTGTAACATGACA----- 5907
Qy 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
Db 5908 -----GCAGTCAAGCACCCCAAGTCCCT 5931
Qy 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSer 2124
Db 5932 TCTTCCC-----CGGATGCTCCAGCC----- 5952
Qy 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
Db 5953 -----CTCTCTGCTCCCATGCCAGCCGAGTTCTTCCACC 5985
Qy 2145 GluProLeuPhePro-----ArgAspLeuLysCysTyrSerValGluThrGlnSer 2162
Db 5986 CTGCAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGGCAGCTGGAAACCTCCCCA 6045
Qy 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSer 2182
Db 6046 AGATTGGCTGTG-CAGGCTCTGGGCATCT-----CTGCGGTCAACAGGTTCAAC 6095
Qy 2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer 2198
Db 6096 TGTACCTCTCTCCGGCAGGCCACCGGAGCAGACAGCTGCTGGACCGCCAGCCAGCAG- 6154
Qy 2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2218
Db 6155 CTCCGGGGCAGCTGCAGACACCGCTCGAGGACAGCTGACCTCTGAGCGACAGCCCGCG 6214
Qy 2219 SerIleSerIleAspProGluSerGlnGlySerArgProProCysSer-----Pro 2236
Db 6215 GCG-----TGCCCTGGGCGCCGCCGCTGCTCCAGGACCCCG 6253
Qy 2237 GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256
Db 6254 GGCCGGCTGTGCCCCCGCGCTGCGCGGCTGAGCTGCGCGCGCGGGGCTCTTTCAG 6313
Qy 2257 ProLeuAspSerThrAlaAspProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db 6314 CTTGGGGGGTGGCGGCGCATCATCGCAGCCAGCAGCGGGGGCTCCACAGCCCGGG 6373

Qy 2277 Leu 2277
Db 6374 CTG 6376

RESULT 10

US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3

Alignment Scores:
Pred. No.: 3,49e-314 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 62.0% Conservative: 235
Best Local Similarity: 52.0% Mismatches: 500
Query Match: 45.1% Indels: 402
DB: 3 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-935-541-3 (1-6855)

Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCCCGCTCTCTATCTGCAGCAGCCCGCTGAGCAGGAGTCCACCGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCTGAGGAGGCTCTGGATGGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCTTCTTCTGCTCGCAGACAGCACCAGCCCGGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCGCTGTTTGAATGTGTGACGATGCTGGTATCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACCGCGTGGCGACACATGGAGTCTGCTGCTCCAGCCG 524
Qy 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValIleGluMetVal 165
Db 525 TGAAGATCTCGAGGCTTTGATGACTTCTTATCTTTTTCATCTTTTTCATGAGATGGTG 584
Qy 166 ValLysMetValAlaLeuGlyIlePhePheGlyLysCysTyrLeuGlyAspThrTrpAsn 185

Db 4470 CGG-----AAGCCAGCGCGCTGCCTACTATGCCACCTATTGT 4508
Qy 1599 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db 4509 CACACCCGGCTGCTCATCTCCACTCCATGTCACACGACCACTACCTGGACATCTTCATCACC 4568
Qy 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
Db 4569 TTCATCATCTGCCTCAAGCTGTCACCATGTCCCTGGAGCAGCTCAATACAGCCACAGTCC 4628
Qy 1639 LeuAspGluAlaLeuLeuIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCCACCATGTCTTTGTCTGGAGGCT 4688
Qy 1659 ValPheLysLeuValAlaPheAlaPheArgPheGlnAspArgTyrAsnGlnLeu 1678
Db 4689 GTGCTGAAGCTGGTGGCATTTGGTCTGAGGGCTTCTTCAAGGACCGATGGAACAGCTG 4748
Qy 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db 4749 GACCTGGCCATTGCTACTGTACGTATGGGCATCACCTGGAGGAGATCGAGATCAAT 4808
Qy 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db 4809 CGCGCCCTGCCCATCAATCCACCATCATCCGCATCATGAGGTTCTCGCATTTGCCGA 4868
Qy 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db 4869 GTGCTGAAGCTGTTGAAGATGCCACAGAAATCGGGCCCTGCTGGACACGGTGGTCAA 4928
Qy 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758
Db 4929 GCTTTGCCCCAGGTGGGAACCTGGGCTCTCTTTCATGCTGCTCTTTTCATCTATGCT 4988
Qy 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1778
Db 4989 GCTCTCGGGTGGAGCTCTTTGGGAAGCTGTTGTCACACGACGAGAACCCGTCGGAGGGC 5048
Qy 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
Db 5049 ATGACCGGCATGCCACCTTCAGAACTTCGGCATGGCTTCCTCACACTCTTCACAGTCTC 5108
Qy 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln 1817
Db 5109 TCCACGGGTGAACTGGAACGGGATCATGAAGACACGCTCGGGAGCTGCACCCAGAC 5168
Qy 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
Db 5169 GAGCGCAGCTGCCTGAGCAGCTGCAGTTTGTGTCGCCGCTGTACTTCTGAGCTTCGTG 5228
Qy 1836 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1855
Db 5229 CTCACCGCGCAGTTCGTGCTCATCAACGTGGTGGTGGTGTGCTCATGAACACCTGGAC 5288
Qy 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMet 1875
Db 5289 GACACCAACAGAGCGCAGAGACGCCGAGATGGATGCGAGCTCGAGCTGGAGATG 5348
Qy 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro--- 1893
Db 5349 GCCCATGGCTGGGCCCTGGCCGAGGCTGCTACCGGCTCCCGGGCGCC---CCTGGC 5405
Qy 1894 -----GlyValGluGlyValAsnSerThrAsp----- 1902
Db 5406 CGAGGCGGGAGGGCGGGCGGGCGGACACCGAGGGCGGCTTGTGCGGGCGCTGC 5465
Qy 1903 ---SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla 1917
Db 5466 TACTCGCTGC---CAGAGGAACCTGTGGCTGGACAGCTCTTTTAATCATCAAGACTC 5524
Qy 1918 AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluValProVal 1937

Db 5525 CTTGAGGG---GGAGCTGACCAT-----CATCGACAACCTGTGCGGCTC 5566
Qy 1938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957
Db 5567 CATCTTCCACACACTACTCTCGCTCGCGCTGCAAGAGTGTCA----- 5611
Qy 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5612 CCACAGCAA-----GCAAGAGGTGAGCTGGTGGTGAGAC 5644
Qy 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db 5645 GGAGGCTTCTCCCTGAACCTCAGACAGGTCTCTCCATCTCTGGTGGTGGACGACCTGAG 5704
Qy 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db 5705 TCTCAGGA-----CCCCACAGC 5722
Qy 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029
Db 5723 CTGCCCACTGG-----CCGAAAGACAGCAAGGTGAGCTGGACCCACCTGAGCC 5773
Qy 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db 5774 CATCGGTGTGGAGACCTGGCGGAATGCTTCTCCCTTGT---CCTCTACGGCCGTCTCGC 5832
Qy 2045 AlaIleArgThrAspSerLeuAspValGlnGlySerArgGluAspLeuLeuSer 2064
Db 5833 CGGATCCAGAGAACTTCTGT---GTGAGATGGAGAGATCCCAT-----TCA 5877
Qy 2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSer 2084
Db 5878 ACCGTGTCGGTCTCGCTGAAACATGACA----- 5907
Qy 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
Db 5908 -----GCAGTCAAGACACCCCAAGTCCCT 5931
Qy 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSer 2124
Db 5932 TCTCCC-----CGGATGCTCTCCAGCC----- 5952
Qy 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
Db 5953 -----CTCTCTCTCCCATCGCAGCCGAGTCTTCCACC 5985
Qy 2145 GluProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSer 2162
Db 5986 CTGCAGTGTCTGCGCAGCCAGAAAGCCAGAAAAGGCGACTGGCAGCTGGAAACCTCCCCA 6045
Qy 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2182
Db 6046 AGATTGCGCTG---CAGGGCTCTCTGGGCATCT-----CTGCGGTACCAAGGGTCAAC 6095
Qy 2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer 2198
Db 6096 TGTACCTCTCTCCGCGAGGCCACCGGAGCCACACGCTCGCTGGACCGCCAGCCAGCAG- 6154
Qy 2199 LeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2218
Db 6155 CTCCGCGGCGAGCTGCAGACACCGCTCGAGGACAGCCTGACCTCGAGCAGACGCCCCG 6214
Qy 2219 SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro 2236
Db 6215 GCG-----TGCCCTGGGCGCGCCGCGGCTGTCTCCAGGACCCCG 6253
Qy 2237 GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256
Db 6254 GGCGGCGCTGCTCCCGCGCTCGCGCGGCTGAGCTGGCGCGCGCGGCGCTCTTCAG 6313
Qy 2257 ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db 6314 CTTGCGGGGCTGCGGGCGCATCAGCCAGCAGCGGGGCTCCACAGCCCGG 6373

```

QY 2277 Leu 2277
Db 6374 CTG 6376

RESULT 11
US-10-425-800-3
; Sequence 3, Application US/10425800
; Patent No. 6893842
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND US$S
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-10-425-800-3

Alignment Scores:
Pred. No.: 3,49e-314 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 62.0% Conservatve: 235
Best Local Similarity: 52.0% Mismatches: 500
Query Match: 45.1% Indels: 402
DB: 3 Gaps: 63

US-09-611-257A-24 (1-2287) x US-10-425-800-3 (1-6855)
QY 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCCCTCTCATCTGCAGCAGCCGCCAGCCCTGAGCCAGGAGTCAACCGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluAlaProArgSer 45
Db 267 CCCGACCCCG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCCAGCCCTGGAGGAGCCTCTGGATGGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCCCTCTCTCGCTGGCAGACACACAGCCCGCCGGAACCTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCGTTTGAATGTGTGACATGCTGGTATCTCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACATTGGCATGTACAGCCGTGCGACGACATGGACTGCTGTCGAGCCGC 524
QY 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValGluMetVal 165
Db 525 TGCAGATCCCTGCAGGTCTTTGATGACTTCATCTTTATCTCTTGGCCATGGATGGTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn 185

585 CTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAGTGCTACCTCGGGGACACATGGAAC 644
186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
645 CGCCTGGATTCTTCATCGTCGAGGAGGATGGTGGAGTACTCCCTCGGACCTTCAGAAC 704
206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
705 ATCAACCTGTGAGCCATCCGACCGTCTGTAGGCCCCCTCAAAGCCATCAACCGC 764
226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
765 GTGCCCATGATGGGATCTCTGTGAACCTCTCTGGACACACTGCCCATCTGCTGGGAAT 824
246 ValLeuLeuLeuCysPhePheValPhePheIleValGlyValGlyValGlnLeuTrp 265
825 GTCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 884
266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
885 GCGGGCTGTGCTGAACCGCTGCTCTCTGAGGAGAACTTCACCATACAAGGGGATGTG 944
286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
945 GCCTTGGCCCCATACCTACCGAGGAGGAGATGATGAGATGCCCTTCATCTGCTCCTG 1004
306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
1005 TCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
1059 ---GGCGTCTGCTGCTCTGCTCAAGGACGAGCTCTACGACTTTGGGGGGGGCGCCAG 1115
340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
1116 GACCTCAATGCCAGCGCCCTCTGTGTCACTGGAAACCGTTACTACAATGTGTGGCGCAG 1175
358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
1176 GGAGCGCCAAACCCCAAGGTTGCCATCACTTTGACACATCGGTATGCTTGGATT 1235
378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
1236 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTATGGAT 1295
398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
1296 GCTCACTCTTACAACTTCACTTCTATCTGCTTATCATAGTGGGCTCTCTTCTTC 1355
418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
1356 ATGATCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1415
438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
1416 CACCGGTGATGCTGGAGAGCGGCGCTACCTGCTCC---TCCAGCACGGTGGCCAGC 1472
458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
1473 TACGCCGAGCGTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCTGC 1532
478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
1533 AAGCCCAAGCGC-----CGGCCCTGGGCTCTACCGAGCCCTGGCAG 1574
498 SerSerProValAlaArgSerGlyGlnProGlnProSerGlySerCysThrArgSer 517
1575 AGC----- 1577
518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537
||||| :|:::

```

Db	1578	----	CGGCGCCAGGCCCTCG	-----	1599
Qy	538	HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp	 	557	
Db	1593	-----	GGCCCGGAG	-----	1601
Qy	558	AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly	 :: ::	577	
Db	1602	-----	GCCCCGGCCCCGCCAAACCTGGGCC	-----	1628
Qy	578	ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro	 	597	
Db	1629	-----	CACGCCAAG	-----	1643
Qy	598	ValArgCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGly	 :: ::	617	
Db	1644	CGGCACCTACGAGCTGTCGCCACATAGCCCCCTGGATCG	 :: ::	1685	
Qy	618	SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys	 	637	
Db	1686	-----	ACGCCCCACACC	-----	1697
Qy	638	AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro	 :: ::	657	
Db	1698	--CTGGTGAC--	-----	1730	
Qy	658	ProGlyProPheSerSerMetHisLysLeuGluThrGlnSerThrGlyAlaCys	:: :: ::	676	
Db	1731	-----	GATCCCCGAGCTGCCCTTCTGCCAG	-----	1757
Qy	677	HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro	:: :: ::	696	
Db	1758	CATGAGACGCCCGCGCCCTCGGCCCTGGCGACACCGACTCGGCCAGGAGGCTCG	:: :: ::	1817	
Qy	697	AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal	:: :: ::	716	
Db	1818	GGCTCC	-----	1853	
Qy	717	MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp	:: :: ::	736	
Db	1854	-----	GATGGGACGGGGCC	-----	1898
Qy	737	LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer	:: :: ::	756	
Db	1899	CTGGGGAAGGAGGAGGAGGAGGACGAC	-----	1940	
Qy	757	SerValLeuAla	-----	774	
Db	1941	GTCTGGCTGTGCGGGATGTGTGCGGGAGACGCGAGCCAAAGTCGCGCATCTGGAC	:: :: ::	2000	
Qy	775	SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly	:: :: ::	794	
Db	2001	AGCAAGTACTTCAACCGGGGATCATGATGCCATCTGTGTCAACCCGTCAGCATGGGC	:: :: ::	2060	
Qy	795	IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal	:: :: ::	814	
Db	2061	ATCAGCACCAACGAGCCGCGAGGAGCTGACCAACATCTCTGGAGATCTGCAATGTGTC	:: :: ::	2120	
Qy	815	PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGly	:: :: ::	834	
Db	2121	TTACACGACATGTTTGCCCTGGAGATGATCTCGAAGCTGGCTGCATTGGGCTCTTCGAC	:: :: ::	2180	
Qy	835	TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGlu	:: :: ::	854	
Db	2181	TACCTGGGTAAACCCCTCAACATCTTCGACAGCATCATGTCATCATCATCTGGGAG	:: :: ::	2240	
Qy	855	IleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal	:: :: ::	874	
Db	2241	ATCTGGGGCAGCGGAGTGGGCTGTCTGGTGCTCGGACCTCTCCGGCTGCTCGCGGTG	:: :: ::	2300	
Qy	875	LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr	:: :: ::	894	
Db	2301	CTGAAACTGGTGCGCTTCATCGCTCCCTCGCGCGCCAGCTCGTGGTGTCTCATGAAGACC	:: :: ::	2360	

Qy	895	MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle	914
Db	2361	ATGGACAACGTGGCCACCTTCTGTCATCTGCTCATGCTCTTCACTTTCATCTTCAGCATC	2420
Qy	915	LeuGlyMetHisIleuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeu	933
Db	2421	CTTGGGATGCATATTTTGGCTGCAAGTTTCAGCTCCGCACGGACACTGGAGACCGGTG	2480
Qy	934	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	953
Db	2481	CCGCACAGGAAGAACTTCGACTCCCTGCTGTGGCCATCGTCACTGTGTTCAGATCTCTC	2540
Qy	954	ThrClnIleAspTrpAsnLysValLeuTyrrAsnGlyMetAlaSerThrSerSerTrpAla	973
Db	2541	ACCAGAGAGACTGGAAAGCTGTTCTTCAATATGGCATGGCTCCCACTTCTCCCTGGGCC	2600
Qy	974	AlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuVal	993
Db	2601	TCCTCTACTTTGTCGCCCTCATGACTTCGCGCAACTATGTGCTCTTCAACCTGTGGTG	2660
Qy	994	AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro	1013
Db	2661	GCCATCCTGTGTGAGGCGCTTCAGAGCGGAGGGTGACGCCAATCGCTCTACTCGGACGAG	2720
Qy	1014	AspPhePheSerProSerVal-----AspGlyAsp	1023
Db	2721	GACCAGAGCTATCCAAACATAGAAAGATTGTATAGCTCCAGGAAGCCCTGGACACGACG	2780
Qy	1024	GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys	1043
Db	2781	GGAGATCCCAAG-----CTCTGCCCAATCCCATGACCCCAATGGGACCTCGGACCCC	2834
Qy	1044	SerLeuLeuProProIleuIleHisThr-----AlaAlaThrProMetSer	1059
Db	2835	AGTCTC-----CCACTGGGTGGCCACTAGTCTCTGGGGCTCGGACCTGCC-----	2885
Qy	1060	HisProLysSerSerThrGlyValGlyAlaLeuGlySerGlySerArgArgThr	1079
Db	2886	---CCCCGACTCTCACTGCACCGGACCCCATCTGCTGGTGGCCCTCCGAAAGAGC	2942
Qy	1080	SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer	1099
Db	2943	AGTGTCATGTCCTA-----GGAGGATGAGCTATGACGAGCGCTCCCTGTCCAGC	2993
Qy	1100	AlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer	1119
Db	2994	TCCCGAGCTCTCTACTACGGGCCCATGGGCGCGAGCGCGCTGGCCAGCCGCTGCTCC	3053
Qy	1120	SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg	1139
Db	3054	AGCTGGGAAC-----AGCCTCAAGCAACAAGCGCGCTCGGCGGAGCAT	3095
Qy	1140	ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerGlu	1158
Db	3096	GAGTCCCTGCTCTCTCGCGAGCGCGCGCGCGCGCGCTGTCGCGAGGTGTCGCGGAC	3155
Qy	1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3156	GAGGGCGCGCGGGCGCGCACCCCTGCACACCCACACCGCCCATCATCAGGG	3215
Qy	1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181
Db	3216	CCCCATCTGGCGCACCGCCACCGCCACCGCGGACGCTGCTCTCGACAACAGGAC	3275
Qy	1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201
Db	3276	TCGCTGACCTGGCGAGCTGGTGCCCGCGGTGGCGGCCACCCCGGGCGCGCTGGAGG	3335
Qy	1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
Db	3336	CGCGAGGCGCGGCCCGCGGATGAGACTGCAATGGCAGTATGCCAG-----ATC	3389

Qy	1220	AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
Db	3390	GCCAAAGACGCTCTTCCACCAAGATGGGCGACCGGGGATATGAGGAGAA	3449
Qy	1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
Db	3450	ATCGACTACACCTGTGCTCCGGTCCGCAAGATGATCAGCTCTATAAGCCGACTGG	3509
Qy	1259	CysArgGluArgAspSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeu	1278
Db	3510	TGCGAGGTCCGCAAGACTGGTGTGTACTCTTCTCCCGAGAACAGTTCGGGTC	3569
Qy	1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIlePhe	1298
Db	3570	CTGTGTGAGACCAATTATTGCCCCAAACTCTTCGACTACGTCGTCTGGGCTTCACTTT	3629
Qy	1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
Db	3630	CTCAACTGCAATCACCATCGCCCTGGAGCGCCTCAGATCAGGCGCGCAGCACCGAACGC	3689
Qy	1319	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
Db	3690	ATCTTCTCACGGTGTCAACTACATCTTCAGGCCATCTTCGTGGCGAGATGACATTG	3749
Qy	1339	LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn	1358
Db	3750	AAGTAGTCTCGCTGGGCCGTGTACTTCGGCGAGCAGCGGTACTACGCAGCAGCTGGAAC	3809
Qy	1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
Db	3810	GTGCTGAGTGGCTTCTTGTCTTCGTGTCTCATCATGACATCGTGGTGTCCCTGGGCTCA	3869
Qy	1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
Db	3870	GCGGGGAGCCAAAGATCTTGGGGTGCTCGAGTCTTGGGGTCTTCGCGCACCTACGC	3929
Qy	1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
Db	3930	CCCTGCGTGTATCAGCCGGCGCGGGCCTGAAGCTGTGTGGTGAGACACTCATCTCC	3989
Qy	1419	SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly	1438
Db	3990	TCCCTCAAGGCCCATCGCAACATCGTGCTCATCTGCTGTGCTTCTTTCATCATCTTTGGC	4049
Qy	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
Db	4050	ATCCTGGAGTGAGCTCTTCAAGGGCAAGTTCACCACCTGTCTGGGCGTGGACCCCGC	4109
Qy	1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
Db	4110	AACATCACCAACCGCTCGGACTGCATGCGCGCAACTACCGCTGGGTCCATCACAATAC	4169
Qy	1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
Db	4170	AAC TTCACAACTGGGCCAGGCTCTGATGTCCCTCTTGTCTCTGGCATCCAGAGATGGT	4229
Qy	1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIleMet	1518
Db	4230	TGGGTGAACATCATGTACAATGGACTGGATGCTGTGCTGGACCAAGCGCTGGACC	4289
Qy	1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
Db	4290	AACCAACCCCTGGATGCTGTACTTTCATCTCTCTCTGCTCATCGTCAGCTTCTTT	4349
Qy	1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln	1558
Db	4350	GTGCTCAACATGTTTGTGGGTGTCTGTGTGGAGAACTTCCACAAAGTGC CGGCAGCACAG	4409
Qy	1559	GluGluGluAlaArgArgArgGluGluLysArgLeuArgLeuGluLysLysArg	1578
Db	4410	GAGCTCAAGAGGACCGCGCGGTGAGAGAAAGCGGTGCGCGGCCCTGGAGAAAGACGC	4469
Qy	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598

	Db	4470	CGG----- ::: TGGCTGCCCTACTATGCACCACTATTGT	4508
	Qy	1599	ArgPheArgLeuValHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1618
	Db	4509	CACACC GGCTGCTCATCCACTCCATGTGCAGCACCACTACCTGGACATCTTCATCACC	4568
	Qy	1619	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1638
	Db	4569	TTCATCATCTGCCTCAACGTGGTGACCATGTCTCCCTGGAGCAGCTACAATCATCACCGCTCC	4628
	Qy	1639	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer	1658
	Db	4629	CTGGAGACACCCCTCAAGTACTCCAATAATGTTCACCACTGTCTTTGTGCTGGAGGCT	4688
	Qy	1659	ValPheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeu	1678
	Db	4689	GTGCTGAAGCTGGTGGCATTTGGTCTGAGCGCTCTTCAAGGACCGATGGAACCAAGCTG	4748
	Qy	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
	Db	4749	GACCTGGCCATTGTGCTACTGTCACTCAGTCATGGGCATCACCTCGGAGGAGATCGAGATCAAT	4808
	Qy	1699	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuAlaArgIleAlaArg	1718
	Db	4809	CGCGCCCTGCCCATCAATCCACCACCATCATCCGATCATGAGGTTCTGCGCATTTGCCCGA	4868
	Qy	1719	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln	1738
	Db	4869	GTGCTGAAGCTGTTGAAGATGGCCACAGGAATCGGGCCCTGCTGGACACGGTGTGCACAA	4928
	Qy	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1758
	Db	4929	GCITTTGCCCGAGGTGGCAACCTGGGGCTCTCTTCATGTGCTCTTCTTCTCATCTATGCT	4988
	Qy	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
	Db	4989	GCTCTCGGGGTGAGGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGCTGCGAGGGC	5048
	Qy	1779	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
	Db	5049	ATGAGCCGGATGCCACCTTCGAGAATCTCGGATGGCTTCTTCACACATCTTCCAGATC	5108
	Qy	1799	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln	1817
	Db	5109	TCCACGGGTGACAACTGGAAACGGATCATGAAGACACCGCTGCGGAGCTGCACCCACGAC	5168
	Qy	1818	GluSerThrCysTyrAsnThrVal----IleSerProIleTyrPheValSerPheVal	1835
	Db	5169	GAGCGCAGCTGCCTGAGCAGCCTGAGTTGTGTGCGCGCTGTACTTCGTGAGCTTCGCTG	5228
	Qy	1836	LeuThrAlaGlnPheValLeuAsnValIleAlaValLeuMetLysHisLeuGlu	1855
	Db	5229	CTACCCGGCAGTTCTGTCATCAACGTTGGTGTGTGCTGTCTCATGAAGACCTCGAC	5288
	Qy	1856	GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMet	1875
	Db	5289	GACAGCAACAGGAGGCGCAGGAGGACGCCAGATGGATGCCGAGCTCGAGCTGGAGATG	5348
	Qy	1876	---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro---	1893
	Db	5349	GCCCATGGCTGGGCCCTGGCCCGAGGCTGCCTACCCGGCTCCCCGGCGGCC---CCTGGC	5405
	Qy	1894	-----GlyValGluGlyValAsnSerThrAsp-----	1902
	Db	5406	CGAGGGCGGAGGGCGGGCGGGGGCGACACCGAGGGCGGCTGTGCCCGCGCTGC	5455
	Qy	1903	---SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla	1917
	Db	5466	TACTCGCTGC-CCAGAGAAACCTGTGGCTGGACAGCGCTCTTTAATCATCAAGGACTC	5524
	Qy	1918	AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluValProVal	1937

Db 5525 CTTGGAGGG---GGAGCTGACCAT-----CATCGACAACCTGTGCGGGTC 5566
Qy 1938 ProLeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957
Db 5567 CATCTTCACCACTACTCTCGCTGCGGCTGCAAGAAGTGTCA----- 5611
Qy 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5612 CCACGACNA-----GCAGAGGTGAGCTGGCTGAGAC 5644
Qy 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db 5645 GGAGGCTTCTCCCTGAACTCAGACAGTCTCGTCCATCTCTGGTGAGCACCTCAG 5704
Qy 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db 5705 TCTCGAGGA-----CCCCACAGC 5722
Qy 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029
Db 5723 CTGCCCACTGG-----CCGCAAGACAGCAAGGCTGAGCTGGACCCACCTGAGCC 5773
Qy 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db 5774 CATCGTGTGGAGACCTGGGCGAATGCTTCTCCCTTGT-CCTCTACGCGCTCTCGC 5832
Qy 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2064
Db 5833 CGGATCCAGAGAACTTCTGT---GTGAGATGGAGAGATCCCAT-----TCA 5877
Qy 2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSer 2084
Db 5878 ACCCTGTCGGTCTCGGTGAAACATGACA----- 5907
Qy 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
Db 5908 -----GCAGTCAAGCACCCCAAGTCCCT 5931
Qy 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSer 2124
Db 5932 TCTCCC-----CGATGCTCCAGCC----- 5952
Qy 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
Db 5953 -----CTCTCTCCCATCCAGCCGAGTCTTCCACC 5985
Qy 2145 GluProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSer 2162
Db 5986 CTGCAGTGTCTGCCAGCCAGAAAGCCAGAAAGGCGACTGGCACTGGAAACCTTCCCCA 6045
Qy 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2182
Db 6046 AGATTGCGCTG-CAGGGTCTCTGGGCATCT-----CTGCGGTCCACCAAGGTCAAC 6095
Qy 2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerSerSer 2198
Db 6096 TGTACCTCTCTCCGCGAGCCACCGGAGCGACACGCTGCTGGAGCGCCAGCCCGACGAG- 6154
Qy 2199 LeuGlyGlyGlnProLeuGlyClyProGlySerArgProLysLysLysLeuSerProPro 2218
Db 6155 CTCGCGGGGAGCTGCAACACCTCGAGGACAGCCTGACCTCGAGCGACGACGCCCGCG 6214
Qy 2219 SerIleSerIleAspProGluSerGlnGlySerArgProProCysSer-----Pro 2236
Db 6215 GCG-----TGCCCTGGGGCCCGCCGCGCTGCTCCAGNACCCCG 6253
Qy 2237 GlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256
Db 6254 GCGCGGCTGTCCCCCGCGCTCGCGCGCTGAGCTGCGCGCGCGGCGCTCTTCAG 6313
Qy 2257 ProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db 6314 CTTGCGGGGCTGGCGGCGCATCAGCGGAGCCACAGCGGGGCTCCACAGCCCGGG 6373

Qy 2277 Leu 2277
Db 6374 CTG 6376

RESULT 12

US-09-404-650-12
; Sequence 12, Application US/09404650
; Patent No. 6309558
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-BEG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12

Alignment Scores:
Pred. No.: 1,94e-313 Length: 6503
Score: 5407.00 Matches: 1234
Percent Similarity: 61.1% Conservative: 241
Best Local Similarity: 51.1% Mismatches: 502
Query Match: 45.0% Indels: 444
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-12 (1-6503)

Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 64 CCCCCGGCGCGCGCTGTCATCGCGCTGCCCTCGCGCGCGCGCA----- 114
Qy 23 SerAspPro-----ProGlyProArgLeuAlaArgGlyTrpThrArgArg 38
Db 115 GCTGATCCCGGAATCCAGGCGTGGCGCGCGGG-GCGCGGGTCTCTCCAGCGCGG 173
Qy 39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla----- 51
Db 174 CTTCCGGGACACGCGTCAACCCCGGCTCTGCGCGGGACGACCCCGCTCGGCCACG 233
Qy 52 -----SerArgSerSerThrTh 57
Db 234 TCCATGCCAAGGCTCCCTGCTCCACGCTGATGGCTGACAGCAACTTACCGCCCTCAT 293
Qy 57 rCysproGlyProGly-----AlaAlaGlyAla-GlySerThrG 70
Db 294 CTGCAGACGCCCCCGCCCTGAGCGGGGAATCACTGACGACCGCGGGCCCGGAGTCCCC 353
Qy 70 LuLysAspProGlySerAlaAspSerGluAlaGluGly-----LeuProTyrP 86
Db 354 CTCCATCCCTCCAGGCTGGAGGAGCATTTGGAAGGAACCAACCTGACGTCCCATC 413
Qy 86 roAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpC 106
Db 414 CAGACCTGGCTCTGTTGCTTCTTCTGCTGCGCCAGACCCAGCGCCACCGAACTGGT 473
Qy 106 ysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeuA 126
Db 474 GCATCAGATGGTTTGTAAACCGTGGTTCGAGTGTGTGAGCATGCTGGTTATTCTGCTGA 533
Qy 126 snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgC 146
Db 534 ACTGTGTGACCTGGGCATGTACCAGCCATGTGATGACATGAGTGCCTGTCGACCGGTT 593
Qy 146 ysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetValV 166

594 GCAAGATCCTGCAGGCTCTTCGATGACTTCATCTTCTTCATCTTCTTCGATGAGATGGTGC 653 Db
166 allYsMetValAlaLeuGlyLeuPheGlyLysLysCysTyrLeuGlyAspThrTrpAsnA 186 Qy
654 TTAAGATGGTGGCCCTGGGCAATTTTGGCAAGAAGTGTCTACCTCGGAGACACATGGAAACC 713 Db
186 rgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnV 206 Qy
714 GCCTGGATTCTTCATTGTTCATGCGAGGATGGTTGAGTACTCTCTGGACCTACAGAAACA 773 Db
206 alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgV 226 Qy
774 TCACCTGTGTCAGCAGCTCGCAGCTGTGGTGTCTTCGAGCGCTCTCAAGCCATCAACCGTG 833 Db
226 alProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnV 246 Qy
834 TACCAGCATGCGGATCTCTGGTGAACCTGTGCTGCTGCACACGCTGCCATGCTGGGGAACG 893 Db
246 alLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA 266 Qy
894 TGCTCCTGCTCTGTTCTTCTGCTCTTCTTCATCTTTCGGCATCATTTGGCGTGCAGCTCTGGG 953 Db
266 laGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValA 286 Qy
954 CAGGCTGTCTACGGAACCGCTGTCTTCTTGGGAAGAGAACTTCACCATACAAGGGGATGTG 1013 Db
286 spLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP 306 Qy
1014 CCCTGCCCCCTTATTACCAACAGAGGAGGATGACGAGATGCCCTTTATCTGTCTCCCTGA 1073 Db
306 roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyG 326 Qy
1074 CTGGGGACATGGCATCATGGCTGCCACGAGATCCCCCACTCAAGAGCAG----- 1126 Db
326 lyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSerS 340 Qy
1127 --GGCCGGAAATGCTGCTGTCCAAAGATGATGTATGACTTCGGGGCGGGCGCCAGG 1184 Db
340 erSerAsnThrThr-----CysValAsnTrpAsnGlnTyrThrAsnCysSerAlaG 358 Qy
1185 ACCTCAACGCCAGCGGTGTGCGCTCAACTGGAAACCGCTACTACAAGCTTGCCTGCCGACGG 1244 Db
358 lyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA 378 Qy
1245 GCAACGCCAACCTCACAGGGCGCCATCAACTTGGACAACATTTGGCTATGCCGGATTG 1304 Db
378 laIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspA 398 Qy
1305 TGATTTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTATGTATGGACG 1364 Db
398 laHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheM 418 Qy
1365 CACATTTCTTCTCAAACTTCACTACTTCTATCTTCTGCTCATCATAGTGGGCTCTTCTTCA 1424 Db
418 etIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438 Qy
1425 TGATCAACTTGTGCTGCTGTGCATGAACCCAGTCTCTGAGACCACAGCAACGGGAGC 1484 Db
438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458 Qy
1485 ACCGGCTGATGCTGGAGCAACGCCAGCGCTACCTGTGCC---TCCAGCAGCGTGGCCAGTT 1541 Db
458 heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478 Qy
1542 ACGTGTAGCCCGGTGATTGCTATGAGGAGATCTTCCAAATATGTCTGTGCATCATCTTCCGA 1601 Db
478 ysAlaAlaArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498 Qy
1602 AAGCCAACGCC-----CGTGGCCTAGGCTCTTACCAGCCCGCTG---- 1639 Db
498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518 Qy
1640 -----CAGA 1643 Db

518 isArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrH 538 Qy
1644 ACCGGCCGACGGC----- 1657 Db
538 isLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558 Qy
1658 --ATGGGCCCGGGGACA----- 1672 Db
558 laAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGlyP 578 Qy
1673 -----CCAGCCCTGCCAAGCCTGGGCC----- 1696 Db
578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598 Qy
1697 -----CATGCCAAG-----GAGCCCA 1712 Db
598 alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlyS 618 Qy
1713 GCCACTGCAAGCTGTGCCACACACACAGCCCTCTGGAC----- 1750 Db
618 erGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLysA 638 Qy
1751 -----CCCACTCCCCACACA----- 1765 Db
638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProP 658 Qy
1766 --CTGGTGCAG----- 1774 Db
658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678 Qy
1775 -----CCCATCTCTGCCATCTCTG----- 1792 Db
678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspS 698 Qy
1793 -----GCCTCTGACCCACGA 1808 Db
698 erCysProTyrCysAlaArg-----ThrGlyAlaGlyLeuProGluS 712 Qy
1809 GCTGCCCTCACTGCCACACGAGCGGCGCCCTCTGGCTGGCGAGCACTGACT 1868 Db
712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732 Qy
1869 CAGGCCAGGAAGGCTCAGGTTCTGTGGCTCTGCAGAGCGCGCAAGCAATGGGATGGAC 1928 Db
732 laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu 749 Qy
1929 TCCAGACGATGGAGTGGGGTCTCTCGGACCTGGGGAAGGAGGAGGAACAGGAGGACG 1988 Db
750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769 Qy
1989 GGG-----CAGCCCGACTGTGTGGG-GATGTGTGGCGGAGACACGAAAAAGCTG 2038 Db
770 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 789 Qy
2039 CGGGGCATCTGTGACACAAAGTACTTCAACAGAGGTATCATGTGGTATCTCTGTGTGAAC 2098 Db
790 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 809 Qy
2099 ACAGTCAGATGGGATCTGAGCACCAAGACAGCCCGGAGGAGCTGACCAACATCTCTGGAG 2158 Db
810 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuVal 829 Qy
2159 ATCTGCAATGGTCTTTCACCAAGTATGTTTGGCTGGAGATGATCTCTGAAACTGGCCGCC 2218 Db
830 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 849 Qy
2219 TTTGGGCTCTTCGACTACCTCGGGAACCTTACAACATCTTTTGACAGCATCATCTGTATC 2278 Db
850 IleSerValTrpGluIleValGlyGlnGlnGlyGlyGlnSerValLeuArgThrPhe 869 Qy
2279 ATCAGCATCTGGGAAATCGTGGGGGAGCGGACCGTGGCTGTCTGTCTGCGCACCTTC 2338 Db

4460	CAC	CAG	GAGGCTGAGGAGGGCCGAGGCGGTGAGGAGAAA	CGGCTGCCGCGCCTGGAAAAAG	4519
1577	Lys	Arg	ArgSerTyrGluLysGlnMetAlaGluAlaGlnCysIysProTyrTyrSerAsp	1596	
4520	AAG	CGCGGT	-----AAGGCTCAGAGGCTGCCTACTATGCTACC	4558	
1597	Tyr	Ser	ArgPheArgLeuValHisIleuCysThrSerHisTyrLeuAspLeuPhe	1616	
4559	TACT	GTCCCCAACAGGCTGCTCATCCATGCCATGCCACCAAGCCACTACCTGGACATCTTC	4618		
1617	Ile	Thr	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro	1636	
4619	ATT	ACCTTCATCATCTGCCTCAATGTTGTACCAATGTCCTGGAGGACACTCAACACGCT	4678		
1637	Gln	Ile	LeuAspGluAlaLeuLeuSileCyAsnTyrIlePheThrValIlePheValPhe	1656	
4679	ACAT	CCCTAGAGACAGCCCTTAAGTACTGCAACTFACATGTTCAACCACTGCTTTTGTCGTG	4738		
1657	Glu	Ser	ValPheLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsn	1676	
4739	GAG	GCTGTGCTGAAGCTGGTGCCAATTTGGCTGAGGCGTTTCTTCAAAGGACCGATGGAAC	4798		
1677	Gln	Leu	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGlu	1696	
4799	CAG	CTGGACCTGGCCCATTTGCTGCTGTCGTATGGGCATCACACTGGAGGAGATCGAG	4858		
1697	Val	Asn	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle	1716	
4859	ATCA	TGCGCCCTTCCCATCAACCCCAACCATCATCCGTATCATGCGGTCTTCGCGTATC	4918		
1717	Ala	Arg	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrVal	1736	
4919	GCC	CGGCTGTGAAGCTATTGAAGATGCCACAGAAATGCGGGCCCTGCCTGGACACAGTG	4978		
1737	Met	Gln	AlaLeuProGlnValGlyAsnLeuClYLeuLeuPheMetLeuLeuPhePheIle	1756	
4979	GTAC	AGGCTCTGCCCCAGGTGGGCAACTGGCGCTGCTCTTTCATGCTGCTCTTCTTCATC	5038		
1757	Phe	Ala	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCys	1776	
5039	TAT	GCTGCTCTGGAGGTGGAGCTCTTCGGAAGCTGGTCTGCAATGACGAGAACCCCTGT	5098		
1777	Glu	Gly	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe	1796	
5099	GAG	GCATGAGCCGGCAGCCACCTTTGMAAACTTCGGCATGGCTGCTCCTCAAGCTCTTC	5158		
1797	Arg	Val	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---	1815	
5159	CAG	GCTCTCCACAGCGGATAACTGGAATGGAAATTAAGAAGGACACCCCTGCGAGACTGT	5218		
1816	Asp	Gln	GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSer	1833	
5219	CAT	GATGAGCGCACGTGCCTTAGCAGCGCTGCAGTTTGTGCACCGCTCTACTTTGTGAGC	5278		
1834	Phe	Val	LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHis	1853	
5279	TTC	GTCGTCAAGCTAGTTCGTCTCATCAACCTGGTGGTGGCGGTGATGATGAACAT	5338		
1854	Leu	Glu	GluSerAsnLysGluAlaIyGluGluAlaGluLeuGluAlaGluLeuGluLeu	1873	
5339	CTG	GATCAGACAACAGAGGAGGCCGAGGAGATGAGAGATGGATGTGTGATGTGAGCTG	5398		
1874	Glu	Met	TyrThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro	1893	
5399	GAG	ATG-----	-----	5404	
1894	Gly	Val	GluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAla	1913	
5405	---	----	-----	5443	
1914	His	tLe	GlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGlu	1933	
5444	---	----	-----	5455	

Qy	1934	GluValProValPro	---LeuGlyProAspLeuLeuThrVal	-----	1941
Db	5456	CCCTGCCCTTGCCTGTGTCTGGCCCGAGCTCCCACTAGTTACCTGGGGCTCGGGG		5457	5515
Qy	1947	ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsn		1948	1966
Db	5516	CGAGGATCGGGAGGGGCGAGTGTCTGGAGGC---GACACCCAGAGTCACTGTGCCGGCAC		5517	5572
Qy	1967	---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGln		1968	1985
Db	5573	TGCTATTCTCCAGCCAGGAGACCTG---TGG		5574	5608
Qy	1986	SerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu		1987	2005
Db	5609	AGCGTCTCTTTAATCATCAAGACTCTCTGGAGGGAGCTGACCATCATTTGACAACCTG		5610	5668
Qy	2006	ProLysAspVal---HisTyrLeuLeuGlnProHisGlyAla	-----	2007	2018
Db	5669	TCTGGTCCGTCTTCCACCACCTACGCTCACCTGACGGCTGTGCAAGTGTCAACATGAC		5670	5728
Qy	2019	-----ProThrTrpGlyAlaIleProLysLeuLeuProPro		2020	2030
Db	5729	AAGCAAGAGACAGGTCTTCATCCATCTCTGTGGGGATGACCTGAGTCTTTGAGGACCCCA		5730	5788
Qy	2031	GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAspSer		2032	2050
Db	5789	CGGCTGCCACAGGGCCCCAAGGAGACAAAGGTGTAAGAGCTTCGGAGGCCCATGTC		5790	5848
Qy	2051	LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu	-----ValSerGly	2052	2068
Db	5849	AGGCTGAGACCTGGATGAATGCTTTTGGCCCTTTGCAAGCGAGCCAGTGTCCACAGGC		5850	5908
Qy	2069	ProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValcIn		2070	2088
Db	5909	CCAGAGAG---CTGCTGTGCCAGAT-----GGGGCCCATTCATTCAACC---CTG		5910	5954
Qy	2089	GlnArgSerGlyIleGlnSerLysValSerLysHisIleArg	-----	2090	2102
Db	5955	TCCAGTCTTGCTCAAAACAGAGAGCAGCAAGCACCCAGAGCCCTTCTCCCCGGATG		5956	6014
Qy	2103	-----LeuProAla	2104	2105	
Db	6015	GCTCCAGCCCTCTCTGTAGATGCCTGTCTTCCACCTGCTGTGTCTGCCAGCC	6016	6074	6133
Qy	2106	-----ProCysProGly	2107	2112	
Db	6075	AGAAGGGCGAGGAACCGGGCATGATGCAGAACCTTCCCCNAG-ATTGCATTTACGGG	6076	6133	
Qy	2113	SerTrpAlaLys---AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeu	2114	2131	
Db	6134	TCCTGGGCATCGTGAAGTCAACGAGTGTCAACTGCACCTCTTTCGCCAGGCTACTGTG	6135	6193	
Qy	2132	SerTrpIleSerGlyAspLeuLeuProSerSerGlnGluProLeuPheProArgAsp	2133	2151	
Db	6194	AGTGACAGCTCTTGGATGCCAGTCTTAGCAGCTCA	6195	6229	
Qy	2152	LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgProGlyPheTrpLeu	2153	2171	
Db	6229	-----	6230	6229	
Qy	2172	AspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg	2173	2191	
Db	6230	-----GGGGCAGCCCTACAGACACACTTGAAGACACTGTGACT-----	6231	6268	
Qy	2192	LeuCysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgPro	2193	2211	
Db	6269	CTGAGTGACAGTCCCCGGGTGCCTCGGGCCCGCGTCCAGGTGCTCTGGG-----CCA	6270	6322	
Qy	2212	LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg	2213	2231	
Db	6323	CGGGCTAGCTGTTCACCGGCCACCCCGGG-----CCGCTCAGCTCGCGGGCCGTGG	6324	6376	

QY 106 ysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuA 126
Db : : : : :
474 GCATCAAGATGGTTGTAAACCGTGTTCGAGTGTGTGAGCATGCTGTTATTCTGCTGA 533
QY 126 snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgC 146
Db : : : : :
534 ACTGTGTGACCTGGGCATGTACCAAGCCATGTGTGATGACATGGAGTGCCTGCGGACCGTT 593
QY 146 ysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetValV 166
Db : : : : :
594 GCAAGATCTTCAGAGTCTTCGATGACTTCATCTTCATCTTCCTTTGCCATGGAGATGGTGC 653
QY 166 alLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsnA 186
Db : : : : :
654 TTRAGATGGTGGCCCTGGGCATTTTGGCAAGAGTGTCTACTCTGGAGACACATGGAAACC 713
QY 186 rgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnV 206
Db : : : : :
714 GCCTGGATTTCTTCATTTGTCATGGCAGGATGGTTGAGTACTCTCTGGACCTACAGAAACA 773
QY 206 alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgV 226
Db : : : : :
774 TCNACCTGTACGCCATCGCATGTGCTGTGCTGCTGAGGCCTCTCAAGGCCATCAACCGTG 833
QY 226 alProSerMetArgIleLeuValThrLeuLeuAspThrLeuProMetLeuGlyAsnV 246
Db : : : : :
834 TACCAGCATGGGATCTCTGTGAACCTGCTGCTGCACACGCTGCCCATGTGGGGAAACG 893
QY 246 alLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA 266
Db : : : : :
894 TGCTCTCTCTGTTCTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGGG 953
QY 266 laGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValA 286
Db : : : : :
954 CAGGCTCTGCTACGGAACCGCTGCTCTCTGGAAGAACTTCACCATCAAGGGGATGTGG 1013
QY 286 spLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP 306
Db : : : : :
1014 CCCTGCCCTTATTACCAACAGAGGAGGATGACAGATGCCCTTTTATCTGCTCCCTGA 1073
QY 306 roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGlyG 326
Db : : : : :
1074 CTGGGGACAATGGCATATGGCTGCCAGAGATCCCCCACTGAAGGAGCAG----- 1126
QY 326 lyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSers 340
Db : : : : :
1127 --GGCGGGAATGCTGCCTGCCAAGATGATGTATGACTTGGGGCGGGGCCAGG 1184
QY 340 erSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaG 358
Db : : : : :
1185 ACCTCAAGCCAGCGGTGTGTGCTCAACTGGAACCGCTACTACAACTCTGCCGCACGG 1244
QY 358 lyGluHiAsnProPheIysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA 378
Db : : : : :
1245 GCAAGCCCAACCTCACAAGGCGCCATCACTTTTGACAACATTTGGCTATGCGCGGATG 1304
QY 378 laIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspA 398
Db : : : : :
1305 TGATTTTCCAGGTGATCACTCTGGAGGCTGGGTGGAGATCATGTACTATGTATGGAGCG 1364
QY 398 laHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheM 418
Db : : : : :
1365 CACATCTTTTACAACTTCATCTACTTCACTTCATCTCATCATATGATGGGCTCTCTTCTCA 1424
QY 418 erIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438
Db : : : : :
1425 TGATCAACTTGTGCTCGTTGTATGAACACCCAGTTCTCTGAGACCAAGCAACGGGAGC 1484
QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
Db : : : : :
1485 ACCGGCTGATGTGGAGCACCAGCGCTACTCTGTCC---TCCAGACGGTGGCCAGTT 1541
QY 458 heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478

Db : : : : :
1542 ACCTGAGCCCGGTGATTGCTATGAGGAGATCTTCCAATATGTCTGTACATCTCTCGCA 1601
QY 478 ysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498
Db : : : : :
1602 AAGCCAAGCG-----COTGCCCTAGGCTCTTACCAGGCCCTG--- 1639
QY 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
Db : : : : :
1640 -----CAGA 1643
QY 518 isArgArgLeuSerValHisLeuValHisHisHisHisHisHisHisHisTyrH 538
Db : : : : :
1644 ACCGCGCCAGGCC----- 1657
QY 538 isLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558
Db : : : : :
1658 --ATGGGCCCGGGGACA----- 1672
QY 558 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578
Db : : : : :
1673 -----CCAGCCCTGCCAGCCTGGGCC----- 1696
QY 578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598
Db : : : : :
1697 -----CATGCCAAG-----GAGCCCA 1712
QY 598 alArgCysGlnAlaProProProProProProProProProGluAlaSerGlyArgThrValGlyS 618
Db : : : : :
1713 GCCATGCAAGCTGTGCCACAGCACACGCCCTGGAC----- 1750
QY 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
Db : : : : :
1751 -----CCACTCCCCACACA----- 1765
QY 638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProP 658
Db : : : : :
1766 --CTGGTGCAG----- 1774
QY 658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678
Db : : : : :
1775 -----CCATCTCTGCCATTCTG----- 1792
QY 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAsps 698
Db : : : : :
1793 -----GCCTCTGACCCCA 1808
QY 698 erCysProTyrCysAlaArg-----ThrGlyAlaGlyGluProGluS 712
Db : : : : :
1809 GCTGCCCTCACTGCCAGCAGCAGCGCGCGCTCTTGGCTGGCGCAGCACTGACT 1868
QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
Db : : : : :
1869 CAGGCCGGAAGGCTCAGTTCTGGTCTCTGAGAGCGCGCAACCCCAATGGGATGAGC 1928
QY 732 laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu 749
Db : : : : :
1929 TCCAGAGCAGTGAAGTGGGTCTCTCGGACCTGGGGAAGAGGAGGAAACAGAGGAGC 1988
QY 750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769
Db : : : : :
1989 GGG-----CAGCCGCACTGTGTGGG-GATGTGTGGCGCGAGACACGAAAAAGCTG 2038
QY 770 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 789
Db : : : : :
2039 CGGGGATCTGTGGACAGCAAGTACTTCAACAGAGGTATCATGTGGCTATCTCTGTGTGAC 2098
QY 790 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 809
Db : : : : :
2099 ACAGTCAGCATGGGCATCGAGCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2158
QY 810 ileSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuVal 829

Db 2159 ATCTGCAATGTGTCCTTACCAGTATGTTTCCCTCGAGATGATCTTGAAACTGGCGCC 2218
Qy 830 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 849
Db 2219 TTTGGGCTCTTCGACTACCTGGGAACCTTACACATCTTTGACAGCATCATCGTCATC 2278
Qy 850 IleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPhe 869
Db 2279 ATCAGCATCTGGGAATCTGTGGGCGAGCGGCGCTGCTGTGCTGCGCACCTTC 2338
Qy 870 ArgLeuMetArgValIleLysLeuValArgPheLeuProAlaLeuGlnArgGlnVal 889
Db 2339 CGGTGTCTGGGGTCTGGAAGCTGGTGGCTTTCATCGCGCGCTGGCGCCAGCTCGTG 2398
Qy 890 ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle 909
Db 2399 GTGCTCATGAAGACCATGGACAGCTGGCCACCTTCTGCATGCTACTCATGCTGTTTCATC 2458
Qy 910 PheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp 929
Db 2459 TTCACTCTCAGCATCTTGGATGCATATCTTGGCTGCAAAATTCAGCCTCGCACGGAC 2518
Qy 930 ---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr 948
Db 2519 ACGGAGACACCGTCTCTGACAGGAAGACTTCGATTCTCTTACTGTGGGCCATCGTCACA 2578
Qy 949 ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer 968
Db 2579 GTGTTCCAGATCTCTACTCAGGAGACTGGAACTGTTCTGTGTACATGTCATGGCCCTCC 2638
Qy 969 ThrSerSerTrpAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeu 988
Db 2639 ACCACCCCTGGGCTCCCTCTATTGTTGGCTCATGACCTTTGGCAACTACGTTCTC 2698
Qy 989 PheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys 1008
Db 2699 TTCAATCTCTGGTGGCTATCTCTGGTAGAGGTTTCAGGCTGAGGGTGATGCTTAATCGT 2758
Qy 1009 SerGluSerGluProAspPheSerProSerValAspGly----- 1022
Db 2759 TCCGTCTCTGATGGAGACAGAGCTCATCCAAATTTGGAGGATTTGACAGCTCCACAGAG 2818
Qy 1023 -----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu 1040
Db 2819 GGCCTGGACAACAGTAGAGATCTCAAGCTCTGCCCAATACCATGACACCAATGGACAC 2878
Qy 1041 LeuArgLysSerLeuProLeuIleIleHis-----ThrAlaAlaThrProMet 1058
Db 2879 CTGACCCCTAGCCTC-----CCTCTGGGTGCGCATCTGGGTCTCTGTGTACCATGGGT 2932
Qy 1059 SerHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg 1078
Db 2933 ACTGCCCCCGCCTCTCTACTGACGACGACCCGCTACTGGTGGCCCTAGACTCTCGGAAA 2992
Qy 1079 ThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProPro 1098
Db 2993 AGCAGTGTATCCCTG-----GGCAGGATGAGTATGATGATGACGATCTCTTGCC 3043
Qy 1099 SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg 1118
Db 3044 AGCTCCGGAGCTCTACTACGGGCGCTGGGGCGCAGTGGGACCTGGGCTAGCGCGCGC 3103
Qy 1119 SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlu 1138
Db 3104 TCCAGCTGGAAC-----AGCCTGAAACACACAGCGCCCTCAGCTGAG 3145
Qy 1139 ArgArgSerLeuLeuSerGlyGluGlnGluSer-----GlnAspGluGluGluSer 1156
Db 3146 CATGAGTCTTACTGTCTGGGAGGGTGGAGGTAGCTGCGTCAGGCGCTGTGAAGGCGCC 3205
Qy 1157 SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3206 CGGGAGGAGGCGCAACTCGCACCGCCCTCGCATGCTCCACACCGCGCACCGCGCAC 3265

Qy 1170 -----ArgHisArgGlySerLeuGluArgGluAla 1179
Db 3266 CATGGACCCACCTGGCACACCGTACCAGCACACCGCGGACTCTGTCCCTGTGATACC 3325
Qy 1180 LysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer 1199
Db 3326 AGGACTCTGTTCACCTGGGAGACTGGTCCCGCTGGTGGTGCCTCCACTCACGGGCGCT 3385
Qy 1200 -----GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGly 1217
Db 3386 TGGAGGGGGCGGCTCAGGCCCTGGGCACAGACTGCAATGGCAGAAATGCCCAAC--- 3442
Qy 1218 ArgLeuAlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsn 1236
Db 3443 ---ATAGCCAAAGATGCTTCCACCAAGATGCATGACCGCCGACCGCGGGAGGACGAG 3499
Qy 1237 AspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuPro 1256
Db 3500 GAGGAGATCGACTATACCTGTGTTCCGGGTCCGCAAGATGATGTGTACAAAGCCG 3559
Qy 1257 AlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPhe 1276
Db 3560 GACTGTGCGAAGTCCGCGAGGACTGGTGGTCTACTCTTCTCCCGGAGAACAGTTC 3619
Qy 1277 ArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIle 1286
Db 3620 CGGATCTGTGTGACAGCATCATTTGCTCACAAGCTTTTGTGACTACGTGGTCTTGGCCTTT 3679
Qy 1297 IlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAla 1316
Db 3680 ATCTTCTCAACTGTATCACCATTGCTCGAGAGACCCAGATTTGAAGCTGTGTAGCACT 3739
Qy 1317 GluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMet 1336
Db 3740 GAGCGATCTTCTCAGGTGTCTTAATCTATCTTACAGCCATCTTCTGGGGGAGATG 3799
Qy 1337 ThrValLysValValAlaLeuGlyTrpCysPheGlyGlnAlaTyrLeuArgSerSer 1356
Db 3800 ACCTGAAGTGTGTTCTCTGGGCTGTACTTTGTTGAGCAGGCGTACCTCGGTAGCAGC 3859
Qy 1357 TrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMet 1376
Db 3860 TGAATGTACTGTATGTTTCTCGGTCTTTGTGTCATCATCATCATCTCGTAGTCTCGTG 3919
Qy 1377 ValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuArgThr 1396
Db 3920 GCCTCTGCTGGGGAGCAAGATTTCTGGGGGTCTCTCGGGTCTCTCGGCTCTCTCGTACC 3979
Qy 1397 LeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValGluThrLeu 1416
Db 3980 TTACGTCTTTGAGGGTTATCAGCCGGGCCCTGGGCTGAAGCTGGTGGTAGACGCTC 4039
Qy 1417 MetSerSerLeuLysProIleGlyAsnIleValIleValIleCysCysAlaPhePheIleIle 1436
Db 4040 ATCTCTCTCCCTCAAGCCATTGGGAACATCGTCTCATCTGCTGTGCTCTTCTTCTCATC 4099
Qy 1437 PheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAsp 1456
Db 4100 TTGGCATCTCTGGGGTGCAGCTTTTCAAGGCAAGTCTTACCATTGTTTGGAGTGGAC 4159
Qy 1457 ThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHis 1476
Db 4160 ACCGAAACATCACCAACCATCTGACTGCTGGTGGCGCAACTACCGCTGGTGCATCAC 4219
Qy 1477 LysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAspSerLys 1496
Db 4220 AAATACAACTTTCACACCTGGGCCAGCATGATGCTCTTGTCTTGTCTTGGCCTCCAAG 4279
Qy 1497 AspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPro 1516
Db 4280 GACGGCTGGTGAACATCATGTATATAGATTAGTCTGTTGCTGTGGACGACGACCA 4339

Db	6230	-----GCGGGCAGCGCTACAGACCACACTGGGAAGACAGTCTGACT-----	6268
Qy	2192	LeuCysProSerProSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgPro	2211
Db	6269	CTGAGTGACACTCCCGCGGTGCCCTGGGGCGCGGTCCAGTGCTGGG-----CCA	6322
Qy	2212	LysLysLysLeuSerProProSerLysSerLysLeuAspProGluSerClnGlySerArg	2231
Db	6323	CGGCGTAGCCTGTACCCGGCCACCCCGCGG-----CCGCTTCAGCTCGGGGCGGTGG	6376
Qy	2232	ProProCysSerPro-GlyValCysLeuArgArgAlaProAlaSer-----	2247
Db	6377	CCTGTTTAGTCTGGTGGGCTCGGGGCCCATCAGCGTAGCCACAGCAGATGGCGGCTCCAC	6436
Qy	2248	-----AspSerLysAspProSer	2253
Db	6437	CAGCCCTGGCTGCACCTACCACGACTCCTGATGACCCCTCT	6476

RESULT 15

```

US-09-949-016-15601
; Sequence 15601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15601

```

Db	10762	AATGTGGNACTCTCAGACCCCACTCTACTACTGTGTCTCACTGACCTGACCCCTCACAGGCC	10821
QY	228	-----	228
Db	10822	CCGTACAGAGAAGGGCTCAGTGGGAGCTGGGATTGCTGGAACAAAATGGAACCTCTGTAAT	10881
QY	228	-----	228
Db	10882	GTGGCACTATGGGAGTTTACCTGGGAAACCCACCTCATTTTAGCCTGGCTTTAGGTGAG	10941
QY	228	-----	228
Db	10942	AGTCTCAGAAACATCTCAGATGACCTCTTCTTCAGCTAGATGACCACTCCCCCAGGA	11001
QY	228	-----	228
Db	11002	GGATAGGGGTGTGGGACTGGAGAGGCTGACAGGCAAGAGTGGACGCAAGTGTCTAATG	11061
QY	228	-----	228
Db	11062	GCCTTTCTAGCCAGAACAGCCTCTCATGTGCAATCTGGTTCTTGTGTGTGAGACAGCTGG	11121
QY	228	-----	228
Db	11122	CCAGCTGAACGTGACTTCTCTCAAGACAAAGGCCACTCCATGTCTCACCTCCCGCTCTG	11181
QY	228	-----	228
Db	11182	TCCCTTCTCCTTCCCGCCCTTCCAAACCAATTGCAGTAACCTGCGGCCCCATTATCT	11241
QY	228	-----	228
Db	11242	AAATTAACATGCTATTGGTTCTGGAGCAGCGAGCCTTTGGCAGCTCTAGTTCTCCCTAC	11301
QY	228	-----	228
Db	11302	ATACTGCCCTCCCTTTGCTCAGGCCCTTTTGCAACTCCCAACCTACACAAGCTGCA	11361
QY	228	-----	228
Db	11362	GATGTCCTCTGTGTGCTTAGGAGTGGGTGGTTGGCAGGAATGCATGTTCTGCGG	11421
QY	228	-----	228
Db	11422	CTCAGTGCCTGTTTGTGTACCTGATGTAGCAGCAGCCCCCTCGCTCTGTGTGTGTGT	11481
QY	228	-----	228
Db	11482	GT	11541
QY	228	-----	228
Db	11542	GCAGAGCTGTTGAATGTGTCTCTCGGGCTCGGGGTGTGTTGGTGTGTTAAACAGAGCTCCA	11601
QY	228	-----	228
Db	11602	GAAGAGGGCATGCCTCGCTCTCTCCGCCCCAGGTGATGGCTGGCAGATTATAGGC	11661
QY	228	-----	228
Db	11662	CTCTGTCTAACCAACCGGTGTAATTCCTTAAATGCAAAACCTGAGGAATTGATCTCAGTTG	11721
QY	228	-----	228
Db	11722	GAGCACAGAGAGCTGAAGGGGATGGGTAGGAGAGGGGAGGAGACTGAGTGAGAA	11781
QY	228	-----	228
Db	11782	AACTGGCTGGCAGGGCGAGCTGGCGCTGCAGTCAACAGAGGGTTAATAGCTGCT	11841
QY	228	-----	228
Db	11842	GCTTAGCAGCTTTTGCCCTGGAGGGCCAGGGGCCATAGATGCACCTTTGGGGTGAAG	11901
QY	228	-----	228
Db	11902	CCAGCCATTAGAGATCTGTCTGTGACGAGGGCTTGGCGACTGGGGGCTGGTTTCAGAC	11961
QY	228	-----	228
Db	11962	CATTTGGCCCGTTGGGTTCTAGACCTGGAGTACGGAGAGAGGAAGTAACCTAACAGG	12021
QY	228	-----	228
Db	12022	GCCTTTGAGAGGGGTTTTCAGTGGCTTTCCTATGAGAGGGGTTGTAATTTGATGACT	12081
QY	228	-----	228
Db	12082	TCTGAGAAGACAGATTGTATCTCTTCAGTCTCTGATTTGGGGATCTGGACCAAGCAGGG	12141
QY	228	-----	228
Db	12142	AATAGTTTCAGGGAAGCAGGGCTCAGAGCCATAGTGAAGCACAGGCATCTTGGCCCTG	12201
QY	228	-----	228
Db	12202	CCTAGAGCTGGCTCTCAAAATGAGATTCCTGCTGCTCATCTCTCTGGAGTTGCT	12261
QY	228	-----	228
Db	12262	GCCTCAGTTTCCCTAATGACTCTGCTGGTGATTAACCTTAGAAAGTCAAGTACTGTGCT	12321
QY	228	-----	228
Db	12322	GTTGAGAGAAGTAGTAGGAGTGTGCGTGTGAATGTGTGCGGTGTGGTGTGTG	12381
QY	228	-----	228
Db	12382	TTGAGAGGGATTCCGAAGCCAAAGCCTGGGTTCCGAGTTCGCGCACCTACACTTAGCAGC	12441
QY	228	-----	228
Db	12442	TGTGTGATCTGGGTGAGTCAAGTCAATTTCTCAAGCCTCAGACTTCTCATCTGTGAATT	12501
QY	228	-----	228
Db	12502	GGGAGTGATATTATCCACATGTGATGTGTTGGAGAGTTAGGAGGGCCACAGTTTCCC	12561
QY	228	-----	228
Db	12562	CAGCTCACTGTTGGTGTACTGTGCAGATTACCTGGGCAAGCCACAAGGGGAAGTGGT	12621
QY	228	-----	228
Db	12622	CGGGCAAGGGCTGCAGAGGCTATCTGGGAGTCAGAGGTGTCTGTTGGTCTCCCTCC	12681
QY	228	-----	228
Db	12682	AGCTTGAGCCGGCGCTCTCAGCCTCAGACTCCCTGTGGGGCCCCCTCCGGGAGTGTGC	12741
QY	228	-----	228
Db	12742	CGGGCCGTGGCAGTCAGCCTAGCCCGGCCACCTGGTGTCCCGAGCTGGTCTTGTGCC	12801
QY	229	-----MetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnVa	246
Db	12802	CACAGGCATGGCATCTTGTTCAGCTGCTGGATACGCTGCCATGCTGGGCAAGT	12861
QY	246	LeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAl	266
Db	12862	CCTGCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	12921
QY	266	aGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeu	281
Db	12922	AGGGCTGCTTCGGAAACCGATGCTTCTTACCTGAGAAATTTACGCTGTGAGTGGTGACAG	12981

Qy	281	-----	281	Qy	412	-----	412	
Db	12982	GGTCCAGGAGACCTGGAGTGGTTATGGGGCTGGGCACCCCCCAAGTTCTCACTTC	13041	Db	14061	CCCGTGGGATGGCGATCCTGGGGACACCTGTGGGGGAGTCCAGAGGGGATAGTT	14120	
Qy	281	-----	281	Qy	412	-----	412	
Db	13042	CGGTTGCTACTGACATATCTGTTCTAAACATCTGAGACATATCTGGTTCTCAAACTTGGCT	13101	Db	14121	TGCTCTGTCTGAAGTTTTTAGCTCTCAGGACAAAGTCTGTAGAGAGGGCATCCATCATAT	14180	
Qy	281	-----	281	Qy	412	-----	412	
Db	13102	ACCATTTGGAACACCTGGGGAGTTTTAAAGACTGATGCTGGGTGGCACCTCCAGA	13161	Db	14181	AGTAGGGGACACACAGATGCAGATGCAGAGTCAAGGTAATCCAAAGGTCAAGGGCGGACTTAAC	14240	
Qy	281	-----	281	Qy	412	-----	412	
Db	13162	GATTCGTATTCAITTCCTGGGGCTCAGCTTGGATGTAAGGATTTTTTCAACCCCTCCA	13221	Db	14241	TGCTATTGGACCTTGGGCAAGTCAITTCATGAGGCCTCCAGCACTGCTCTGGGCCTC	14300	
Qy	281	-----	281	Qy	412	-----	412	
Db	13222	GTGATCCTAACTTGCAGTGAATTTGAAATCACTATTCCAGGATGTGACCTTCCAACAT	13281	Db	14301	TGTTTCTTCATGGGTAAATGAATGGTTCTCAACCTGAGATGATACCACCTCTCCACAG	14360	
Qy	281	-----	281	Qy	412	-----	412	
Db	13282	CCTGAGTCTGAGTTTCCCACTCAGGCCTCATGCTCCTGTGGTGGCCCAAAATCCTCGCC	13341	Db	14361	GGCATTGGAAATGGGAAAGGGTGATTCTGGTTTTTGATTTTTTTTAATAGCTTTATTGAG	14420	
Qy	281	-----	281	Qy	412	-----	412	
Db	13342	TGCCAGTCCCTTCCCATCTTGGTTCTGCGCTGCTCACCTATATGCTTCGAGCACTC	13401	Db	14421	ACATAACTCACATATCATTTCAATTCATCCCTTTGAATGAATCCAGTGGTTTTTTTAAGCAT	14480	
Qy	281	-----	281	Qy	412	-----	412	
Db	13402	GTGCCATCTCTCCTTCTCTGGGCCCTCTCCCTGGAGAGCCACTCCCCAGTCTCACCCCT	13461	Db	14481	GTTTACAGAGTTCTGTTTTTTTGTAGGACAAGGGAGTGCAATTGGCAATTTGTTACTG	14540	
Qy	282	-----	ProLeuSerValAspLeuGluProTyrTyrGlnThrG1	294	Qy	412	-----	412
Db	13462	GTTCCTTCCCACTCTGACGCCCTTGAGCGTGGACCTTGAGCGCTATTACCCAGACAGA	13521	Db	14541	GGGAGGGGAGAGAGCTAAACATCTCGAAATGCTTGCAAAATAAGAAATTTATTCTACCCA	14600	
Qy	294	uAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCy	314	Qy	412	-----	412	
Db	13522	GAACAGAGATGAGAGCCCTTCATCTGCTCCACGCCAGCGAGAACGGCATGCGGTCTG	13581	Db	14601	AAATTCGTGATCAGTGATCAATTTGGTGTAAATGCTGCTGTGATCTCTTATTCTCTGCCAGTT	14660	
Qy	314	sArgSerValProThrLeuArgGlyGlyGlyGlyProProCysSerLeuAspTy	334	Qy	412	-----	412	
Db	13582	CAGAAAGCTGCCACGCTCGCGGGGACGGGGCGGTGGCCACCTTGGGTCTGGACTA	13641	Db	14661	CAGAAATTCGCAGACTTTAAGNAGGACAGAGCGGAGGCAAAAGCAGCAATATTTAATAG	14720	
Qy	334	rGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAs	354	Qy	412	-----	412	
Db	13642	TGAGGCCCTACAAACAGCTCCAGCAACACCCCTGTCAACTGGAAACAGTACTACACAA	13701	Db	14721	TTTTAATCACTACCATTCATAGTTAATAACTTCATCGCCACCACCTTTGAGCTAATATTTA	14780	
Qy	354	nCysSerAlaGlyGluHisAsnProPheLysGlyValAlaIleAsnPheAspAsnIleGlyTy	374	Qy	412	-----	412	
Db	13702	CTGCTCAGCGGGGAGCACAAACCTTCAAGGGCGCCATCACTTTGACAACATTGGCTA	13761	Db	14781	TTGAGCACTTTACTATGCGCCAGCCCTTGATCTAAGCACTTTCAATGTGCTGGTGCAITTA	14840	
Qy	374	rAlaTrpIleAlaIlePheGln-----	381	Qy	412	-----	412	
Db	13762	TGCTCGATCGCCATCTTCAGGTGGGCGAGCCTGGGCGCGGAGCTTCCCCAGAACAC	13821	Db	14841	ATCCTCACCGTGATCTCTCCATTTTACAGATGAGAAACTGACATTTTCCTCATTTATCT	14900	
Qy	381	-----	381	Qy	412	-----	412	
Db	13822	CAGCCCCAGGACACAGCCAGGATCGGAGTGGTCTCTCAGGTTGGGGTGGGGTCAA	13881	Db	14901	GACCTTACCAGACGCTTGGCTATGCTGTGTATTAAATCTCCAAGAGTGGGGCATCACTGC	14960	
Qy	381	-----	381	Qy	412	-----	412	
Db	13882	GGCCTCTGGAGGACTGAAGGAGATTGTTGGTGGGCCCATAGTCAGCCTGCCCTCTGCA	13941	Db	14961	TGACGTATGTGTAACATCTGCTGCTGTTTAAATCTCGTCTGCTCCCTGTGAGGTGCCAG	15020	
Qy	382	-----	ValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaH	399	Qy	412	-----	412
Db	13942	CCCCCTAGGTATCATCAGCGTGGAGGCTGGGTGCGACATCATGCTACTTTGTGATGATGCTC	14001	Db	15021	GGCAGGGATTGTGTGCCCATCTCTTAAATGAGAAATTCAGCGCCCCAGAGGGTGGGTAC	15080	
Qy	399	isSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle-----	412	Qy	412	-----	412	
Db	14002	ATTCCTTCTACAATTTTCACTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	14060	Db	15081	TGGGCCAAGATCACACAGAAAAGTAAGCGGCTGGGGCTGAGNATTCAGTCCCGAGCTAACG	15140	
Qy	412	-----	412	Qy	412	-----	412	

Db	15141	ACTCCACATTTCAGCCTTCTCTCCATGTCCACCAAGGCCAACGACAGACAGAGG	15200
Qy	412	-----	412
Db	15201	GACAGACATTGAGAGAAAGAGATTAAAGAAAGATTAAAGATCTACTCAGGACCTAGGACTAG	15260
Qy	412	-----	412
Db	15261	CTCCAGAGAGAGATGAAGACAAATAAGCGAGCTCCTTGTGAGAGACAGAGGGTAGGCC	15320
Qy	412	-----	412
Db	15321	TGAGAAAGACAGTCCCAAGGCCACCTCATTTCTGCCCTGGTAACTTCCCTCTGGTGG	15380
Qy	412	-----	412
Db	15381	AAGAGTGGCAGGCTTGGGGGGAAGCCTGACTGGAGGCCCTGTTCCTCCATCCCTGGCCACCA	15440
Qy	412	-----	412
Db	15441	CCTCAAGGGGTGAGGCCAGTGCTTCAGGGAAGTGGGGTCTTCTCACCATGTGCCCCCCC	15500
Qy	412	-----	412
Db	15501	ACCCCACTCCCTTTCCCTCTCGGCTTGGGAGGGGAAGAACGACAGAGGAGATA	15560
Qy	412	-----	412
Db	15561	AGGGCCTAGTTTCCACCCTCCACACACCCCTGAAAAATCTTTCTTAACAGCTCTCTG	15620
Qy	412	-----	412
Db	15621	GAATCACACTAGTGAAGCTAATTATCAATAATTACTAGGACAGGATCTAGAAAAAATAAT	15680
Qy	412	-----	412
Db	15681	CTGCTTTGTCAACATAAATATTCAATTTCTTCATTGGGATGTTGTTCCAAGCAATGGCT	15740
Qy	412	-----	412
Db	15741	GTTCAGAGTTCTGGGGAACTGAGGCGTGGAGATGGGGCTGGGGTAGTGTGAGCAAGT	15800
Qy	412	-----	412
Db	15801	CAGGTGGCAGCCTGACTAGTCTGTAGGCTCAAGGTTTCAGGCCCTCCACATCTGAGGGA	15860
Qy	412	-----	412
Db	15861	GGGGGCACAGGGAAATGGGACAGACAAGSCCAATGGTCCCTGTTTTCAGATGAGGAT	15920
Qy	412	-----	412
Db	15921	ATGAGTCCCATGGCTAAGGCTCTCTCGCCAAAGTCAACAGCTAGAAATTGGGCTAGA	15980
Qy	412	-----	412
Db	15981	AGCAGGAGTCTGTAAATGATGTTTTTGTCAAGATCTCAAGGCTCAATATAATTGAAAA	16040
Qy	412	-----	412
Db	16041	CCCCATGTCCTTAATTGGTTCATTTCCACAGCATTCGCTACTCTTAATGGAATTGC	16100
Qy	412	-----	412
Db	16101	GGAAGGGGTGCTGCTCTCGCAGGTGTGCGTGTAGGGACAGGGAATTTGAGAGATTG	16160
Qy	412	-----	412
Db	16161	CAGGATAACACCATGTTCAATAGCAATATCTTGGAAATTTATAGAGCTTGGTTCCAGTCT	16220
Qy	412	-----	412
Db	16221	TAGCCTTGCTCTGAATTAGCTGAGTGATCTTGGGCAAAATGTTTGACCTCTGTGACCTGA	16280
Qy	412	-----	412
Db	16281	GTTTCTTACCTGCTGATGGAGATTACAATAGCATCACCTCTGTGAGGCTGCTTTAAAAA	16340
Qy	412	-----	412
Db	16341	TAAATGAGATAATGCTTGGAAAAATACTGAGCGTGGCGCTTGGCTCATAGGAATGCCTC	16400
Qy	412	-----	412
Db	16401	CGTATGTGGTGGCATTTGATTCACATTTCTTCAGGACATTTCTCTTCCTGTGCC	16460
Qy	413	-----ValGlySerPhePheMetIleAenLeuCysLeuValValIleAlaThrG	429
Db	16461	CACCCCTACAGGTGGGTCTCTTCATGATCAACCTGTGCTGTGCTGTGATGCCACGC	16520
Qy	429	InPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheL	449
Db	16521	AGTTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGATCGGGAGCAGCGTGTGCGTTCC	16580
Qy	449	euSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGlnLeuL	469
Db	16581	TGTCAAACGCCAGCACCTGGCTAGCTTCTCTGAGCCCGCAGCTGTATGAGGAGCTGC	16640
Qy	469	euLysTyrLeuValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgA	489
Db	16641	TCAAGTACCTGGTGTATCATCTTCGTAAAGCAGCCCGCAGCTGGCTCAGGTCTCTCGGG	16700
Qy	489	laIleGlyValArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProG	509
Db	16701	CAGCAGGTGTGCGGTGGCTGCTCAGCAGCCCGCAGCACCTCGGGGGCCAGGAGACCC	16760
Qy	509	InProSerGlySerCysThrArgSerHisArgArgLeuSerValHisIleuValHisH	529
Db	16761	AGCCCAGCAGCAGCTGCTCTCGCTCCACCCCGCTATCCGTCCACCATCTGCGTGGCACC	16820
Qy	529	isHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgA	549
Db	16821	ACCACCCACCATCACCCACCATCACCCCTGGGCAATGGACGCTCAGGGCCCCCGGG	16880
Qy	549	laSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProp	569
Db	16881	CCAGCCCGGAGATCCAGGACAGGATGCCAATGGTCCCGCGCTCATGTGTCACACAC	16940
Qy	569	roSerThrProThrProSerGlyProProArgGlyAlaGluSerValHisSerPheT	589
Db	16941	CCTCAGCGCTGCCCTCTCGGGGCCCCCTGTGGCGCAGAGTCTGTGCACAGCTTCT	17000
Qy	589	YrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgCysProS	609
Db	17001	ACCATGCCAGTGCACCTTAGAGCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCAT	17060
Qy	609	erGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerP	629
Db	17061	CTGAGGCATCCGCGAGGACTGTGGGCAGCGGAAGGTGTATCCACCGTCGACACAGCC	17120
Qy	629	roProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProp	649
Db	17121	CTCCACCGGAGCGCTGAAGGAGAGGCATCTAGTAGAGGTGGCTGCCAGCTCTTGGGCCCC	17180
Qy	649	roThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuG	669
Db	17181	CAACCTCACCAGCTCAACATCCACCCGGGCCCTACAGCTCCATGACAAAGCTGCTGG	17240
Qy	669	luThrGlnSerThr-----	673
Db	17241	AGACACAGTACAGGTGAGAACTCTGGGTGGAGGCATGTGGGTGCCCTCGTCTGGGGAC	17300
Qy	673	-----	673
Db	17301	TGGGTGGCGTCCACAGGGGACTAGGGGGTCTGGAGTCTGAGGGGACAGGGGCTTATATTC	17360

Qy	673	-----	673	Qy	673	-----	673
Db	17361	TCATGCTGCCTCTCATGGCTTAGGCACCTTCAACCAAGTCACATCCCTGCTATGAGCTCGA	17420	Db	18441	CATGCACGTGTCTGGTGTTCATATGCATATGTGTGCACATGTGTGCTTGTATGTGTAGGTG	18500
Qy	673	-----	673	Qy	673	-----	673
Db	17421	ATTTTCTCATCTGCTAAAGTGAAGTCACTAATATCTTACATTTGTAATAGCAGTAATCA	17480	Db	18501	CATGTGCGATGTGAAGCTCTTCTTGGTGTGTGCATGTGTGCATATGTCTGGCATAT	18560
Qy	673	-----	673	Qy	673	-----	673
Db	17481	TGTAATAAGCACCTGCTTCGTCTGTTGCAATGATGTGTAGCAACTGTGTGCACACAGCA	17540	Db	18561	GTCCCGTGTGAATGTGTTTGTGCACACATGTGTTGGTATGTGCATGTATGTGTGCCCA	18620
Qy	673	-----	673	Qy	673	-----	673
Db	17541	ATGCTGTGTGCTGTGCATGCTTTGCGGCAAAATTCATTGGATCCTCTCTACCCAT	17600	Db	18621	TATGTTGTTGCCAAATAGTATACATGTGTACACAGTGTGCGCATCTGGAGCACGTGTG	18680
Qy	673	-----	673	Qy	673	-----	673
Db	17601	TAAGTGATAGGCTTTCTTAGCATCCCATTTGTGTGATGAGAACAGGAGGCTTGAGGGG	17660	Db	18681	CAGGTGCACGTGTCTGTGTGGTGTGTGTGCAAGTGCACGTGTGTGGCGGTGTCTTAAG	18740
Qy	673	-----	673	Qy	673	-----	673
Db	17661	ATTGCATGACTTGCCCAAGGCTTTGCTATTGGTGAGGGGCGGACTCGGGGCCCCCACTCG	17720	Db	18741	GATCCCATGAAAGTGTCTGTCTCAGAACAGTGTTCATGTAGTCTCTGGCTTCTGGGAAGGG	18800
Qy	673	-----	673	Qy	673	-----	673
Db	17721	GGACTCCTTGTGTGAGGCTCAGAGAGGAATGGTGTGACTGTGTGCCAGCTTCATGCC	17780	Db	18801	AAGGGAGCAGGCTCTTCTGTGAAGCACCTTAGGATATAGGAGCTGTCCAGGACCTCAG	18860
Qy	673	-----	673	Qy	673	-----	673
Db	17781	CCACTGGCTAAACCTGAGTCTCATTTGCTCTCGGCACAGGAGACCCAGTTCAGGAGCTGC	17840	Db	18861	AGGACATCCAGGCCACCTCTCTGAGCCCCAGGACACTCAGCAGTGTACTGTCAATGAAGTG	18920
Qy	673	-----	673	Qy	673	-----	673
Db	17841	TTGTCTGATGGTGACACTCCAGTGTCTGGGGGCGAGTGAGACACATAGGAGCTCGGG	17900	Db	18921	CTATTGACATTAGGGCATCTTGTGGGTCAAGACTGCCACCTTGCCTTGACATTGACGACC	18980
Qy	673	-----	673	Qy	673	-----	673
Db	17901	CTCTCCCCAGCAGACAGGTTCACTGTAGTGTGACGCCACCGCCTGTGTTTCAGGAAGGAT	17960	Db	18981	CCTGGCCCCATAAGTGTCTAGCACCCCATCACTGTATAACACCCAGACTCCCTGACTCAT	19040
Qy	673	-----	673	Qy	673	-----	673
Db	17961	GTGCACTGTGGGAGCAGCGGATATTCTGTGGGATGTTACGTGGGAATGTGGCTGGGA	18020	Db	19041	TTTACATACTCACAGGGCAGGGTAGCCCCAGTACGAGACTGTGGAGCCTCTCACCTC	19100
Qy	673	-----	673	Qy	674	-----	688
Db	18021	CCAGAAGGTGCTATCACAGAACCCAGAGCGAAAGGTTTCTATGCCAGCTCTCCACTACC	18080	Db	19101	TACTCTCTCTTCCAGGTGCTGCCAAAGTCTTTGCAAGATCTCCAGCCCTTGTGAAA	19160
Qy	673	-----	673	Qy	689	AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGly	708
Db	18081	CTGCCACGGGACGTGGGCCAGTCACATGCCACCCACGTTTTATTTCCTCTGTGTAAAAG	18140	Db	19161	GCAGACAGTGGAGCCTGTGGTCCAGACAGCTGCCCTTACTGTGCCGGCGCGGCGAGG	19220
Qy	673	-----	673	Qy	709	GluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPhe	728
Db	18141	GCAAGGCTGGGCCCATTAATTACTCTCAGTGGGTGCTTACTGACTCCCTCTGTGTGCAGA	18200	Db	19221	GAGGTGAGTTCGCGCACCTGAAATGCCTGACTCAGACAGCGAGGAGTTTATGAGTTC	19280
Qy	673	-----	673	Qy	729	ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSer	748
Db	18201	TGCAGTCAAGGAGAAATGTCTGAGAGCCACCTGGGGCCAGGCCCTGAGCGGGGGG	18260	Db	19281	ACACAGATGCCAGCACAGGACCTCCGGGACCCCCACAGC---CGGCGGCAACGGAGC	19337
Qy	673	-----	673	Qy	749	LeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThr	768
Db	18261	TTCCACATCCATGCTTTACCTGGTACTCTCTGAGGTTCTCATATCTGTGATCAAGCTG	18320	Db	19338	CTGGGCCAGATGCAGAGCCAGCTCTGTGTGGCTTCTGGAGGCTAACTGTGACACC	19397
Qy	673	-----	673	Qy	769	PheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleVal	788
Db	18321	GATTTAAAGGACATTTGATGTCTTGGGCTAGGTCCCTGAGTGTGTGGCAGCAGTGCATC	18380	Db	19398	TTCCGAAGATTTGGACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTCTGTC	19457
Qy	673	-----	673	Qy	789	AsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeu	808
Db	18381	TAGTATGCGTGTATGCGTCTATGTATGCCATGAAGGGGTCAGTGTGTGTGTGCTGTGTG	18440	Db	19458	AACACACTCAGATGGGCATCGAATACACAGCAGGAGGTAGGAGAGTGGCGAGAGGCA	19514
				Qy	809	GluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeu	828

```

Db 19515 -----GGGCTCTGCAGCTGCTTTTCGCCTGGGCTG--- 19547
      |||
Qy 829 ValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal 848
      |||
Db 19548 -----GGGCTTCTACCTCCCTCCGACCCCTCTCTCTGAGCTCAGCTTCTCTCCATG 19601
      |||
Qy 849 VallleSer-ValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgTh 868
      |||
Db 19602 CTGCTAGCCACCTGGCAGGTAGGAGGGAGGTGGGTGATGGA-----GCAATGCATGG 19655
      |||
Qy 868 rPheArgLeuMetArgValLeuLysLeuValArgPhe----- 880
      |||
Db 19656 GGATTCTCTAGAGGAGTGCTTAAGTCTCTGAGTATGGAGTGCCTCAGGTAGGCCAC 19715
      |||
Qy 881 -----LeuPro-----AlaLeuGlnArgGlnLeuValVal 890
      |||
Db 19716 AGGGTATGTTCTACCCAGGAAGGCTGCTCAGAGGAGGCTGGCTTTG 19761
      |||

```

Search completed: July 10, 2006, 07:21:54
 Job time : 1331.74 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 10, 2006, 06:41:45 ; Search time 4670.36 Seconds

(without alignments)
8942.712 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGBESQGRFSM.....PKKDVLISGLSPADLDP 2266

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlp
-Q=/abse/ABSSWEB_spool/US09611257/runat_10072006_064126_6972/app_query.fasta.1
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs06p
-USER=US09611257 @CNC 1 1 7492 @runat_10072006_064126_6972 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11815.5	99.3	7648	9	US-10-377-139-10
					Sequence 10, Appl

2	11815.5	99.3	7648	9	US-10-757-262-15
3	11815.5	99.3	7825	10	US-10-756-149-31
4	11815.5	99.3	7825	10	US-10-786-148-120
5	11353	95.4	8116	7	US-10-062-674-2011
6	11111	93.3	7129	3	US-09-383-894-1
7	11111	93.3	7285	3	US-09-383-894-3
8	10945	91.9	6942	9	US-10-377-139-7
9	6315.5	53.1	3993	9	US-10-930-301-51
10	6215.5	52.2	7898	10	US-10-483-467-3
11	5496.5	46.2	6990	9	US-10-377-139-8
12	5496.5	46.2	6990	15	US-11-000-688-609
13	5492.5	46.1	6816	7	US-09-935-541-1
14	5492.5	46.1	6816	7	US-10-425-800-1
15	5484	46.1	6855	3	US-09-935-541-3
16	5484	46.1	6855	7	US-10-425-800-3
17	5418.5	45.5	6503	3	US-09-935-541-12
18	5418.5	45.5	6503	7	US-10-425-800-12
19	5382.5	45.2	5562	16	US-11-180-074-3
20	4013.5	33.7	7969	13	US-11-097-143-8135
21	3959.5	33.3	5562	3	US-09-030-482B-18
22	3867	32.5	6073	9	US-10-377-139-11
23	3461.5	29.1	6933	10	US-10-450-763-10945
24	1786.5	15.0	7376	6	US-10-033-026-3
25	1784.5	15.0	7362	8	US-10-375-253-11
26	1782.5	15.0	7364	3	US-09-954-456-1179
27	1782.5	15.0	7364	6	US-10-033-026-5
28	1782.5	15.0	7364	9	US-10-736-883-31
29	1782.5	15.0	7364	10	US-10-843-641A-4206
30	1782.5	15.0	7364	10	US-10-483-467-5
31	1782.5	15.0	7364	15	US-11-096-281-10
32	1778	14.9	7175	6	US-10-375-253-13
33	1776	14.9	7177	6	US-10-033-026-7
34	1776	14.9	7177	9	US-10-736-883-33
35	1776	14.9	7177	10	US-10-483-467-7
36	1773.5	14.9	6792	8	US-10-627-370-1
37	1757.5	14.8	7121	9	US-10-736-883-43
38	1755.5	14.7	6984	9	US-10-736-883-37
39	1752	14.7	7185	9	US-10-736-883-39
40	1751.5	14.7	7113	9	US-10-736-883-41
41	1751.5	14.7	9695	9	US-10-736-883-27
42	1751.5	14.7	9695	10	US-10-486-706-207
43	1751.5	14.7	9695	15	US-11-096-281-12
44	1738.5	14.6	7363	9	US-10-723-860-5192
45	1728.5	14.5	7011	6	US-10-033-026-9

ALIGNMENTS

RESULT 1
US-10-377-139-10
; Sequence 10, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Protein
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-10

Alignment Scores:	0	Length:	7648
Pred. No.:	11815.50	Matches:	2264
Score:			

QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2101 CAGCACAGACCTCCGGACACCCACAGCGCGGCAACAGAGCTGGGCCACATGCA 2160
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2161 GAGCCACGCTCTGCTCGCTCTTCCTGGAGGCTAACTCTGTGACACCTTCGGAAGATTGT 2220
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2221 GACACAGTACTTTGGCGGGGAATCATGATCGCATCTCTGGTCAACACACTCAGCATG 2280
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2281 GGCATCGAATACACAGCAGCGCCGAGGAGCTTACCAACGCGCTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800
Db 2341 GTCTTTCACGCGCTCTTTGGCTGGAGATGCTGCTGAAGCTGCTTGTGTATGTCCTCTT 2400
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820
Db 2401 GCCTACATCAAGAAATCCCTACAAACATCTTCGATGGTGTCATTGTGTCATCAGCGTGG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2461 GAGATCGTGGCGCAGCAGGGGGCGCTGTCGGTGCTCGGACCTTCCGCTGTATGCGT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2521 GTGCTGAAGCTGGTGGCTTCTGCGCGGCTGTCAGCGCAGCTGGTGTGCTCATATGAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2581 ACCATGGACAAGCTGGCCACCTTCTGCATGCTGCTTATGCTCTTCTCATCTTTCAGC 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 2641 ATCTCTGGCATGTCATCTCTGGCTGCAAGTTTGGCTCTGAGCGGATGGGGACACCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 2701 CCAGACCGGAAGAAATTTGACTCTCTGCTGCGGCATCGTCACCTCTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db 2761 ACCCAGGAGGACTGGAAACAAGTCTCTACAAATGGTATGGCTCCACGTCGTCCTGGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 960
Db 2821 GCCCTTTATTTTCATTCGCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
Db 2881 GCCATTCTGTGTGGAGGGTTCCAGCGGAGAAATCAGCAAAACGGGAAGATCGCAGTGG 2940
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 2941 CAGTTAAGCTGTATTTCAGCTGCTCTGCATCTCCAGGGGGAGATGCCAAACAAAGTCCGAA 3000
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3001 TCAGAGCCCGATTCTTCTCACCCAGCTGGATGGTGTGGGACAGGAAGAGTGTG 3060
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
Db 3061 GCCTTGGTGTCTCCGGAGAGCACCGGAGCTGCGGAAAGAGCTGCTGCGCGCTCTCATC 3120
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3121 ATCCACAGCGCGCCACACCCATGCTGCTGCCAAAGACACAGCAGCGGGCTGGGCGAG 3180

QY 1061 AlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3181 GCGCTGGGCCCTCGCTCGCGCGCACACAGCAGCAGCGGTGGCAGAGCTTGGGGCGGCC 3240
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3241 CACGAGATGAAGTCAACGCCCCAGCGCCGAGCTCTCCGCAAGAGCCCTTGGAGCGCTGCA 3300
QY 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3301 AGCAGCTGGACACGACGCGCTCCAGCCGGAACAGCTTCCGCCGTGACACCCAGCTGAAG 3360
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln 1140
Db 3361 CGGAGAAGCCCAAGTGGAGAGCGCGCTCTGTTGTGGGAGAAGGCGCAGGAGAGCCAG 3420
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3421 GATGAAGAGGAGAGCTCAGAAGAGAGCGCGCCAGCCCTGCGGGCAGTGACCATCGCCAC 3480
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3481 AGGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3540
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3541 CCAGGGCTGCATCGCAGTCCGAGTGGCGAGGGTCTGCTTCTGAGCACACAGGACTGCAAT 3600
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220
Db 3601 GGCAAGTCCGCTTCCAGGGCGCTGCGCGCGCCCTGCGCGCTGTAGACCCCTCATGAT 3660
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyArgValArgAlaTrpIle 1240
Db 3661 GGGGATGACGCGCATGACAGGGCAACCTTGAGCAAAAGGGGAACGGGTCCGCGCGTGGATC 3720
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 3721 CGAGCCCGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 3781 CCTCAGTCCAGGTTCGCGCTCTGCTGCTCAGCGGATCATCCCAAGATGTTTCAGCCAC 3840
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3841 GTGTCTTGTTCATCATCTTCTTAACATGTCATCACCATCGCATGGAGCGGCCCAAAATT 3900
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3901 GACCCCAACAGCGCTGAACGTCATCTTCTGACCCCTCTCCAATTACATCTTACCCGAGTC 3960
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
Db 3961 TTTCTGCTGTAATACACAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 4020
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4021 TACTTGGGACGAGTGGAAACGTCGTGGACGGGCTGTTGGTGGTGGTGGTGGTGGTGG 4080
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4081 ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCTCTGGGTCATGCTGAGGGT 4140
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4141 CGGCTGCTGCGGACCCCTGCGCCGCTCAGGGTGTATCAGCCGGGCGCAGGGGCTGAAGCTG 4200
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 4201 GTGTGGAGACGCTGATGTCCTCACTGAACCCCATCGCAACATTTGTAGTCATCTGCTGT 4260
QY 1421 AlaPheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440


```
Qy 2050 ProProLeuAlaArgAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGlnHis 2069
Db 6481 CCGCCCTGGCCCGCCCTACTCTTCTTGGGGCCAGTCAAGTACCAGGACAGCAGCAC 6540
Qy 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
Db 6541 TCCCGCAGCCACAGCAAGATCTCCAAAGCACATGACCCCGCCAGCCCTTGGCCAGGCCCA 6600
Qy 2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
Db 6601 GAACCAACTGGGCAAGGGCCCTCCAGAGACCAGAACAGCTTAGATTGGACACGGAG 6660
Qy 2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSerPro 2129
Db 6661 CTGAGCTGGATTTCAGGAGACTCTCGCCCTGGCGGCCAGGAGGCCCCATCCCA 6720
Qy 2130 ArgAspLeuLysLysCysTySerValGluAlaGlnSerCysGlnArgArgProThrSer 2149
Db 6721 CGGGACCTGAAGAAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCTACGTC 6780
Qy 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169
Db 6781 TGGCTGGATGAGCAGAGAGACACTCTATGCCGTCAGCTGCTGGACAGCGGCTCCCA 6840
Qy 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyProGlySer 2189
Db 6841 CCCACCTGGGCACAGACCCCTTAACCTTGGGGCCAGCCCTTGGGGGGCCCTGGGAGC 6900
Qy 2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209
Db 6901 CGGCCCAAGAAAAAATCAGCCGCTAGTATCACATAGACCCCGCCGAGACCAAGGT 6960
Qy 2210 ProArgThrProProSerProGlyLysCysLeuArgArgAlaProSerSerAspSer 2229
Db 6961 CCTCGACCCCGCCAGCCCTGGTATCTGCTCCGGAGAGAGCTCCCTGACGAGACTCC 7020
Qy 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249
Db 7021 AAGGATCCCTGGCCCTCTGGCCCTGACAGCATGGCTGCTCGCCCTCCCAAGAAA 7080
Qy 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7081 GATGTGCTGAGTCTCTCGGGTTATCTCTGACCCAGCAGACCTGGACCCC 7131

RESULT 2
US-10-757-262-15
; Sequence 15, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
```

```
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7134)
US-10-757-262-15

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 11815.50 Matches: 2264
Percent Similarity: 95.3% Conservative: 1
Best Local Similarity: 95.2% Mismatches: 111
Query Match: 99.3% Indels: 111
DB: 9 Gaps: 2

US-09-611-257A-37 (1-2266) x US-10-757-262-15 (1-7648)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGACGAGGAGGAGGATGGAGCGGGGCCGAGGAGTCGGGACAGCCCGGAGCTTCATG 60
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CGGCTCAACGACCTGTGGGGGCCGCGGGGCCGCGGGGCCGCGGGGTGACGAGAAAAGGAC 120
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGCGACGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGCGGCTGCCCGCGGTGTT 180
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTTGAGCCAGGACAGCGCGCCGCGGAGCTGGTGTCTCCGACCGGTCTGTAA 240
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCCTGGTTGAGCGCATCAGCATGTTGGTCACTCTTCACTGCGTGACCTGGGCATG 300
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCCGGCCATCGGAGGACATCCCTGTGACTCCCGGCGCTCCCGGATCCTGCGAGCCCTT 360
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValMetValAlaLeuGly 140
Db 361 GATCACTTCATCTTTGGCTCTCTTGGCCGTGAGATGGGGTGAAGATGGTGGCCCTGGGC 420
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 421 ATCTTTGGAAAAAGTGTACTCTGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC 480
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATCGCAGGATGCTGGAGTACTCGCTGGACCTCGCAGAACGTCAGCTTCTCAGCTGCAGG 540
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGTCGCGACCGCTCAGGGCCATTAAACCGGGTCCCGCAGCATCGCATCCTT 600
```


2761 Db ACCCAGGAGGACTGGAACAAAGTCTCTACAAATGGTATGGCTCCACAGCTCGTCTGGGCG 2820
941 Qy AlaleuTyrPheIleAlaleuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
2821 Db GCCCTTTATTTTCATTGGCCCTCATGACCTTCGGAACACTAGTGCTCTTCAATTTGCTGGTC 2880
961 Qy AlaleuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
2881 Db GCCATTCTGGTGGAGGCTTCCAGGCGGAGGAAATCAGCAACGGAAGATCGAGTGA 2940
981 Qy GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
2941 Db CAGTTAAGCTGTATTTCAGCTGCTGTGCACTCCAGGGGGAGATGCCAACAAGTCCGAA 3000
1001 Qy SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
3001 Db TCAGAGCCGATTTCTTCTCACCCAGCTGGATGGTGTATGGGACAGGAAGATGCTTG 3060
1021 Qy AlaleuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProProLeuIle 1040
3061 Db GCCTTGGTGTCTGGAGAGACCCGAGAGCTGCGGAAGAGCTGCTGCCGCTCTCATC 3120
1041 Qy IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlu 1060
3121 Db ATCCACACGGCCGCCACACCCATGTCGTGCCCAAGAGCACCAGCACGGGCCCTGGCGAG 3180
1061 Qy AlaleuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1080
3181 Db CGCTGGGCGCTGCTGCGCGCGCACACAGCAGCGGCTGCGAGAGCTGGGCGGCGC 3240
1081 Qy HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAla 1100
3241 Db CACGAGATGAATCACCGCCACAGCCCGCCAGCTCTCCGCACAGCCCTGGAGCGCTGA 3300
1101 Qy SerSerTrpThrSerArgArgSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
3301 Db AGCAGCTGACACGAGCGGCTCCAGCGGAAACAGCCTCGGCCAGCCCTGACCCAGCTGA 3360
1121 Qy ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGluGlnGluSerGln 1140
3361 Db CGGAAGAGCCCAAGTGGAGCGGCTCCCTTGTGCGGGAAGGCGGAGAGCGGAG 3420
1141 Qy AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
3421 Db GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCGCCCTGCGGCGAGTGACCATCGCCAC 3480
1161 Qy ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
3481 Db AGGGGGTCCCTGGAGCGGAGGCCAAGAGTTCCTTTGACCTGCCAGACACACTGCGAGGTG 3540
1181 Qy ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
3541 Db CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGCTCTGCTTCAGACCCAGGACTGCAAT 3600
1201 Qy GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220
3601 Db GGCAGTTCGGCTTCAGGGCGCTTGGCCCGGCGCTTGGCGCTGATGACCCCCCATGATG 3660
1221 Qy GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
3661 Db GGGGATGACCGCATGACGAGGGCAACCTGAGCMAAGGGAACGGGCTCCGCGCTGGATC 3720
1241 Qy ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTrpIlePhePro 1260
3721 Db CGAGCCCGACTCCCTGCCCTGCTGCTCGAGCGGAGACTCTGTTGTCAGCCCTACATCTTCCCT 3780
1261 Qy ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
3781 Db CTTCAGTCCAGGTTCCGCTCTGTGTACCGGATCATCACCCACAAGATGTTCCGACCAC 3840
1281 Qy ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300

3841 Db GTGFTCTTGTTCATCATCTTCTTAACTGCATCACCATCGCATGGAGCGGCCCAAAATT 3900
1301 Qy AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
3901 Db GACCCCAACAGCGCTGAACGCATCTTCTGACCTCTCCAATTACATCTTCCACCGAGTC 3960
1321 Qy PheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
3961 Db TTTCTGGCTGAAATGACAGTGAAGTGGTGGCAGTGGCTGGTGGTGGGAGCAGGCG 4020
1341 Qy TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuValLeuLysSerValIleAsp 1360
4021 Db TACCTGCCGAGCAGTGGAAACGTGCTGACCGGGCTGTTGGTCTCATCTCCGCTCATCGAC 4080
1361 Qy IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
4081 Db ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGATGCTGAGGGTGTG 4140
1381 Qy ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
4141 Db CGGCTGCTGCGGACCCCTGCGCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTG 4200
1401 Qy ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
4201 Db GTGTGGAGAGCGCTGATGCTCTCACTGAACCCATCGGCAACATTTGATGCTATCTGCTGT 4260
1421 Qy AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal 1440
4261 Db GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCGAGCTCTTCAAGGGGAAGTTTTTCGTG 4320
1441 Qy CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
4321 Db TGCCAGGCGGAGGATACCCAGGAACATCACCAATAAATCGGATGCTGCCCGCAGGCGATTAC 4380
1461 Qy ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
4381 Db CGGTGGGTCCCGGCAACAGTACAACTTTGACAACTTTGGCCAGGCGCTGATGCTCTGTTTC 4440
1481 Qy ValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
4441 Db GTTTTGGCTCCNAGGATGGTTGGGTGGACATCATGTACGATGGGCTGATGCTGTGGGC 4500
1501 Qy ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
4501 Db GTGGACACGAGCGCCATCATGAACCAACCAACCCCTGGATGCTGCTGATCTCTCGTTC 4560
1521 Qy LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
4561 Db CTGCTCATTTGGGCTCTTTGTCTGAACATGTTTGTGGGTGTGGTGGGAGAACTTC 4620
1541 Qy HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu 1560
4621 Db CACAAGTGTGGCAGCACCCAGGAGAGAGGAGGCGCCGCGGGGAGGAGAACGCCCTA 4680
1561 Qy ArgArgLeuGluLysLysArgArg 1568
4681 Db CGAAGACTGGAGAAAAAGAGAGGAATCTAATGCTGGACCATGTAATGCTTCCGCGCAGC 4740
1569 Qy -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582
4741 Db TCAGCCAGCGCTGCTGCAAGAGCCCGAGTGCAAACTTACTCTCGACACTACCTCCGCTTC 4800
1583 Qy ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspPheIleThrGlyVal 1602
4801 Db CGGCTCTCTGCTCCACCATTTGTGCACCGACCACTACCTGGACCTCTTCATCACAGGTGC 4860
1603 Qy IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622
4861 Db ATTCGGCTGAACGTGGTCAACCATGGCATGGGAGCACTACCCAGCAGCCCCCAGATTCGTGAT 4920
1623 Qy GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
4921 Db GAGGCTCTGAAGATCTGCAACTACATCTTCTACTGTCATCTTGTCTTGGAGTCAGTTTTC 4980

1643 LysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeu 1662
1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleLeuValAsnAlaSer 1682
5041 GCATTTGCTGCTGCTCCATCATCGGCATCAGCTGGAGGAATCGAGGTCAACGCCCTCG 5100
1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702
5101 CTGCCCATCAACCCACCATCATCGCATCATGAGGGTCTCGGCATTTCGCCGAGTGTCTG 5160
1703 LysLeuLeuLysMetAlaValAlaGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
5161 AAGCTGCTGAAGATGCTGTGGCATGTGGCGATGCGGGCGCTGCTGGACACGGTGATGACGGCCCTG 5220
1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742
5221 CCCAGGTGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTCAGCTCTG 5280
1743 GlyValGluLeuPheCysAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762
5281 GCGGTGGAGCTCTTTGGAGACCTTGGAGTGTGACGAGACACACCCCTGTGAGGGCCCTGGGC 5340
1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
5341 CGTCATGCCACCTTTTCGGAACCTTTGGCATGGCCCTTCTTAACCCCTCTTTCGAGTCTCCACA 5400
1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
5401 GGTGACAAITGGAAATGGCAATTATGAAGGACACCTCCGGGACTGTGACACGAGTCCACC 5460
1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
5461 TGTACAAACACGGTCACTCGCCTATCTACTTTGTGTCTTGTCTGTCGTGTCGCGCCCGAGTTTC 5520
1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluLeuSerAsnLysGlu 1842
5521 GTGCTAGTCAAGTGTGTATGCCGTGCTGATGAAGCACTCGAGAGAGCAACAGGAG 5580
1843 AlaLysGluAlaGluLeuAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862
5581 GCCAAGGAGAGCGCGAGCTAGAGGCTGAGCTGAGCTGGAGTGAAGACCTCGACGCC 5640
1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882
5641 CAGCCCCACTCGCCACTGGGCAGCCCCCTTCTCTGCGCTGGGGTCGAGGGCCCCCGACAGC 5700
1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902
5701 CCGCAGAGCCCCAAGCCTGGGCTGTGCACCCAGCGGCCCGCCAGGATCAGCCCTCCAC 5760
1903 PheSerLeuGluHisProThr----- 1909
5761 TTTTCCCTGGAGACACCCACGGACAGGCAGCTGTTTTCACACCATATCCCTGTGTGTCCAG 5820
1909 ----- 1909
5821 GGCTCCCTGGAGTGGGAGCTGAAGCTGATGGAGCTGGCAGGCCAGGGGCCAGGCC 5880
1909 ----- 1909
5881 TCTGCCCTTCCCTTCTGCCCCCGACCTGGGAGGGCTCGACCCACAGATCCCTCTAGCTGAG 5940
1909 ----- 1909
5941 ATGGAGGCTCTGTCTCTGACGTCAAGATTTGTCTCTGAACCGTCCCTGTCTCTAGCTCTG 6000
1909 ----- 1909
6001 ACGGATGACTCTTTGCTGATGACATGCACACACTCTTACTTAGTGCCCTGGAGAGCAAT 6060

1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929
6061 ATGCAGCCCCACCCACGAGGCTGCAGGACGAGCTTACTGACTGTGCGGAAGTCTGGG 6120
1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949
6121 GTCCGCCGAACGCACTCTCTGCCCAATCACAGCTACATGTGTGCGCATGGGAGCACTGCC 6180
1950 GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu 1969
6181 GAGGGGCCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGCTTTG 6240
1970 SerValHisSerGlnProAlaAspThrSerTrpIleLeuGlnLeuProLysAspAlaPro 1989
6241 TCCGTTCACTCCACGACGAGATACAGCTACATCTCTGCAGCTTCCCAAAAGATGCACCT 6300
1990 HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro 2009
6301 CATCTGCTCCAGCCCCACAGCGCCCAACCTGGGCGACCATCCCCAAACTGCCCCCCACCA 6360
2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029
6361 GGACCTCTCCCTTTGGCTCAGAGGCCACTCAGCGCCGAGCGAGCAATAAGAGCTGACTCC 6420
2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049
6421 TTGGACGTTTCAGGCTCTGGGCAGCCGGGAGACCTGCTGGCAGAGGTGAGTGGGCCCTCC 6480
2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHis 2069
6481 CGGCCCTTGGCCGGGCTACTCTTTCTGGGGCCAGTCAAGTACCAGCAGCACAGCAGCAC 6540
2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
6541 TCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCAGCCCTTGGCCAGGCCCA 6600
2090 GluProAsnTrpGlyLysGlyProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
6601 GNAACCACTGGGGCAAGGGCCCTCCAGAGACCAGAGACAGCTTAGAGTTGGACAGGAG 6660
2110 LeuSerTrpIleSerGlyAspLeuLeuProGlyGlyGlnGluGluProProSerPro 2129
6661 CTGAGCTGGATTTTCAGGAGACCTCTCTGCCCTTGGCGGCCAGAGAGGCCCTCATCCCCA 6720
2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149
6721 CCGGACCTGAAGAAGTGTCTACAGCGTGGAGGCCAGAGCTGCCGCCCGCTACGCTCC 6780
2150 TrpLeuAspGluGlnArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169
6781 TGGCTGGATGACAGAGGAGACACTCTATCGCGCTCAGCTGCTGAGACAGCGGCTCCCAA 6840
2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer 2189
6841 CCCCACCTTGGGCACAGACCCCTCTAACTTGGGGGCCAGCCCTTTGGGGGGCTGGGAGC 6900
2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProGluSerGlnGly 2209
6901 CCGGCCAAGAAAANAACCTCAGCCCCGCTAGTATCACCATAGACCCCCCGAGAGCCAGGT 6960
2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229
6961 CCTCGGACCCCGCCAGCCCTGGTATCTGCTCTCGGAGGAGGGCTCCGTCAGCGACTCC 7020
2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249
7021 AAGGATCCCTTGGCCTCTGGCCCCCTTGACACATGGCTGCTGCTGCCCTCCCCAAAGAAA 7080
2250 AspValLeuSerSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
7081 GATGTGCTGAGTCTCTCCGTTTATCTCTGACCCCGACAGACTGGACCCC 7131

RESULT 3

US-10-756-149-31
; Sequence 31, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756.149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patent version 3.2
; SEQ ID NO 31
; LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-31

Alignment Scores:
Pred. No.: 0 Length: 7825
Score: 11815.50 Matches: 2264
Percent Similarity: 95.3% Conservative: 1
Best Local Similarity: 95.2% Mismatches: 1
Query Match: 99.3% Indels: 111
DB: 10 Gaps: 2
US-09-611-257A-37 (1-2266) x US-10-756-149-31 (1-7825)

Qy	1	MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20
Db	373	ATGGACGAGGAGGAGTGGAGCGGGCCCGGAGGATCGGACACGCCCGGAGCTTTCATG	432
Qy	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
Db	433	CGGCTCAACGACCTGTTCGGGGGCGGGGGCGGGCGGGGGCGGGGTACGAGAAAGGAC	492
Qy	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal	60
Db	493	CCGGGACGCGGACTCCGAGCGGAGGGGTGCGGTACCCCGCGCTGGCCCGGTGGT	552
Qy	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
Db	553	TTCTTTACTTTGAGCAGACAGCGCGCGCGGAGCTGGTGTCTCCGACACGGTCTGTAAC	612
Qy	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	613	CCCTGGTTTGGCGCATCAGCATGTGTGTCTCTTCTCAACTGCGTGACCTGGGCATG	672
Qy	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	673	TTCCGGCCATCGGAGGACATCGCTGTGACTCCCGAGCGCTCCGATCCTCGAGGCCTTT	732
Qy	121	AspAspPheIlePheAlaPhePheAlaValGluMetValLysMetValAlaLeuGly	140
Db	733	GATGACTTTCATCTTGGCTTCTTGGCGGTGGAGATGGTGGTGAAGATGGTGGCTTGGGC	792
Qy	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
Db	793	ATCTTTGGGAAAAGTGTTACTCTGGGAGACACTTGGAAACCGGCTTGACTTTTCATGTC	852
Qy	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	853	ATCGCAGGATGCTGGAGTACTCGCTGGACCTGCGAGACGTCAGCTTCTCAGCTGTCCAG	912
Qy	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	913	ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACCGGGTGGCCAGCATGCGCATCTT	972
Qy	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	973	GTCAGTGTGCTGGATACGTCGCCCATGCTGGGCAACGCTCTGCTCTCTCTCTCTCTC	1032

Qy	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	1033	GTCTTCTTTCATCTTCGGCATCGTCCGGCTCCAGCTGGGCGAGGCTCTTCGGAACCGA	1092
Qy	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln	260
Db	1093	TGCTTCTTCTTACCTGAGAATTTTCAGGCTCCCTCAGCGTGGACCTGGAGCGCTATTACCA	1152
Qy	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	1153	ACAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACCGAGACGCGATCGG	1212
Qy	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	1213	TCCTGCAGAGCGTGCACACGCTCGCGGGGACGGGGCGGTGGGCCACCTTGGCGTCTG	1272
Qy	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	1273	GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCACTGGAACAGTACTAC	1332
Qy	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
Db	1333	ACCAACTGCTCAGCGGGGAGCACACCCCTTCAAGGGCGCATCACTTTGACAACATT	1392
Qy	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Db	1393	GGCTATGCTGGATCGGCATCTTCAGGTATCATCGCTGAGGGGTGGGTGCACATCATG	1452
Qy	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle	380
Db	1453	TACTTTGTGATGGATGCTCATCTTCTACAAATTTTCATCTTCTCATCTCTCTCATATC	1512
Qy	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1513	GTGGGCTCTCTTCATGATCAACTGTGCTGCTGGTGGTATGTCACGCGAGTCTTCAGAG	1572
Qy	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1573	ACCAAGCAGCGGAAAGCCAGCTGATCGGAGCAGCGTGTGCGGTTCTCTGTCCAACGCC	1632
Qy	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
Db	1633	AGCACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATAGGAGCTCTCAAGTACCTG	1692
Qy	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1693	GTGTACATCTTCTGTAAGGAGCCCGCAGGCTGCTCAGGTCTCTCGGCGAGCAGGTGTG	1752
Qy	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1753	CGGTTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC	1812
Qy	481	SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis	500
Db	1813	AGCTGCTCTGCTCCACCGCGCTATCTCCGTCACCACTCTGGTGGTGCACACCCAGCAC	1872
Qy	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1873	CATCACCACTTACCACTTGGGCAATGGGACGCTCAGGGCCCCCGGGCGAGCCCGGAG	1932
Qy	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	1933	ATCCAGGACAGGATGCAATGGGTCCCGCGGCTCATGCTGCCACCACTCTCGACGCT	1992
Qy	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1993	GCCCTCTCCGGGGCCCCCTTGTGGCGCAGAGTCTGTGCACAGCTTCTACATGCCGAC	2052
Qy	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	2053	TGCCACTTAGAGCAGTCCGCTGTCAGGCGCCCCCTCCAGGTCCTCCATCTGAGGATCC	2112
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600

Db 2113 GCGAGGACTGTGGGAGCGGGAGAGTGATGCCACCGTGACACAGCCCTCCACGGAG 2172
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 2173 ACGCTGAAGGAGAGGCACTAGTAGAGGTGGCTGCAGCTCTGGGCCGCCCAACCCCTACC 2232
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrClnSer 640
Db 2233 AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCAACAAGCTGCTGGAGACACAGAGT 2292
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2293 ACAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGGACAGACAGTGA 2352
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2353 GCCTGTGGTCCAGACAGAGCTGCCCTACTGTGCCGGCGGGGACAGGGAGGTGGAGCTC 2412
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrClnAspAla 700
Db 2413 GCGGACCGTGAAATGCCGTACTCAGACAGCGAGGAGGATTTATGAGTTTCAACAGGATGCC 2472
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2473 CAGCACAGGACCTCGGGACCCCAACAGCGCGCGCAACGAGCCTGGGCCACAGTGA 2532
Qy 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2533 GAGCCAGCTCTGTGTGGCCCTCTGGAGGCTTAATCTGTGACACCTTCGGAAGATTGTG 2592
Qy 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2593 GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTCGTCAACACACTCAGCATG 2652
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2653 GGCATCGAATACACAGCAGCGCCGAGGAGCTTACCAAGCCCTAGAAATCAGCAACATC 2712
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800
Db 2713 GTCTTACCAGGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTTGTGTATGTCCTCTTT 2772
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
Db 2773 GGCTACATCAAGAATCCCTTACAAACATCTTCGATGGTGTCAATGTGTCATCAGCGTGG 2832
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2833 GAGATCGTGGGCACAGGGGGGGCGGCTGTGGTGCTCGGACCTTCGCGCTGATGCGT 2892
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2893 GTGCTGAAGCTGGTGGCTTCTGCGCGGCTGTCAGCGGCGAGCTGGTGGTGTCTCATGAAG 2952
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2953 ACCATGGACAAGTGCGCACTTCTCGGCTGCAAGTTTGGCTCTGAGCGGAGTGGGACACCCCTG 3012
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3013 ATCTCTGGGATGCATCTCTTCGGCTGCAAGTTTGGCTCTGAGCGGAGTGGGACACCCCTG 3072
Qy 901 ProAspArgGlyAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3073 CCAGACCGGAAGAAATTTGACTCTCTGCTCGGGCATCGTCACTGTCTTTTTCAGATCTCTG 3132
Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db 3133 ACCAGGAGACTGGAAACAAAGTCCTTACAATGGTATGGCTTCCACGTCGTCCTGGGCG 3192
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960

Db 3193 GCCCTTTATTTTCATTTGCCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTC 3252
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluLeuIleSerLysArgGluAspAlaSerGly 980
Db 3253 GCCATTCTGGTGGAGGGCTTCAGCGGAGGAAATCAGCAACGGGAAGATCGCGAGTGA 3312
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 3313 CAGTTAAGCTGATTCAGCTGCTGCTGCTCCAGGGGGGAGATGCCCAACAAGTCCGAA 3372
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3373 TCAGAGCCGATTTCTTCTCACCCAGCCTGGATGGTATGGGGAAGGAGTGGCTTG 3432
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
Db 3433 GCCTTGGTGTCCCTGGGAGACACCCGAGCTGGGAAGAGCTGCTGCCGCTCTCATC 3492
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3493 ATCCACAGCGCGCCACACCCATGTCGTGCCAAGAGACACAGCAGCGGCTGGCGAG 3552
Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3553 GCGCTGGGCCCTGCGTCGCGCGCACACAGCAGCAGCGGTGCGCAGAGCCTGGGGCGGCC 3612
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3613 CACGAGATGAAGTACACGCCCGCCGCGAGCTCTCCGCACAGCCCTTGAGACCGCTGCA 3672
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3673 AGCAGCTGGACACAGCAGCGGCTCCAGCGGAAACAGCCTCGGCGGTGACCCAGCCTGAAG 3732
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlyGlnGlnSerGln 1140
Db 3733 CGGAAGACCCCAAGTGGAGAGCGGCGTCCCTGTTGTGGGAGAAGGCGCAGAGAGCCAG 3792
Qy 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3793 GATGAAGAGGAGAGCTCAGAAGAGAGCGGCGCCAGCCCTGCGGGCAGTGACCATGGCCAC 3852
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3853 AGGGGTCTCTGGAGCGGAGGCCCAAGAGTTCTTTTGACCTGCCAGACACACTGCGAGTG 3912
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3913 CCAGGGCTGCATCGCACTGCCAGTGGCGAGGGTCTGCTTCTGAGCACCCAGGACTGCAAT 3972
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3973 GGCAAGTGGCTTTCAGGGCGCTTGGCGCGGCCCTGCGGCCCTGATGACCCCCACTGGAT 4032
Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyArgValArgAlaTrpIle 1240
Db 4033 GGGGATGACCGCGATGACGAGGGCAACCTGAGCAAAAGGGAAACGGGTCCGCGCTGGATC 4092
Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 4093 CGAGCCCGCACTCCCTGCTGCTGCTCGAGCGAGACTCCTGCTGAGCCTACATCTTCCCT 4152
Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 4153 CCTCAGTCCAGGTTCGCGCTCTGTCACCGGATCATCCCCACAGATGTTTCGACCAC 4212
Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 4213 GTGGTCTTGTTCATCATCTTCTTAACGTGATCACCATCGCCATGGAGGCGGCCCAAAAT 4272
Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 4273 GACCCCAACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATTTACATCTTTCACCGCAGTC 4332

QY 1321 PheLeuAlaGluMetThrValIysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
| | | | |
Db 4333 TTTCTGGCTGAAATGACAGTGAAGTGTGGCACTGGCTGGTCTTCGGGAGCAGCG 4392
| | | | |
QY 1341 TyrLeuArgSerSerTrpAsnValLeuLeuAspGlyLeuValLeuLeuLeuValIleSerValIleAsp 1360
| | | | |
Db 4393 TACCTGCCGAGCAGTGGAAACGTGTCGACCGGGCTGTGGTGTCTCATCTCCGTCAATCGAC 4452
| | | | |
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
| | | | |
Db 4453 ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTCTG 4512
| | | | |
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
| | | | |
Db 4513 CGGCTGCTGCGGACCTGCGCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTG 4572
| | | | |
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
| | | | |
Db 4573 GTGGTGGAGACGCTGATGCTCTCACTGAACCCATCGGCACATTTGTAGTCATCTGCTGT 4632
| | | | |
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal 1440
| | | | |
Db 4633 GCCTTCTTCATTTTCGGCAATCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTTCGTG 4692
| | | | |
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
| | | | |
Db 4693 TGCCAGGCGGAGGATACCCAGGAACATCACCATAAATCGGACTGTGCCGAGGCCAGTTAC 4752
| | | | |
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
| | | | |
Db 4753 CGGTGGTCCCGCACAGTACAACTTTGACAACCTTGCCAGGCCCTGATGTCCCTGTTT 4812
| | | | |
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
| | | | |
Db 4813 GTTTTGGCTTCAAGATGGTTTGGGTGGACATCATGTAGATGGGCTGATGCTGTGGGC 4872
| | | | |
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
| | | | |
Db 4873 GTGGACGAGCAGCCCATCATGAACACACACCCCTGGATGCTGTACTTCATCTCGTTC 4932
| | | | |
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
| | | | |
Db 4933 CTGCTCAITTTGGCCCTCTTTGCTCCTGAACATGTTTGTGGTGTGGTGGAGAACTTC 4992
| | | | |
QY 1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu 1560
| | | | |
Db 4993 CACAAAGTGTGGCAGCACAGGAGGAAGAGGAGGCCCGCGCGGAGGAAGCGCCTA 5052
| | | | |
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568
| | | | |
Db 5053 CGNAGACTGGAGAAAAGAGAGGAATCTAATGCTGGACGATGTAATTGCTTCGGCAGC 5112
| | | | |
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582
| | | | |
Db 5113 TCAGCCAGCGCTGCGTCAGAAAGCCAGTGCACAACTTACTACTCCGACTACTCCTCCGCTTC 5172
| | | | |
QY 1583 ArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602
| | | | |
Db 5173 CGGCTCCTCGTCCACACTTGTGCACCACTACCTACCTGGACCTCTTCATCACAGGTGTC 5232
| | | | |
QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622
| | | | |
Db 5233 ATCGGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACCAGACGCCCCAGATTCGGAT 5292
| | | | |
QY 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
| | | | |
Db 5293 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTCTTGTCTTGGAGTCAGTTTTTC 5352
| | | | |
QY 1643 LysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeuAspLeu 1662
| | | | |
Db 5353 AAAATTGTGGCCCTTTGGTTTCGTGGTTCTTCCAGGACAGGTGGAACCGAGCTGGACCTG 5412
| | | | |

QY 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682
| | | | |
Db 5413 GCCATTGTGCTGCTTCATCATGGCATCAGCTGGAGAAATCGAGTCAACCCCTCG 5472
| | | | |
QY 1683 LeuProIleAsnProThrIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702
| | | | |
Db 5473 CTGCCCATCAACCCACCATCATCCGATCATGAGGTGCTGCGCATTTGCCGAGTGTG 5532
| | | | |
QY 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
| | | | |
Db 5533 AAGCTGCTGAAGATGGCTGTGGCATCGGGCTGCTGGACACGCTGATGCAGGCCCTG 5592
| | | | |
QY 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaLeu 1742
| | | | |
Db 5593 CCCAGGTGGGAAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGACGCTG 5652
| | | | |
QY 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762
| | | | |
Db 5653 GCGGTGGAGCTCTTTGGAGACTCTGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGGC 5712
| | | | |
QY 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
| | | | |
Db 5713 CGTCATGCCACTTTCGGAACCTTTGGCATGGCTTCTTAACCTCTTCCGAGTCTCCACA 5772
| | | | |
QY 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
| | | | |
Db 5773 GGTGACAATTTGGAATGGCATTTATGAAGACACCCCTCCGGGACTGTGACGAGGAGTCCACC 5832
| | | | |
QY 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
| | | | |
Db 5833 TGCTACAACACGGTCTCTCGCTTACTTGTGTTGTTGCTTCTGCTGACGGCCGAGTTT 5892
| | | | |
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842
| | | | |
Db 5893 GTGCTAGTCAACGTGGTGTATGCCGTGCTGATGAAGCACCTGGAGAGAGCAACAAGAG 5952
| | | | |
QY 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862
| | | | |
Db 5953 GCCAAGGAGGAGCGCGAGCTAGAGCTGAGCTGGAGCTGGAGATGAAGACCTTCAGCCCC 6012
| | | | |
QY 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882
| | | | |
Db 6013 CAGCCCCACTCGCCACTGGGAGGCCCTTCTCTGCTGGGTGAGGGGCCCCGACAGC 6072
| | | | |
QY 1883 ProAspSerProLysProGlyValAlaLeuHisProAlaIleHisAlaArgSerAlaSerHis 1902
| | | | |
Db 6073 CCCGACGCCCCAGCCCTGGGGCTCTGACCCAGCGGCCACGCGGAGATCAGCCCTCCCAC 6132
| | | | |
QY 1903 PheSerLeuGluHisProThr----- 1909
| | | | |
Db 6133 TTTTCCCTGGAGCACCCACCGACAGGCGCTGTTTGACCCATATATCCCTGCTGTATCCAG 6192
| | | | |
QY 1909 ----- 1909
| | | | |
Db 6193 GGCTCCCTGGAGTGGAGCTGAAGCTGATGAGACGAGCTGGCAGGCCAGGGGCCAGCC 6252
| | | | |
QY 1909 ----- 1909
| | | | |
Db 6253 TCTGCTTCCCTTCTGCCCCCAGCCTGGGAGGCTCCGACCCACACATCCCTCTAGCTGAG 6312
| | | | |
QY 1909 ----- 1909
| | | | |
Db 6313 ATGAGGCTCTGCTCTCTGACGTCAGAGATTGTGTCTGAACCGCTCCTGCTCTCTAGCTCTG 6372
| | | | |
QY 1909 ----- 1909
| | | | |
Db 6373 ACGGATGACTTTTGGCTGATGACATGCACACACTTCTTACTTAGTGCCTCGAGAGCAAT 6432
| | | | |
QY 1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929
| | | | |
Db 6433 ATGACGCCCCACCCACCGAGCTGCCAGGACCACTTACTGACTGTGGGAAGTCTGG 6492
| | | | |
QY 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949
| | | | |

```
Db 6493 GTACGCCAAGCACTCTCTGCCAATGACACTACATGTGCGCATGGGAGCACTGCC 6552
Qy 1950 GluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeu 1969
Db 6553 GAGGGCCCTGGGACACAGGGGCTGGGGCTCCCCAAGCTCAGTCAGGCTCCGCTGTG 6612
Qy 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989
Db 6613 TCCGCTTCACTCCAGCCAGCAGATACCACTGCTGAGCTTCCCAAGATGCACCT 6672
Qy 1990 HisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLeuProProPro 2009
Db 6673 CATCTGCTCCAGCCACAGCCGCCCACTGGGGACCATCCCCAACTGCCCCACCA 6732
Qy 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029
Db 6733 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGCGCCAGGAGCAATAAGGACTGACTCC 6792
Qy 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049
Db 6793 TTGGAGCTTCAGGGCTGCGGCAGCCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCC 6852
Qy 2050 ProProLeuAlaArgAlaTyrSerPheTyrGlyGlnSerSerThrGlnAlaGlnHis 2069
Db 6853 CCGCCCTTGGCCCGGCCCTACTCTTTCTGGGGCCAGTCAAGTACCAGGCACAGAGCAGC 6912
Qy 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
Db 6913 TCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGGCCAGGCCA 6972
Qy 2090 GluProAsnTyrGlyGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
Db 6973 GAACCCAACTGGGGCAAGGGCCCTCCAGAGACAGCAAGCAGCTTAGAGTTGGACACGGAG 7032
Qy 2110 LeuSerTyrIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSerPro 2129
Db 7033 CTGAGCTGATTTACAGAGACCTCTCGCCCTTGGCGGCAGAGAGGCCCTCATCCCA 7092
Qy 2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149
Db 7093 CGGGACCTCAGAAAGTGCTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCTACGTCC 7152
Qy 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169
Db 7153 TGGCTGGATCAGCAGAGGAGACACTCTATCGCGCTCAGCTGCTGGACAGCGGCTCCCA 7212
Qy 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyProGlySer 2189
Db 7213 CCCCACCTGGGCACAGCCCTCTAACCTTGGGGCCAGCCTTGGGGGGCTGGGAGC 7272
Qy 2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209
Db 7273 CGGCCCAAGAAAAAATCAGCCCGCTAGTATCACCATTAGACCCCGCCGAGAGCCAAAGT 7332
Qy 2210 ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer 2229
Db 7333 CCTCGGACCCCGCCAGCCCTTGGTATCTGCTCCGGAGAGGGCTCCGTCAGCGACTCC 7392
Qy 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249
Db 7393 AAGATCCCTTGGCCCTTGGCCCCCTTGACAGCATGGCTGCTGCGCCCTCCCAAGAAA 7452
Qy 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7453 GATGTGCTGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGAGCCCC 7503
```

RESULT 4

```
US-10-786-148-120
; Sequence 120, Application US/10786148
; Publication No. US20050191634A1
; GENERAL INFORMATION:
; APPLICANT: LIN, SHIU-RU
```

```
; APPLICANT: WANG, JAW-YUAN
; TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER
; FILE REFERENCE: BHT/3230-85
; CURRENT APPLICATION NUMBER: US/10/786,148
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-148-120

Alignment Scores:
Pred. No.: 0 Length: 7825
Score: 11815.50 Matches: 2264
Percent Similarity: 95.3% Conservative: 1
Best Local Similarity: 95.2% Mismatches: 1
Query Match: 99.3% Indels: 111
DB: 10 Gaps: 2

US-09-611-257A-37 (1-2266) x US-10-786-148-120 (1-7825)
```

```
Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGGACGAGGAGGAGTGGAGCGCGCGGAGAGTGGGACACGCCCGGAGCTTCATG 432
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACAGCACTCTCGGGGCGCGGGCGCGGGGCTCAGCAGAAAAAGGAC 492
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaAlaProValVal 60
Db 493 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCCGCGCTGGCCCCGGTGT 552
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 553 TTCTTCTACTTGAGCCAGACAGCCCGCGCGAGCTGGTGTCTCCGACCGTCTGTAA 612
Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 613 CCTGGTTTGAAGCATCAGCATGTGGTTCATCTTCACTGGCTGACCTGGGCGATG 672
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 673 TTCCGGCCATGCGAGACATCGCTGTGACTCCAGCGCTCGGATCTCTGAGGCTTT 732
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 733 GATGACTTCATCTTTGGCTTCTTTGCCGTGGAGATGGTGTGAAGATGCTGGCTTGG 792
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160
Db 793 ATCTTTGGAAAAAGTTTACCTGGGAGACACTTGGAAACCGGCTTTGACTTTTTCAT 852
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 853 ATCGAGGAGATGCTGAGTACTCGCTGGACCTGCGAGACGTGAGCTTCTCAGCTGT 912
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 913 ACAGTCCGTGTGCTGGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCGCAT 972
Qy 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 973 GTACGCTTCTGCTGGATACGCTGCCCATATGCTGGGCAACGCTCTGCTGCTCTCT 1032
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
Db 1033 GTCTTCTTCTATCTTCGGCATCTGCGCGCTCCAGCTGTGGCGAGGCTGCTTCGAA 1092
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrGln 260
```

Db 1093 TGCCTCTACCTAGAGAAATTCAGCCTCCCTCGAGCGTGGACCTCGAGCGCTATTACCAG 1152
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1153 ACAGAGACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGNACGGCATGGCG 1212
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
Db 1213 TCCCTCAGAAAGCGTCCACGCTGCGGGGAGCGGGCGGTGGCCACCTTGGCGGTCTG 1272
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1273 GACTATGAGCCCTACAAACGCTCCAGCAACACCACTGTGTCACTTGAACACGACTACTAC 1332
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheIleGlyValAlaIleAsnPheAspAsnIle 340
Db 1333 ACCAACTGCTCAGCGGGGAGCACAACTTCAGAGGGCGCCATCACTTTGACAACTT 1392
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPheValAspIleMet 360
Db 1393 GGCTATGCTGTGATCCCATCTTCAGAGTTCATCGCTGGAGGGCTGGGTGACATCATG 1452
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
Db 1453 TACTTTGTGATGGATGCTCATCTTCCTACAAATTCATCTACTTCATCTCCTCATCATC 1512
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400
Db 1513 GTGGGCTCTCTTCATGATCAACTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1572
Qy 401 ThrIleGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1573 ACCAAGCAGCGGAAAGCAGCTGATCGGAGCAGCGTGTGCGGTTCCTGTCCAAACGCC 1632
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuIleTyrLeu 440
Db 1633 AGCACTCTGGGTAGCTTCTCTGAGCCCGCAGCTGCTATGAGAGCTGCTCAAGTACCTG 1692
Qy 441 ValTyrIleLeuArgIleAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1693 GTGTACATCTTCGTAAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGTGTG 1752
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1753 CGGGTGGGTGCTCAGCAGCCAGCAGCCCTCGGGGCGCAGGAGCAGCCAGCCAGCAGC 1812
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1813 AGCTGCTCTCGCTCCACCGCGCTATCCGTCACCACTGGTGGTGCACCAACCAACCCAC 1872
Qy 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1873 CATCACCACTACCACTGGGCAATGGGAGCTCAGGGCCCCCGGGCCAGCCCGGAG 1932
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1933 ATCCAGGACAGGATGCCAATGGGTCCCGCGCTCATGCTGCCACCACTCCGAGCCT 1992
Qy 541 AlaLeuSerGlyAlaProProGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1993 GCGCTCTCGGGGCCCCCTCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATCCGAC 2052
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 2053 TGCCACTTAGACCAAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCATCTGTAGGACATCC 2112
Qy 581 GlyArgThrValGlySerGlyIleValTyrProThrValHisThrSerProProProGlu 600
Db 2113 GGCAGGACTGTGGCAGCGGGAAGGTATCCACCGTGCACACAGCCCTCCACCGGAG 2172
Qy 601 ThrLeuLeuGlyAlaLeuValGluValAlaIleAlaSerSerGlyProProThrLeuThr 620
Db 2173 AGCTGAAAGGAGAGGCACCTAGTAGAGTGGTGTGCTGTGGGCCCCCAACCTCACC 2232

Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2233 AGCCTCAACATCCACCCCGGCCCTACAGCTCCATGCACNAGTCTCTGGAGACACAGAGT 2292
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLeuAlaAspSerGly 660
Db 2293 ACAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGACACAGAGTGA 2352
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2353 GCCTGTGTTCAGACAGCTGCCCTACTGTGCCGGGCGGGGCGAGGAGGTGGAGCTC 2412
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2413 GCCGACCGTGAATGCTCTGACTCAGACAGCGAGGCGAGTTTATGAGTTCACACAGGATGC 2472
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2473 CAGCACGCGACCTCCGGGACCCCGGAGCGGCAACGAGGCTGGGGCCAGATGCA 2532
Qy 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2533 GAGCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCGAAAGATTGTG 2592
Qy 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2593 GACAGCAAGTACTTTGGCCGGGGAATCATGATCGCATCTGGTCAACACACTCAGCATG 2652
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2653 GGCATCGAATACACGAGCAGCGGCGGAGGCTTACCAACGCGCTAGAAATCAGCAACATC 2712
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800
Db 2713 GTCTTCACAGCCTCTTTGGCCTGGAGATGCTGTGAAGCTGCTTGTATGGTCCCTTT 2772
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
Db 2773 GGCTACATCAAGAATCCCTACCAACATCTTCATGGTGTGTCATTCAGCGTGTGG 2832
Qy 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2833 GAGATCGTGGCGCAGCAGCGGGCGGCGCTGCTGGTGTGCTGGAGACCTTCGCGCTGATGCT 2892
Qy 841 ValLeuLysLeuValAlaGlyPheLeuProAlaLeuGlnArgGlnLeuValLeuMetLys 860
Db 2893 GTGCTGAAGCTGGTGGCTTCTCGCGCGCTGACGCGGAGCTGGTGGTCTCATGAAG 2952
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
Db 2953 ACCATGGACAAGTGGCCACCTTCTGCATGCTGCTTATGCTTCTTCATCTTCAGC 3012
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3013 ATCTCTGGGCATGCTCTCTCGGCTGCAAGTTTGGCTCTGAGCGGATGGGGACACCTG 3072
Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3073 CCAGACCGGAAGAATTTTGACTCTCTGGGCCATCGTCACTGTCTTTCAGATCTCTG 3132
Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 3133 ACCCAGGAGGACTGGAAACAAGTCTCTACAAATGGTATGGCTCCACGCTCGTCTGGGCG 3192
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 3193 GCGCTTTATTTCAITTCGCTCATGACCTTCGCAACTACGTCTCTCAATTTGCTGTGTC 3252
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluLysSerLysArgGluAspAlaSerGly 980
Db 3253 GCCATTCTGGTGGAGGGCTTCAGCGCGAGGAAATCAGCAACCGGGAAGATGCGGAGTGA 3312

Qy	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAlaAspAlaAsnLysSerGlu	1000
Db	3313	CAGTTAAGCTGTAATTCAGCTGCCTGTTCGACTCCACGGGGGAGATGCCAACAGTCCGAA	3372
Qy	1001	SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgIysLysCysLeu	1020
Db	3373	TCAGAGCCCGAATTTCTTCTCACCCAGCCTCGATGGTATGGGACAGGAAGTGGCTTG	3432
Qy	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle	1040
Db	3433	GCCTTGTGTGTCCTGGGAGAGACACCGAGACTCGGAAGAGCCTGTTCGCCCTTCATC	3492
Qy	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
Db	3493	ATCCACACGGCCGCCACACCCATGCTGCTGCCAACAGAGCACACAGCGGCTTGGCGGAG	3552
Qy	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
Db	3553	CGCGTGGGCCCTGCGTCCGCGCACACAGCAGCAGCGGCTCGCGAGAGCTTGGGGGGCGC	3612
Qy	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
Db	3613	CACGAGATGAAGTCAACCGCCAGCGCCCGCAGCTCTCCGACACGCCCTCGAGCGCTGCA	3672
Qy	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
Db	3673	AGCAGCTGGACCACGAGCGGCTCCAGCCGGAAACAGCCCTCGGCCGTGCACCCACGCTGAAG	3732
Qy	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGluSerGln	1140
Db	3733	CGGAGAAAGCCCAAGTGGAGAGCGCGGCTCCCTGTTGTGGGAGAAAGCCACAGGAGCCAG	3792
Qy	1141	AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3793	GATGAAGAGGAGAGCTCAGAAGAGAGCGGGCCAGCCCTCGGGCGAGTGACCATGCCAC	3852
Qy	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3853	AGGGGTCCCTGGAGCGGGAGCCCAAGATTCTCTTGACCTGCCACACACACTGCCAGTG	3912
Qy	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3913	CCAGGGCTGCATCGACTGCCAGTGGCGGAGGCTCGCTTCTGAGCACACAGGACTGCAAT	3972
Qy	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3973	GGCAAGTCGGCTTCAGGGCGCTCGGCCGGGCCCTCGCGGCTGATGACCCCCCAGCTGGAT	4032
Qy	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
Db	4033	GGGGNTGACCGCGATGACAGGGGCNACTGAGCAAAAGGGNAACGGGTCCGCGGTGGATC	4092
Qy	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrllePhePro	1260
Db	4093	CGAGCCGACTCCCTGCTGCTGCTCGAGCGAGACTCCTGGTCAGCTACATCTTCCCT	4152
Qy	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	4153	CCTCAGTCAGGTTCCGCGCTCCTGTGTACCGGATCATCACCACAGAATGTTTCGACCAC	4212
Qy	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	4213	GTGGTCTCTGTTCATCATCTTCTTTAACTGCAATCACCATCGCCATGGAGCGCCCAAAAT	4272
Qy	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrllePheThrAlaVal	1320
Db	4273	GACCCCCACAGCGCTGAACGCATCTTCTCGACCCCTCTCCAATTAATCATCTTCCCGCAGTC	4332
Qy	1321	PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla	1340
Db	4333	TTTCTGGCTGAAATGACAGTGAAGGTGTGGCACTGGGCTGGTCTTCGGGGGACGACGGC	4392
Qy	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360

4393	Db	TACCTCGGAGCAGTTGGAACTGCTGGACGGGCTGTGGTGTCTCATCTCCGTCATCGAC	4452
1361	Qy	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
4453	Db	ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATCTGAGGGTGGCTG	4512
1381	Qy	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
4513	Db	CGGCTGTCGGACCCCTCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTG	4572
1401	Qy	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
4573	Db	GTGGTGAGACGCTGATGTCTCCTCAGTGAACCATCGGCAACATGTAGTCACTTCGTCTGT	4632
1421	Qy	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
4633	Db	GCCTTCTTCATCATTTTCGCATCTTGGGGGTGCGACTCTTCAAGAGGAAGTTTTCGTG	4692
1441	Qy	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
4693	Db	TGCCAGGCGGAGGATACCAAGAAACATCACCAATAAATCGGACTGTGCCGAGGCAGTTAC	4752
1461	Qy	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
4753	Db	CGGTGGGTCCGGCACAAAGTAACTTTTGACAACCTTTGGCCAGGCCCTGATGTCCCTGTTT	4812
1481	Qy	ValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
4813	Db	GTTTTGGCTTCCAAAGATGGTTGGTGGACATCATGTACCATGGCTGGATGCTGTGGGC	4872
1501	Qy	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
4873	Db	GTGGACAGCAGCCCATCATGAACCAACACCCCTGGATGTGCTGTACTTCACTCGCTTC	4932
1521	Qy	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
4933	Db	CTGCTCATTTGGGCTTCTTTTGTCTCTGAACATGTTTGTGGGTGTGGTGGAGAACTTC	4992
1541	Qy	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu	1560
4993	Db	CACAAGTGTGGCAGCACACAGGAGGAGAGGAGCCCGCGCGGAGGAGAGACGGCTA	5052
1561	Qy	ArgArgLeuGluLysLysArgArg- - - - -	1568
5053	Db	CGAAGACTGGAGAAAAAGAGAAAGAAATCTAATGCTGGACGATGTAATTGCTCCGGCAGC	5112
1569	Qy	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1582
5113	Db	TCAGCCAGCGCTGCGTCAGAAAGCCAGTCGAAACCTTACTACTCCGACTACTCCCGCTTC	5172
1583	Qy	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
5173	Db	CGGTCTCTCTGTCACCACTTGTGTGCACCAACCACTACTCTGGACCTTCTTCATCACAGGTGC	5232
1603	Qy	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1622
5233	Db	ATCGGCTGAACGTGGTTCACCATGGCCATGGACACTACCAGCAGCCCCAGATTCTGGAT	5292
1623	Qy	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
5293	Db	GAGGCTCTGAAGAGATCTGCAACTACATCTCTCACTGTCTTGTCTTGGAGTCAGTTTTC	5352
1643	Qy	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrPAsnGlnLeuAspLeu	1662
5353	Db	AAACTTGTGGCCTTTGGTTTCGTCGGTCTCTCCAGGACAGTGGAGCCACCGCTGACCTG	5412
1663	Qy	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682
5413	Db	GCCATTGTGCTGCTGCCATCATGGGCATCACGCTGGAGGAAATCGAGGTCAACGCCTCG	5472
1683	Qy	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702

Db 5473 CTGCCCATCAACCCACCACATCATCCGCATCATGAGGGTCTGCGCATTTGCCGAGTGTCTG 5532
Qy LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
Db AAGCTGCTGAAGATGGCTGTGGGCATGGGGGCTGCTGGACACGGTGATGCAGGCCCTG 5592
Qy ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742
Db CCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGCAGCTCTG 5652
Qy GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762
Db GCGGTGGAGCTCTTTGGAGACTGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGGC 5712
Qy ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
Db CGTCATGCCACCTTTCGNACTTTGGCATGGCTTCCTTAACCTCTTCGGAGTCTCCACA 5772
Qy GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
Db GGTGACAATTGGAATGGCATATTGAAGGACACCCCTCCGGACTGTGACAGAGTCCACC 5832
Qy CysThrAsnThrValIleSerProIleThrPheValSerPheValLeuThrAlaGlnPhe 1822
Db TGCTACAACACGGTCACTCGCCTATCTACTTTGTCTCTGCTGCTGACGGCCAGTTTC 5892
Qy ValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842
Db GTGCTAGTCAACGTGTGATCGCCTGTGATGAAGCACCTGGAGGAGACACAAAGGAG 5952
Qy AlalysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862
Db GCCAAGGAGGAGCCGAGCTAGAGCTGAGCTGGAGCTGGAGATGAAGACCTCAGCCCC 6012
Qy GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882
Db CAGCCCCACTGGCCACTGGGACGCCCTTCCTCTGGCTGGGGTGGAGGCCCGACAGC 6072
Qy ProAspSerProLysProGlyValAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902
Db CCGGACGCCCAAGCCTGGGCTCTGCACCAGCGGCCCGCCAGCATCAGCTCCAC 6132
Qy PheSerLeuGluHisProThr----- 1909
Db TTTTCCCTGGAGACACCCACGACGAGCGAGCTGTTTGACCATATCCTGCTGATCCAG 6192
Qy 1909 ----- 1909
Db GGCTCCCTGGAGTGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCCGAGGCCAGCCC 6252
Qy 1909 ----- 1909
Db TCTGCCTTCCCTTCTGCCCCCAGCCTGGAGGCTCCGACCCACAGATCCCTCTAGCTGAG 6312
Qy 1909 ----- 1909
Db ATGGAGGCTCTGCTCTGACGCTCAGAGATTGTGTCTGAACCGTCTGCTCTAGCTCTG 6372
Qy 1909 ----- 1909
Db ACGGATGACTCTTTGCTGATGACATGACACACACTTTACTTTAGTGGCCCTGGAGACAA 6432
Qy MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929
Db ATGACGCCCCCACCAGGAGCTGCAGACCCAGACTTACTGACTGTGCGGAAGTCTGGG 6492
Qy ValSerArgThrHisSerLeuProAsnAspSerThrMetCysArgHisGlySerThrAla 1949
Db GTACGCCGAAGCACTCTCTGCCCAATGACAGCTACATGTGTGGCATGGGAGCACTGCC 6552
Qy GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu 1969
Db GAGGGGCCCCGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGCTCTG 6612

Qy 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989
Db TCCGTTCACTCCAGCCAGCAGATACACAGCTACATCTCTGACGTTCCCAAGATCACCT 6672
Qy HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro 2009
Db CATCTGCTCCAGCCCCACAGCGCCCAACCTTGGGGCACCATCCCCAAATCTGCCCAACA 6732
Qy GlyArgSerProLeuAlaGlnArgProLeuLeuArgGlnAlaAlaIleArgThrAspSer 2029
Db GGACGCTCCCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGAGCAGCAATTAAGACTGCT 6792
Qy LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049
Db TTGGACGTTTCAAGGTCTGGGCAGCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCC 6852
Qy ProProLeuAlaAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHis 2069
Db CCGCCCTGGCGCGGCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGACACAGCAGCAC 6912
Qy SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
Db TCCGCGACGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGCCAGGCCCA 6972
Qy GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
Db GAACCAACTGGGCGCAAGGCCCTCCAGAGACCAAGACAGCTTAGAGTTGGACACGAG 7032
Qy LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlnGluGluProProSerPro 2129
Db CTGAGCTGGATTTTCAGGAGACTCTCTGCCCTCTGGCGCCAGGAGAGCCCCCATCCCA 7092
Qy ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgProThrSer 2149
Db CGGACCTTGAAGAAGTGTCTACAGCGTGAGGCCCCAGAGCTCCAGCGCGGCTACGTC 7152
Qy TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169
Db TGGCTGGATGAGCAGAGGAGACACTCTATCCGCTGCTGCTGGACAGCGGCTCCCAA 7212
Qy ProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySer 2189
Db CCCACCTGGGCACAGACCCCTCTAACCTTGGGGCCAGCCTCTTTGGGGGGCTGGAGC 7272
Qy ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly 2209
Db CGGCCCCAAGAAAAAACACTCAGCCCGCTAGTATCACCATAGACCCCGCCGAGAGCAAGT 7332
Qy ProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAspSer 2229
Db CCTCGACCCCGCCAGCCCTGTTATCTGCTCTCGGAGAGGGCTCCCTCCAGCGACTCC 7392
Qy LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249
Db AAGGATCCCTTGGGCTCTGGCCCCCTGACAGCATGGCTGCTGCTCCCTCCCAAGAAA 7452
Qy AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db GATGTGTGAGTCTCTCGGGTTTATCTCTGACCCAGCAGACCTGGACCCC 7503

RESULT 5

US-10-062-674-2011
; Sequence 2011, Application US/10062674
; Publication No. US2004000559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24

```
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2011
; LENGTH: 8116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US2004000559A1 404183.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ... (8116)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-2011

Alignment Scores:
Pred. No.: 0 Length: 8116
Score: 11353.00 Matches: 2204
Percent Similarity: 93.5% Conservative: 19
Best Local Similarity: 92.7% Mismatches: 20
Query Match: 95.4% Indels: 135
DB: 7 Gaps: 5

US-09-611-257A-37 (1-2266) x US-10-062-674-2011 (1-8116)

QY 1 MetAspGluGluAspSerGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
DB 413 ATGGACGAGGAGGATGGAGCGCGCGGAGGAGTGGGACACGCCCGGAGCTTCATG 472
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40
DB 473 CGGCTCAACAGCTGTGCGGGGCCGGGGCCGGCCGGGGCCGGGGTCAGCAAAAGGAC 532
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 533 CCGGCGAGCGGACTCCGAGCGGAGGGGCTGCCGTACCGCGCGTGGCCCCGGTGT 592
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
DB 593 TTCTTCTACTTGAGCGACACAGCGCGCGGAGCTGGTGTCTCGCACGGTCTGTAAAC 652
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 653 CCTGGTTTGAGCGCATCAGCATGTGGTCATCCTTCTCAACTGGCTGACCTTGGGCATG 712
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 713 TTCCGGCCATGCGAGACATCGCTGTGACTCCAGCGCTGCCGATCCTGCAGGCGCTTT 772
QY 121 AspAspPheIlePheAlaPheAlaValGluMetValLysMetValAlaLeuGly 140
DB 773 GATGACTTCATCTTGTCCCTTCTTTGCCGGTGGAGATGGTGGTGAAGATGGTGGCTTGGGC 832
QY 141 IlePheGlyLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160
DB 833 ATCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACGGCTTGACTTTTTCATCGTC 892
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 893 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAGCTGCAGCTTCTCAGCTGTTCAGG 952
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB 953 ACAGTCCGTGTGTGGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTT 1012
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
DB 1013 GTACAGTTGCTGTGTGATAGCTGCCCATGCTGGGCAACGTCTCTGTCTCTCTTCTTC 1072
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
DB 1073 GTCTTCTTCTATCTTCGCGCATCGTGGCGTCCAGCTGTGGCAGGGTGTCTTCGGAACCGA 1132

241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
1133 TGCCTTCTTACCTGAGATTTTCAGCTCTCCCTGAGCGTGGACCTTATGAGCGCTATACACAG 1192
261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
1193 ACAGAGAACGAGGATGAGAGCCCTTCTATCTGCTCCACGACCGCAACGGCATGCGG 1252
281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProCysGlyLeu 300
1253 TCCTGCAGAGCTGCCACAGCTCGCGGGGACGGGGCGGTGGCCACCTTGGCGGTCTG 1312
301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr 320
1313 GACTATGAGGCTTACACAGCTCCAGCAACACCTGTGTCACTGGAAACGAGTACTAC 1372
321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
1373 ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGGCATCAACTTTGACAACATT 1432
341 GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
1433 GGCTATGCTGGATCGCCATCTTCAGGTTCATCAGCTGGAGGGCTGGGTCCACATCATG 1492
361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
1493 TACTTTGTGATGATGCTCATCTTCTTACAATTTTCATCTACTTCTCTCTCATCATC 1552
381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
1553 GTGGGCTCCTTCTTCTATGATCAACCTGTGCTGGTGGTGAATGGCACGCACTTCTCAGAG 1612
401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
1613 ACCAAGCAGCGGAAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTCTCTGTGCCAACGCC 1672
421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
1673 AGCACCTTGGCTAGCTTCTTCTGAGCCCGGACGCTGCTATGAGGAGCTGCTCAAGTACCTG 1732
441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
1733 GTGTACATCTTCGTAAAGCAGCGCGGAGCTGGCTCAGGCTCTCTCGGGCAGCAGGTGTG 1792
461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
1793 CGGGTTGGGCTGCTCAGCAGCCCGACCCCTCGGGGGCCAGAGACCAGCCGCCACGAGCAGC 1852
481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
1853 AGCTGCTCTCGCTCCACCGCCGCTATCCGTCACCACTTGGTGNNNNNNNNNNNNN 1912
501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
1913 NNNNNNNNNNTACACCTGGGCAATGGGAGCGCTCAGGGCCCCCGGGCCAGCCCGGAG 1972
521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
1973 ATCCAGGACAGGAGTGGCAATGGGTCCCGCGGCTCATCTGCCACACCCCTCGACGCT 2032
541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
2033 GCCCTCTCGGGGCCCTCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2092
561 CysHisLeuGluProValArgCysGlnAlaProProProProProProProProProPro 580
2093 TGCCACTAGAGCCAGTCCGCTGCCAGGGCGCCCTCCAGAGTCCCATCTGAGGCGATCC 2152
581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
2153 GGAGGACTGTGGGACGCGGAGGTGTATCCACCGTGCACACAGCCCTCCACCGGAG 2212
601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
```

Db 2213 |||||ACGCTGAAGAGGAGCGCACTAGTAGAGGTGGCTGCGAGCTCTGGGCCCCCAACCCCTCACC 2272
Qy 621 |||||SerLeuAniLeProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2273 AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAGT 2332
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2333 ACAGGTGCTGCGCAAAAGCTCTTTGCAAGATCTCCAGCCCTTGCTTCAAAAGCAGACAGTGA 2392
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2393 GCCTGTGTCCAGACAGCTGCCCTTACTGTGCCGGCGCGGGCAGGGAGGTGGAGCTC 2452
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2453 GCGGACCGTGAATGCCCTGACTCAGACAGCGAGGCGATTATGAGTTTACACAGGATGCC 2512
Qy 701 GlnHisSerAspLeuArgAspProHisSerArg-ArgGlnArgSerLeuGlyProAspAl 720
Db 2513 CAGCACGCGAACTTCGGGAAACCCCAAAAGCGGGGGCAACGGAGCCCTGGGCCACAGATGC 2572
Qy 720 aGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVa 740
Db 2573 AGAGCCCAAGCTCTGTGCTGGCCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGT 2632
Qy 740 LasSerLysTyrPheGlyArgGlyLeuMetIleAlaIleLeuValAsnThrLeuSerMe 760
Db 2633 GGACAGCAAGTACTTTGGCCGGGGAATCATGATCCCATCTCTGGTCAACACACTCAGCAT 2692
Qy 760 tGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIl 780
Db 2693 GGGCATCGAATACCACGAGCAGCGCCGAGGAGCTTACCACGCCCTAGAAATCAGCAACAT 2752
Qy 780 eValPheThrSerLeuPheAlaLeuLeuMetLeuLysLeuLeuValTyrGlyProPh 800
Db 2753 CGTCTTCCACAGCCTCTTTGGCCCTGGAGATGCTGTGAAGCTGCTTGTATGTGTCCTT 2812
Qy 800 eGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTr 820
Db 2813 TGCTTACATCAAGAAATCTCTACAACTTCTCGATGGTGTCAATGGTCAACAGCGGTGTG 2872
Qy 820 pGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetAr 840
Db 2873 GGAGATCGTGGCCACGAGCGGGGGCGGCTGTGCGTGTGCGGACCTTCCGGCTGATCG 2932
Qy 840 gValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValLeuMetLys 860
Db 2933 TGTGCTGAAGCTGTGTGCGCTTCTCCCGCGCTGCAGCGGAGCTGTGTGCTCATGAA 2992
Qy 860 sThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSe 880
Db 2993 GACCATGACAAACGTGGCCACCTTCTGATGCTGCTTATGCTTCTTCACTTCACTTCAG 3052
Qy 880 rIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLe 900
Db 3053 CATCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCT 3112
Qy 900 uProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLe 920
Db 3113 GCCACCGGAAGAAATTTTGACTCTCTGCTGGGCCATCGTCACTGTCTTTCAGATCCT 3172
Qy 920 uThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAl 940
Db 3173 GACCAGGAGGACTGGAAACAAAGTCTCTACAAATGGTATGGCCTCCACGTCTCTGGGC 3232
Qy 940 aAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 3233 GGCCCTTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGT 3292
Qy 960 lAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGl 980
|||||

Db 3293 CGCCATTCTGTGAGGGCTTTCAGAGCGGAG- 3323
Qy 980 yGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGl 1000
Db 3324 -----GGAGATGCCAACAGTCCGA 3343
Qy 1000 uSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLe 1020
Db 3344 ATCAGAGCCCGATTCTTCTCACCGCTGGATGGTGTATGGGACAGGAAGTGTCTT 3403
Qy 1020 uAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIl 1040
Db 3404 GGCCTTGTGTCTCTGGAGAGCACCCCGAGCTGCGAAGAGCCTGCTGCGCCCTCTCAT 3463
Qy 1040 eIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1060
Db 3464 CATCCACAGCGCCGCACACCCATGTGCTGCCCAAGAGCACACAGCGGCCCTGGCGGA 3523
Qy 1060 uAlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaAl 1080
Db 3524 GCGCTGGGCCCTGCTGCGCGCACCCAGCAGCGGGTCCGACAGAGCCTGGGGCGGC 3583
Qy 1080 aHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAl 1100
Db 3584 CCACGAGATGAAGTCAACGCCCGCGCCGAGCTCTCCGACAGCCTGGAGCGCTGC 3643
Qy 1100 aSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3644 AAGCAGCTGGACACAGCAGCGCTCAGCCGGAACAGCTCGGCCGTGCACCCAGCCTGAA 3703
Qy 1120 sArgArgSerProSerGlyGluArgArgSerLeuSerGlyGlyGlnGluSerGl 1140
Db 3704 GCGAGAAGCCCAAGTGGAGAGCGCGTCCCTGTTGTCGGAGAAGCCAGGAGGCA 3763
Qy 1140 nAspGluGluLeuSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHi 1160
Db 3764 GGATGAAGAGAGAGCTCAGAAAGAGGAGCGGCCAGCCTCGCGGACGTGACCATCGCCA 3823
Qy 1160 sArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVa 1180
Db 3824 CAGGGGTCTCTGGAGCGGGAGGCCAAGAGTTCCTTTGACCTGCAGACACACACTGCAGGT 3883
Qy 1180 lProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAs 1200
Db 3884 GCCAGGGCTGCATCGCACTGCGCAGTGGCGGAGGGTCTGCTCTGAGCACACAGGACTGCAA 3943
Qy 1200 nGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAs 1220
Db 3944 TGGCAAGTCGGCTTTCAGGGCGCCTGGCCCGGGCCTGCGGCTGATGACCCCCACTGGA 4003
Qy 1220 pGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIl 1240
Db 4004 TGGGGATGACCCCATGACGAGGGCACTCAGCAAGGGGNAACGGGTCCGCGCTGAT 4063
Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260
Db 4064 CCGAGCCGACTCTGCTGCTGCTCGAGGAGACTCTCTGGTCAGCCTACATCTTCTCC 4123
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 4124 TCCTCAGTCCAGGTTCGCGCTCTGCTGTCACCGGATCATACCCCAAGATGTTTCAGCCA 4183
Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIl 1300
Db 4184 CGTGGTCTTGTCTATCATCTTCTTNACTGATCATCATCGCCATCGGAGCGGCCCAAAAT 4243
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 4244 TGACCCCCACAGCGCTGAACGCATCTTCTGACCTCTCCAATTTACATCTTTCACGCGAGT 4303
Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
Db 4304 CTTTCTGGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGTCTTTCGGGAGCAGGC 4363


```
Db 6524 GGCTGGGGGCTCCCAAAAGCTCAGTCAGGCTCCGCTTGTGCGTTCACTCCAGCAGCA 6583
Qy 1977 AspThrSerTrpIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSer 1996
Db 6584 GATACCACTACATCTCTGACGCTTCCCAAGATGACCACTCATCTGCTCCAGCCCAACAGC 6643
Qy 1997 AlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGln 2016
Db 6644 GCGCCAACTGGGCACTCCCAAACTGCCCCCACCAGGAGCTCCCTTTGGCTCAG 6703
Qy 2017 ArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGly 2036
Db 6704 AGGCACCTCAGCGCCAGCGAGCAATAAGGACTGACTCTTGGAGCGTTTCAGGGCTGGGC 6763
Qy 2037 Ser-ArgGlnAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTy 2056
Db 6764 AGCCCGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCCCGCCCTTGGCCCGGCCCTA 6823
Qy 2056 rSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysI 2076
Db 6824 CTCCTTCTGGGGCCAGTCAAGTACCAGGCACAGCAGCACTCCCGCACACAGAT 6883
Qy 2076 eSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysG 2096
Db 6884 CTCCAAGCACATGACCCCGCAGCCCTTGCACAGCCAGCCAGAACCAACTGGGGCAAGGG 6943
Qy 2096 yProProGlnThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAs 2116
Db 6944 CCCTCCAGAGACCAAGACAGCTTAGAGTTGGACACGGAGCTGAGCTGGATTTTCAGGAGA 7003
Qy 2116 pLeuLeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTy 2136
Db 7004 CCTCTGCCCCCTGGCGGCCAGGAGGCCCCCATCCCCACGGACCTGAAGAAGTGCTA 7063
Qy 2136 rSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgAr 2156
Db 7064 CAGCTGGAGGCCAGAGCTGCCAGCGCCGCTACGTCCTGGCTGGATGAGCAGAGGAG 7123
Qy 2156 gHisSerIleAlaValSerCysLeuAspSerGly-SerGlnProHisLeuGlyThrAspP 2176
Db 7124 ACCTCTATCGCCGTCAGCTCGCTGGACAGCGGCTTCCCAACCCCACTGGGGCACAGACC 7183
Qy 2176 roSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuS 2196
Db 7184 CCTCTAACCTTGGGGGCCAGCTCTTGGGGGCCCTGGGAGCGCGCCCAAGAAACTCA 7243
Qy 2196 erProProSerIleThrIle-AspProProGluSerGlnGlyProArgThrProProSer 2215
Db 7244 GCGCGCCTAGTATCACCAATTAGACCCCCCGGAGAGCCAAAGTCTCGGACCCCGCCAGC 7303
Qy 2216 Pro-GlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSe 2235
Db 7304 CCTGGGNTTCGCTTCGGAGAGGGCTCCCTGCGAGCGACTCCAAGGATCCCTTGGCCCTC 7363
Qy 2235 rGlyProPro--AspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeu 2254
Db 7364 TGGGCCCCCTGAACAGCATGGCTGCTCGCCCTCCCAAGAAAGATGCTGCTGAGTCTC 7423
Qy 2255 SerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7424 TCCGGTTTATCTCTGACCCAGCAGACCTCGGACCCC 7459
```

RESULT 6
US-09-383-894-1
; Sequence 1, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26

```
; EARLIER APPLICATION NUMBER: US 60/098,004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399  
; EARLIER FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 7129  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-383-894-1  
  
Alignment Scores:  
Pred. No.: 0 Length: 7129  
Score: 11111.00 Matches: 2135  
Percent Similarity: 94.8% Conservative: 35  
Best Local Similarity: 93.3% Mismatches: 95  
Query Match: 93.3% Indels: 24  
DB: 3 Gaps: 5  
  
US-09-611-257A-37 (1-2266) x US-09-383-894-1 (1-7129)  
  
Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20  
Db 1 ATGGACGAGGAGGAGATGGAGCGGCGCCGAGAGTCGGACAGCCCGGTAGCTTCAG 60  
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyValArgProGlyProGlySerAlaGluLysAsp 40  
Db 61 CAGCTCAACGACCTGTCCGGGCGCGGGCGCGGCGGGGTCACCGGAAAGGAC 120  
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60  
Db 121 CCGGGCAGCGGAGCTCCGAGCGGAGGGGTGCGGTACCCGCGCTAGCCCGGTGTT 180  
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
Db 181 TTCCTTACTTGAACCCAGGACAGCGCGCGGAGTGGTGTCTCCGACCGTCTGTAAAC 240  
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCAACTGTGTGACTCTGGGTATG 300  
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 301 TTCAGGCGGTGTAGGACATTCCTGTGACTCCAGCGCTCCGCGATCCTGCAGGCTTC 360  
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
Db 361 GATGACTTCATCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCTTTTGGCT 420  
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160  
Db 421 ATCTTTGGGAAGAAATGTTACTTGGGAGACACTTTGGAAACCGGCTTGACTTTTCAATTGTC 480  
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 481 ATTCCAGGATGCTGGAGTATTTCGTGACCTGAGAACAGTCAGCTTCTCCGAGTCAGG 540  
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCGTGTGCTGGACCGCTCAGGGCCCAATAACCGGGTGGCCAGCATCGGCAATCTC 600  
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGCTTCTGCTGCTCTGTTTCTTC 660  
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCCTTTTTCATCTTTTGGCATCGTGGGGGTCCAGCTGTGGGCGAGGACTGCTTCGCAACCGA 720  
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrCln 260  
Db 721 TGCTTCCTCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780
```

QY 261 ThrGluAenGluAspGluSerProPheIleCysSerGlnProArgGluAasnGlyMetArg 280
DB 781 ACAGAGAATAGGACGAGAGCCCTTCTATCTGCTCTCAGCCCTCGGAGAAATGGCATGAGA 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
DB 841 TCCCTCAGAGAGTGTCCACACTGGCTGGGGAAGCGGTGGGCCACCCCTCGCAGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
DB 901 GACTATGAGACCTATAACAGTTCAGACAACACCACTGTGTCAACTGGAAACCACTACTAT 960
QY 321 ThrAsnCysSerAlaGlyCyluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
DB 961 ACCAACTGCTCTCGCGGGGAGCACAAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
DB 1021 GGCTATGCTGGATCGCCATCTTCAGAGTTCATCACTGAGGGCTGGGTGCACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
DB 1081 TACTTCGTAATGAGCGCTCACTCTCTACAACTTCATCTACTTCTTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400
DB 1141 GTGGGCTCCTCTCATGATCAACCTGTGCTGGTGGTGAATGTCACGCACTTCCTCCGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
DB 1201 ACCAAACAGCGGAGAGTCAGCTGATGCGGGAGCAGCGGTATACGATTCTGTCCAATGCT 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
DB 1261 AGCACCTTGCAAGCTTCTCTGAGCCAGGACAGCTGCTATGAGAGCTACTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaIleVal 460
DB 1321 GTGTACATCTCCGAAAAGCAGCCGAGGCTGGGCCAGGCTCTAGGGCTATAGGCGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
DB 1381 CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGACAGAGCCCGCCAGTGGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
DB 1441 AGCTGCACCTCGCTCACACCGTCTGCTGTCTGCCACCACTGGTCCACCACCATCACCAC 1500
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
DB 1501 CACCATCACCACTACCACTGGGTAAATGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
DB 1561 ATCCAGGACAGGATGCCAATGGGTCTCCCGGCTCATCTGCTACCAACCCCTCTACACC 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB 1621 ACTCCCTCTGGGGCCCTCCGAGGGGTGGCGAGTCTGTACACAGCTTCTACCATGTGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
DB 1681 TGCCACTTGGAGCCAGTGTGCCAGGCAACCCCTCCAGATGCCCATCGGAGGCGATCT 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
DB 1741 GGTAGACTGTGGTGTAGTGGAGAGGTATCCCCACTGTGCATACAGGCCCTCCACCAGAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
DB 1801 ATACTAGAGGATAAAGCACTAGTGGAGGTGGCCCCCAGGCCCTGGGGCCCCCACCCTCACC 1860

QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
DB 1861 AGCTTCAACATCCCACTGGGCCCTTTCAGCTCCATGCAAGCTCCTCGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysSerLeuLysAlaAspSerGly 660
DB 1921 ACGGGAGCTGCCATAGCTCTGCAAAATCTCCAGCCCTTCTCCTCAAGCAGACAGTGGGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
DB 1981 GCCTCGGGCGGAGCAGTTGTCTCTACTGTGCCCGGACAGGAGCAGGAGACGACAGTCC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
DB 2041 GCTGACCATGTCATGCTGCTGACTCAGACAGCAGGCTGTGTATGATTTCCACAGAGACGCT 2100
QY 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719
DB 2101 CAGCACAGTACCTCCGGGATCCCCACAGCGCGGCGACAGCGGAGCCTGGGCCACAGAT 2160
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
DB 2161 CGAGAGCCTAGTCTGTGCTGCTGCTTCTGGAGGCTGATCTGTACACATTCGGAAGATC 2220
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
DB 2221 GTAGATAGCAAAATACTTTGGCCGGGAATCATGATCGCCATCCTGCTCAATACACTCAGC 2280
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
DB 2281 ATGGCATCGATACACAGCAGCCCGAGGAGCTCACCAAGCCCTGGAAATCAGCAAC 2340
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
DB 2341 ATCGCTTTCACACAGCCTCTTCGCCCTGGAGATGCTGCTGAAACTCTGTCTACCGTCCC 2400
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
DB 2401 TTTGCTACATTAAGAAATCCCTACAAACATCTTTGATGTTGTTGTTGTTGTTGTTGTTG 2460
QY 820 TrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
DB 2461 TGGGAGATTGGGCCAGCAGGAGGTGGCCTGTCCGTGCTCGGACCTTCGCCCTGTATG 2520
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
DB 2521 CGGGTGTCAAAGCTGGTGGCTTCTCGCGGCGCTCGCAGCGCCAGCTCGTGTGTTCTATG 2580
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879
DB 2581 AAGACCATGGACACAGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2640
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
DB 2641 AGCATCTTGGGCATCATCTCTTGTGTCAAAGTTCCGATCTCGCATCTGAAACGGATGGGACAG 2700
QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
DB 2701 TTTGCCAGACCGGAAGAAATTCGACTCCCTGCTGGGCCATCGTCATCTCTTTTCAGATT 2760
QY 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939
DB 2761 CTGACTCAGGAACACTGGNAATAGTCTCTACACGGCATGGCCCTCCACATCGTCTTGG 2820
QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
DB 2821 GCTGCTCTTACTTCTATCGCCCTCATGCTTTTGGCAACTATGCTGCTCTTTAACTCTGCTG 2880
QY 960 ValAlaIleLeuValIleGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer 979
DB 2881 GTGGCCATCTTGTGGAAGGATTTCAGGCGAGAGAAATCGGCAAAACGGGAAGATGCGAGT 2940
QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999

Db	2941	GGACAGTTAAGCTGTTAAGCTGCTGCTCAACTCTCAGGGGGAGATGCCACCAAGTCT	3000	Db	4021	CAGGCTACCTGCGCAGCAGCTGGAATGTGCTGGACGGCTTCTGCTGCTCATCTCCGTC	4080
Qy	1000	GluSerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019	Qy	1359	lleAspilleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	3001	GAGTCAGACCTGATTTCTTTTCGCCAGTGTGGATGGTGTGGGACGAAAGAGCGC	3060	Db	4081	ATCGACATCTTGCTCTCATGCTCCGACAGCGGCACCAAGATCTTTGGCATGCTGAGG	4140
Qy	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039	Qy	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	3061	TTGGCCCTGGTCTTGGGAAACACGCGGAACACGAAAGAGCCTTTTGCACCCCTC	3120	Db	4141	GTGCTGCGCTGCTCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4200
Qy	1040	llelleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059	Qy	1399	LysLeuValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValIle	1418
Db	3121	ATCATCCATACCGCTCGCACCAATGTCTACTACCCCAAGAGCTCCAGCAGGTGGGG	3180	Db	4201	AAGCTGGGTGGTAGAGACTCTGATGTCATCCCTCAAAACCCATTTGGCAACATTTGGTCAT	4260
Qy	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAla	1079	Qy	1419	CysCysAlaPhePheIlelePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	3181	GAAGCACTGGGCTCTGGCTCTCGAGTACAGTAGCAGTGGGTCCGCTGAGGCTGGAGCT	3240	Db	4261	TGCTGTGCTTCTTCTCATCATTTTGGAAATCTTCGGGTGCAGCTCTTCAAGGGAAGTTC	4320
Qy	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098	Qy	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	3241	GCCACCATGAGATGAATCTCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGGAGT	3300	Db	4321	TTCTGTGTGTGAGGTGAGACACACAGGAACATCACTAACAAATCCGACTCGCTGAGGCC	4380
Qy	1099	AlaAlaSerSerTrpThrSerArgArgSerArgAsnSerLeuGlyArgAlaProSer	1118	Qy	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	3301	CGCGCAAGCAGCTGGACACGACGAGCGCTCCAGCAGGAACAGGCTGGCGCGGCCACAGC	3360	Db	4381	AGCTACCATGGTCCGCGCACAAAGTACAACATTTGACAACTTGGCCAGGCTCTGATGTCC	4440
Qy	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu	1138	Qy	1479	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498
Db	3361	CTAAAGCGAGGAGCGCGGAGCGGAGGAGTCCCTGCTGTCTGGAGGGGCCAGGAG	3420	Db	4441	CTGTTTGTGCTGGCTCCAGGATGGTTGGGTGTGACATCATGTATGATGGGTGATGCT	4500
Qy	1139	SerGlnAspGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis	1158	Qy	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
Db	3421	AGTCAGGATGAGAGGAAATTCAGAGAGAGGACCGCGCCAGCCAGCAGCAGTCAACAT	3480	Db	4501	GTGGGTGGTATCAGCAGCCCATCATGAACCAACACCCCTGGATGCTGTATCTCATC	4560
Qy	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178	Qy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	3481	CGCCACAGGGGTTCCTTGGAACTGAGGCAAGAGTTCCTTTGACCTGCTGACACTCTG	3540	Db	4561	TCCTTCCTCCTCATCGTGGCTTCTTTGTCTGGAACATGTTGTGGCTGTGGTGGAG	4620
Qy	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198	Qy	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys	1558
Db	3541	CAGGTGCGGGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCTCTGAGCACCACAGAC	3600	Db	4621	AACTTCCATAGTGCAGACAGCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	4680
Qy	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProPro	1218	Qy	1559	ArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	3601	TGTAATGGCAAGTCGGCTTCAGGGCTTTGGCCCGCAGCCCTCAGGACTGATGACCCCAA	3660	Db	4681	CGACTACGAGGCTGAGAAAAAGAGAGGAATCTAATGTTGGACGATGTAATTTGCTTC	4740
Qy	1219	LeuAspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238	Qy	1569	-----LysAlaGlnCysLysLysProTyrTyrSerAspTyrSer	1580
Db	3661	CTGGATGGGATGATGACAAATGATGAGGGAATCTGAGCAAAAGGGGAACGCATACAAGC	3720	Db	4741	GGCAGCTCAGCCAGCGCTCGCTCAGAACCCAGTCAAGCCCTACTACTCTGACTACTCG	4800
Qy	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle	1258	Qy	1581	ArgPheArgLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1600
Db	3721	TGGTCAGATCCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3780	Db	4801	AGATTCCGGCTCCTTGTCCACCACCTGTGTACCCAGCCACTACTGGACCTCTTCTACT	4860
Qy	1259	PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278	Qy	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
Db	3781	TTTCTCTCTCAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3840	Db	4861	GGTGTCTCGGCTGAACTGGTGTCTATGGCATGGCAACATTAACAGCAGGCCAGATC	4920
Qy	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298	Qy	1621	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer	1640
Db	3841	GACCATGTGCTGCTCATCATCTTCTCAACTGTATCACCATCGCTATGGAGGCGCCC	3900	Db	4921	CTGGACAGGGCTCGAAGATCTGCAATTTACATCTTTTACCGTCATCTTTGTCTTTAGTCA	4980
Qy	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318	Qy	1641	ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu	1660
Db	3901	AAAAATGACCCACAGCGCTGAGCGCATCTTCTGACCCCTCTCAAACTACATCTTCAG	3960	Db	4981	GTTTTCAAACTTGTGGCTTTGGCTTTCGCGTTTCTCCAGGACAGGTGGAAACGAGCTG	5040
Qy	1319	AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGlu	1338	Qy	1661	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1680
Db	3961	GCAGTCTTCTAGCTGAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGGTGGGAG	4020	Db	5041	GACCTGGCTATTGTGCTTCTGCTCATCATGGGCATCACACTGGAGAGATTGAGGTCAAT	5100
Qy	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358	Qy	1681	AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
Db		GGACAGTTAAGCTGTTAAGCTGCTGCTCAACTCTCAGGGGGAGATGCCACCAAGTCT	3000	Db	5101	GCCTGCTGCCCATCAACCCCATCATCGTATCATGAGGGTCTCCGCAATTGCTTCTCGA	5160

```
QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuLeuAspThrValMetGln 1720
Db 5161 GTTCTGAAGCTGTTGAAGATGCTGTGGGCATGCGGGCACTCTGGACACGGTGTATGCAG 5220
QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
Db 5221 GCCCTGCCCCAGGTGGGAACCTGGGACTCTCTTCATGTTATTGTTTTTCATCTTTGCA 5280
QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
Db 5281 GCTCTGGGGCTGGAGCTCTTTGGAGACCTGGAGTGTGATGACACACACCCCTTTGTGAGGCG 5340
QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5341 TTGGGTGCGCATGCCACCTTTAGGAACCTTTGGTATGGCCCTTTCTGACCCCTCTTCGAGTGC 5400
QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
Db 5401 TCCACTGGTGACAACCTGGAACTGTTATTATGAAGGACACCCCTCCGGGACTGTGACCAAGGAG 5460
QY 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820
Db 5461 TCCACCTGCTACACACTGTCATCTCCCTATCTACTTTGTGTCTGTCTGTGACGGCC 5520
QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840
Db 5521 CAGTTTGTGTGTCACCTGCTCATAGCTGTGCTGATGAAGCACCTCGGAAGAAAGCAAC 5580
QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeu 1860
Db 5581 AAGAGGCCAAGAGAGAGCCGAGCTTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTC 5640
QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
Db 5641 AGCCCGCAGCCCCACTCCCGCTGGGCAGCCCCCTCTCTGGCCCGGGTGGAGGGTGC 5700
QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaHisAlaArgSerAla 1900
Db 5701 AACAGTCTCTGACAGCCCTAAGCCTGGGGCTCCACACACACTGCCCCACATTGGAGCAGCC 5760
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918
Db 5761 TCGGGCTTCTCCCTTGAGACACCCACGATGTTACCCACCCCGAGAGGTGCAGTCCCC 5820
QY 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db 5821 CTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGCACTCTCTGCC 5880
QY 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957
Db 5881 AATGACAGCTACATGTGCCGAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGC 5940
QY 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db 5941 TGGGGCTCCCCAAGCCCAAGTCAGGCTCATCTTGTTCGTTCACTCCCAACACGAGCAGAC 6000
QY 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997
Db 6001 ACCAGCTGCATCTACAGCTTCCCAAGATGTGCACTATCTGTCTCCAGCCCTCATGGGGCC 6060
QY 1998 ProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2017
Db 6061 CCCACTGGGGGCCCATCTCCCTAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGG 6120
QY 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037
Db 6121 CCTCTCAGGGCCGAGGAGCAATAAGACTGACTCTCCCTGATGTGAGGGCCCTGGGTAGC 6180
QY 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db 6181 CGGGAGACCTGTTGTGAGAGGTGAGTGGGGCCCTCTCGCCCTCTGTGACCCCGTCTCATCC 6240
```

```
QY 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077
Db 6241 TTCTGGGCGGGTCCAGCATCCAGGTGAGCAGCGCTTCGGCATCCAGAGCAAGTCTCC 6300
QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 6301 AAGCACATCCGGCTCCAGCCCTTGGCCAGGCTTGGAAACCCAGCTGGGCCAAGGACCT 6360
QY 2098 ProGluThrArgSerSerLeuLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 6361 CCAGAGACCAGAAGCAGCTTAGAGCTGACACGGAGCTGAGTGGATTTTCAGGAGACCTC 6420
QY 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSer 2137
Db 6421 CTT----CCAGCAGCCAGGAAGACCCCTGTCTCCACCGGACCTGAAGAAGTGTCTACAGT 6477
QY 2138 ValGluAlaGlnSerCysGlnArgProThrSerTrpLeuAspGluGlnArgArgHis 2157
Db 6478 GTAGAGACCAGAGCTGCAGCGCGCAGGCTGGGTCTCTGGCTAGATGAACAGCGGAGACAC 6537
QY 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177
Db 6538 TCATTTGCTGTGCTGCTGTGACACGCGCTCCCAACCCCGCTATGTCCAAGCCCTCA 6597
QY 2178 AsnLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerPro 2197
Db 6598 AGCCTCGGGGGCAACCTCTTGGGGTCTTGGAGCGGCTTAAGAAAAAATCAGCCCCA 6657
QY 2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217
Db 6658 CCAGTATCTCTATAGACCCCGGAGAGCAGGGCTCTCGGCCCCCATGTCAGTCTCTGGT 6717
QY 2218 IleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237
Db 6718 GTCTGCTCAGAGGAGCGCGCGCTTAAAGATCCCTCGGTCTCCAGCCCC 6777
QY 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257
Db 6778 CTTGACAGCAGCGCTGCCTCACCTCCCAAGAAAGACACGCTGAGTCTCTCTGTTTG 6837
QY 2258 SerSerAspProAlaAspLeuAspPro 2266
Db 6838 TCTTCTGACCAACACATGAGCCCC 6864
RESULT 7
US-09-383-894-3
; Sequence 3, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004, 00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7285
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-3
Alignment Scores:
Pred. No.: 0 Length: 7285
Score: 11111.00 Matches: 2135
Percent Similarity: 94.8% Conservative: 35
Best Local Similarity: 93.3% Mismatches: 95
Query Match: 93.3% Indels: 24
DB: 3 Gaps: 5
```

US-09-611-257A-37 (1-2266) x US-09-383-894-3 (1-7285)

Qy 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 157 ATGGACGAGGAGGATGGAGCGGGCGCGAGGAGTGGGAGACGCCCGCTAGCTTCAGC 216

Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 217 CAGCTCAACAGCTGTCTCGGGGCGGGGCGCGAGCGGGGCTCGACGGAAGGAC 276

Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 277 CCGGGCAGCGCGAGCTCCAGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 336

Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 337 TTCCTTACTTGAGCCAGACAGCGCGCGGAGCTGGTGTCTCGACAGGTCGTGTAAC 396

Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 397 CCGTGGTTCGAGCGAGTCAGTATGTGTGTCACTTCTCAACTGTGTGACTCTGGGTATG 456

Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 457 TTCAGGCGGTGTGAGGACATTGCCCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTC 516

Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 517 GATGACTTCATCTTTGCCCTCTTTGCTGTGGAATGGTGGTGAAGATGGTGGCCCTTGGGC 576

Qy 141 IlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 577 ATCTTTGGAGAAATGTTACCTGGGAGACACTTGGAAACCGCTTGACTTTTTTCATTGTC 636

Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 637 ATTGAGGGATCTGGAGTATTTCGTGGACCTGCAAGACGTCAGCTTCTCGCAGTCAGG 696

Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 697 ACAGTCCGTGTGTCGACCGCTCAGGGCCATTACCGGGTGCCGAGCATGGGCATCTTC 756

Qy 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 757 GTCACTTACTGCTGGACACCTTGCTATGCTGGGCAACGCTCTGCTGCTGTTCTTC 816

Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 817 GTCTTTTTCATCTTTGGCATCTGGGCGCTCCAGCTGTGGGCAAGGACTGCTTCGCAACCGA 876

Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 877 TGTCTTCTCCCGAGAACTTACGCTCCCTCGAGCGTGAGCCTGGAGCTTATTACCAG 936

Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 937 ACAGAGATGAGACAGAGAGCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGA 996

Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 997 TCCTCAGAGAGTGTCCACACTGCTGGGGAAGCGGTGTGGGCCACCCCTGCAGTCTG 1056

Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1057 GACTATGAGACCTATAACAGTTTCCAGCAACACCACTGTGTCACTGGAACCACTACTAT 1116

Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyValAlaIleAsnPheAspAsnIle 340
Db 1117 ACCAACTGCTCTCGGGCGAGCACAAACCCCTTCAAGGGCCCATCAACTTTGACAACTT 1176

Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPheValAspIleMet 360
Db 1177 GGCTATGCTGGATCGCCATCTTCAGGTTCATCACACTGGAGGCTGGGTTCGACATCATG 1236

Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1237 TACTTGGTANTGGACGCTCACTCTTACAACTTCATCTACTTCTTCTTCATCATC 1296

Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1297 GTGGGCTCTCTTTCATGATCAACCTGTGCTGTGGTGGTATGCCACGCGAGTCTCCGAG 1356

Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1357 ACCAAACAGCGGAGAGTATGATGCGGAGCAGCGGTACGATTCCTGTCCAATGCT 1416

Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1417 AGCACCTTGGCNAAGCTTCTCTGAGCCAGGAGCTGCTATGAGGAGCTACTCAAGTACCTG 1476

Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1477 GTGTACATCTCCGAAAGCAGCCGAAAGGCTGGCCAGGCTCTTAGGGCTATAGGCGTG 1536

Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1537 CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGAGGAGCCCGCCAGTGGC 1596

Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHis 500
Db 1597 AGCTGCATCTGCTACACCGTCTGCTGTCTGTCCACCACTGGTCCACCACTCATCCAC 1656

Qy 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1657 CACCATCACCACTACCACTGGGTAAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAG 1716

Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1717 ATCCAGGACAGGATGCAATGGGTCTCGCGGCTCATGCTACCAACCCCTCACCCC 1776

Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1777 ACTCCTCTGGGGCCCTCCGAGGGGTGGGAGTCTGTACAGAGTCTTACCATGCTGAC 1836

Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1837 TGCCACTTGGAGCCAGTCCGTGTCAGGACCCCTCCAGATGCCATCGGAGGCGATCT 1896

Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 1897 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACAGAG 1956

Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1957 ATACTGAAGATTAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGGCCCCCCTCACCC 2016

Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2017 AGCTTCAACATCCCACTGGGCCCTTCAGTCCATGCCACAAAGCTCTTGAGAGACAGAGT 2076

Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2077 ACGGAGGCTCCCATATGCTCTGCAAAATCTCCAGCCCTTGTCTCAAGGCGACAGAGTGA 2136

Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeu 680
Db 2137 GCCTCGGGCGGACAGTGTTCCTTACTGTGCCCGGACAGGAGGAGGAGGAGGAGTCC 2196

Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2197 GCTGACCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2256

Qy 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719
Db 2257 CAGCAGTGTACCTCCGGGATCCCCACAGCGGGCGGCGACAGCGGAGCTTGGGCCCAT 2316

Qy	720	AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle	739	Qy	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098
Db	2317	GCAGAGCCTAGTTCTGTGCTGGCTTCTGGAGGCTGATCTGTGACACATTCGGGAAGATC	2376	Db	3397	CCCCACCATGAGATGAATCTCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGGAGT	3456
Qy	740	ValAspSerLysTyrrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer	759	Qy	1099	AlaAlaSerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118
Db	2377	GTAGATAGCAATACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAATACATCAGC	2436	Db	3457	CGGCAACGACGTGGACCGAGCGCTCCAGCAGGAACAGCTGGCGCGGCCCCACG	3516
Qy	760	MetGlyIleGluTyrrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn	779	Qy	1119	LeuLysArgArgSerProSerGlyClyArgArgSerLeuLeuSerGlyClyClyGlnGlu	1138
Db	2437	ATGGGCATCGAGTACACAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC	2496	Db	3517	CTAAAGCGAGAGCCGAGCGGAGCGAGGTCCTGCTGTCTGGAGAGGCGCCAGAG	3576
Qy	780	IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrrGlyPro	799	Qy	1139	SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis	1158
Db	2497	ATCGTCTTACCAGCGCTTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGCTCC	2556	Db	3577	AGTCAGGATGAGAGGAAAGTTTCAGAGAGGACCGGGCCAGCCAGCAGGACGTGACCAT	3636
Qy	800	PheGlyTyrrIleLysAsnProTyrrAsnIlePheAspGlyValIleValIleSerVal	819	Qy	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178
Db	2557	TTTGGCTACATTAAGAATCCCTACACATCTTTGATGGTGTCAATGTGGTCAATCAGTGTG	2616	Db	3637	CGCCACGGGTTCTTGGAACTGAGGCCAAGAGTTCTTTGACCTGCTGACACTCTG	3696
Qy	820	TrpGluIleValClyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet	839	Qy	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198
Db	2617	TGGGAGATTGTGGCCAGCAGGAGGTGGCTGTGGTGTCTGGGACCTTCCGCCCTGATG	2676	Db	3697	CAGGTGCCGGGCTGCACCGCACAGCGCCGAGCTCTGCCTCTGAGCACCAAGAC	3756
Qy	840	ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet	859	Qy	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro	1218
Db	2677	CGGTTCTGAGCTGTGGCTTCTTCCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCATG	2736	Db	3757	TGTAATGGCAAGTCGGCTTCAGGGTTTGGCCCGCACCCCTGAGGACTGATGACCCCAA	3816
Qy	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe	879	Qy	1219	LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyClyArgValArgAla	1238
Db	2737	NAGACCATGGACAACGTGGCCACTTCTGCATGCTCTCATGTGTTCATCTTCATCTTC	2796	Db	3817	CTGGATGGGATGATGACAATCATGAGGGAATCTGAGCAAAAGGGAGCATACAAGCC	3876
Qy	880	SerIleLeuGlyMethIleLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899	Qy	1239	TrpIleArgAlaArgLeuProAlaCysTyrrLeuGluArgAspSerTrpSerAlaTyrrIle	1258
Db	2797	AGCATCTGGCGATGATCTCTTTGGTTCGAGTTGCGATCTGAAACGGATGGGACAGC	2856	Db	3877	TGGGTGAGTCCGGCTTCTGCTGTTGCCGAGACGAGATTCCTGGTGGGCTATATC	3936
Qy	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919	Qy	1259	PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278
Db	2857	TTGCCAGCCGGAAGAAATTCGACTCCCTGCTCTGGGCCATCTGCTCTTCAGATT	2916	Db	3937	TTTCTCTCTCAGTCAAGTTTCTCTCTGTGTCCCGGATCATCACCCACAGAAGTGT	3996
Qy	920	LeuThrGlnGluAspTrpAsnLysValLeuTyrrAsnGlyMetAlaSerThrSerTrp	939	Qy	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	2917	CTGACTCAGGAAGACTGGAATAAAGTCTCTACACGGCATGGCCCTCCACATCGTCTTG	2976	Db	3997	GACCATGTGCTCTGTCATCTCTCTCACTGATCATCATCATCATCATCATCATCAT	4056
Qy	940	AlaAlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuLeu	959	Qy	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrrIlePheThr	1318
Db	2977	GCTGCTCTTACTTCTATCGCCCTCATGACTTTTGGCNACTATGTGCTCTTAACTGCTG	3036	Db	4057	AAAAATTGACCCCCACAGCGCTGAGCGCATCTTCTGACCCCTCTCAACTACATCTTCACG	4116
Qy	960	ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer	979	Qy	1319	AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGlu	1338
Db	3037	GTGCCATTCTTGTGGAAGGATTCAGGCAGAGGAAATCGGCAACCGGGAAGATGCGAGT	3096	Db	4117	GCAGTCTTCTAGCTGAATGACAGTGAAGTGTGGTGGCTGGCTGGCTGGTGGGAG	4176
Qy	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999	Qy	1339	GlnAlaTyrrLeuArgSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	3097	GGACAGTTAAGCTGTATTCAGTGCCTCAACTCTCAGGGGAGATGCCAACAGTCT	3156	Db	4177	CAGGCTTACCTGCGCAGCAGCTGGAATGTCTGCGACGGCTTGTGGTGTCTCATCTCGCTC	4236
Qy	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019	Qy	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	3157	GAGTCAGAGCTGATTTCTTTTCCGCCAGTGTGTGATGTGATGGGACAGAAAGACGC	3216	Db	4237	ATCGACATCTGCTGCTCCATGGTCTCCGACGGGACCAAGATCTCTTGGCATGCTGAGG	4296
Qy	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039	Qy	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	3217	TTGGCCCTGGTGGCTTTGGGAGAACACCGCGAACTACGAAAGACCTTTTGGCACCCCTC	3276	Db	4297	GTGCTGGGCTGTGCGGACCTTGGCTCCACTCAGGGTTCATCAGCGGGCCCGAGGACTG	4356
Qy	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059	Qy	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle	1418
Db	3277	ATCATCCATACGGTGGCACCAATGTCACTACCCAAAGAGCTCCAGCAGAGGTGGGG	3336	Db	4357	AAGCTGGTGTAGAGACTCTGATGTCATCTCCCTCAAAACCCATTTGGCAACATTTGGCTCAT	4416
Qy	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAla	1079	Qy	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	3337	GAAGCACTGGGCTCTGGCTCTCGAGTACCAAGTAGCAGTGGTCCGCTGAGCCTGGAGCT	3396	Db	4417	TGCTGTGCTCTTCTCATCATTTTTTGGAAATCTTCGGGGTGCAGCTCTTCAAGAGGAGTTC	4476
				Qy	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458

Db 4477 T T C G T G T G C A G G G T G A G G A C C A G G A A C A T C A C T A A C A A A T C C G A C T G C G C T G A G G C 4536
Qy SerThrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4537 A G C T A C C G A T G G G T C C G G C A A G T A C A C T T T G A C A A C C T G G C C A G G C T C T G A T G T C 4596
Qy LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
Db 4597 C T G T T T G T G T G C C T C C A A G A T G T T G G T T G A C A T C A T G T A T G A T G G C T G G A T G C T 4656
Qy ValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db 4657 G T G G G T G T G A T C A G A C A G C C C A T C A T G A A C C A C A C C C T G G A T G C T G T A T A C T T C A T C 4716
Qy SerPheLeuLeuIleValAlaPheValLeuAsnMetPheValGlyValValValGlu 1538
Db 4717 T C C T T C C T C A T C G T G C C T T C T T T G C C T G A A C A T G T T G T G G C G T G T G T G G A G 4776
Qy AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaAlaArgArgGluGluLys 1558
Db 4777 A A C T T C A T A A G T G C A G A C A C C A G G A G G A G G A G G C G A G G C G T G A G G A A G 4836
Qy ArgLeuArgArgLeuGluLysLysArgArg----- 1568
Db 4837 C G A C T A C G A G G C T G A G A A A A G A G A G A A T C T A A T G T T G A C G A T G T A A T T G C T T C C 4896
Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580
Db 4897 G G C A G C T A C G A C G C C T G C T A G A A G C C C A G T G C A A G C C C T A C T A C T G A C T A C T C G 4956
Qy 1581 ArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600
Db 4957 A G A T T C C G G C T C C T T G C C A C C A C C T G T G A C C A C C A C T A C C T G G A C C T C T T C A C A C T 5016
Qy GlyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
Db 5017 G G T G C A T C C G G C T A A C T G T G C A T A T G G C C A T G G A A C A T T A C C A G A C G C C C A G A T C 5076
Qy 1621 LeuAspGluAlaLeuLysLysCysAsnTyrIlePheThrValIlePheValLeuGluSer 1640
Db 5077 C T G G A C A G G C T G A A G A T C T G C A A T T A C A T C T T T A C C G T C A C T T T G T C T T T G A G T C A 5136
Qy 1641 ValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeu 1660
Db 5137 G T T T T C A A A C T T G T G C C T T T G C C T T C C G C G T T C T T C C A G G A C A G G T G G A A C C A G C T G 5196
Qy 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsn 1680
Db 5197 G A C C T G G C T A T T G C T T C T G C C A T C A T G G G C A T C A C A C T G G A G A G A T T G A G G T C A A T 5256
Qy 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
Db 5257 G C T T G C T C C C A T C A A C C C C A C C A T C A C C G T A T C A T A G G G T G C T C C G C A T T G C T C G A 5316
Qy 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
Db 5317 G T T C T G A A C T G T T G A A G A T G C T G T G G C A T C A T G G G C A C T G C T G G A C A C G G T A T G C A G 5376
Qy 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
Db 5377 G C C C T G C C C A G T G G G A A C C T G G A C T T C T C T C A T G T A T T G T T T T C A T C T T T G C A 5436
Qy 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
Db 5437 G C T C T G G G C G T G A G C T C T T T G A G A C C T G G A G T G T A T G A C A C A C C C T T G T G A G G C 5496
Qy 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5497 T T G G G T C G C A T C C A C C T T T A G G A A C T T T G T A T G G C C T T T C T G A C C C T C T T C C G A G T C 5556
Qy 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800

Db 5557 T C A C T G T G C A C A A C T G G A A T G G T A T T A T A A G G A C A C C C T C C G G A C T G T G A C C A G G A G 5616
Qy 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820
Db 5617 T C A C C T G T A C A A C A C T G T C A T C C C C T A T C T A C T T T G T G T C C T T G T G C T G A C G G C C 5676
Qy 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840
Db 5677 C A G T T T G T G C T G G T C A A C G T G T C A T A G T G T G T G A A G C A C C T G G A A G A A A C A A C 5736
Qy 1841 LysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu 1860
Db 5737 A A A G A G G C C A A G A G A G C C G A G C T C G A G G C G A C T G G A G T G A A G A C G C T C 5796
Qy 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
Db 5797 A G C C C G A C C C A C T C C C C G T G G C A C C C C T C C T C T G G C C C G G G T G G A G G T G T C 5856
Qy 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5857 A A C A G T C C T G A C A G C C C T A A G C C T G G G G C T C C A C A C A C C A C T G C C C A C A T T G G A G C A G C C 5916
Qy 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGlnLeuPro----- 1918
Db 5917 T C G G G C T T C C C T T T G A C A C C C A C G A T G G T A C C C C A C C C G A G A G G T G C C A G T C C C C 5976
Qy 1919 ---GlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db 5977 C T A G A C C A G A C C T G T G A C T G T G A G A A G T C T G T G T C A G C C G A C G C A C T C T T G C C C 6036
Qy 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957
Db 6037 A A T G A C A G C T A C A T G T G C C G C A A T G G A G A C A C T G C T G A G A G A T C C C T A G A C A C A C A G G G C 6096
Qy 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db 6097 T G G G G C T C C C C A A A G C C A G T C A G G C T C A T C T T G C G T T C A C T C C C A C C A C A G A G A C 6156
Qy 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuGlnProHisSerAla 1997
Db 6157 A C C A C T G C A T C C T A C A G C T T C C C A A A G A T G T G C A C T A T C T G C T C A G C C T C A T G G G C C 6216
Qy 1998 ProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2017
Db 6217 C C C A C C T G G G G C C A T C C C T A A A C T A C C C C A C C T G G C C G C T C C C C T C T G C T C A G A G G 6276
Qy 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037
Db 6277 C C T C T C A G C G C C A G G A C A A T A A G G A C T G A C T C C C T G A T G T G C A G G C C C T G G G T A G C 6336
Qy 2038 ArgGluAspLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db 6337 C G G A A G A C C T G T G A G A G T G A G T G G G C C C T C T G C C C T C T G A C C G G T C C T C A T C C 6396
Qy 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077
Db 6397 T T C T G G G C G G T C G A G C A T C A G T G C A G A C G C T T C C G G C A T C C A G A C C A A A G A G T C C C 6456
Qy 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 6457 A A G C A C A T C C G C T C C G A C C C C T T G C C A G C C C T G G A A C C C A C C A G G C C A A G A C C C T 6516
Qy 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 6517 C C A G A G A C C A A G A G C C T T A G A G C T G G A C A C G A G C T G A G C T T T C A G A G A C C T C 6576
Qy 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysCysTyrSer 2137
Db 6577 C T T ---C C C A G C A G C A G A A A C C C C T G T C C C A C C G G A C C T G A A G A A G T G C T A C A G T 6633
Qy 2138 ValGluAlaGlnSerCysGlnArgProThrSerTrpLeuAspGluGlnArgHis 2157
Db 6634 G T A G A C C C A G A G C T G C A G G C C A G G C C T G G G T C C T G G C T A G A T A C A A C A C C A G C G A G A C A C 6693

QY	2158	SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer	2177	QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	6694	TCCATTGCTGTGAGTGTCTGACAGCGGCTCCCAACCGGCTATGTCCAAAGCCCTCA	6753	DB	354	CCGTGGTTCGAGCGAGTCAGTATGCTGTGTCATTCTTCTCAACTGTGTGACCTCGGGTATG	413
QY	2178	AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysIleValSerPro	2197	QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	6754	AGCCTCGGGGGCAACCTCTTGGGGTCTCGGAGCGCGCTTAAGAAAAAATCTCAGCCCA	6813	DB	414	TTCAGCGCGTGTGAGGACATTGCTGTGACTCCAGCGCTGCGGATCCTGCGAGCCCTTC	473
QY	2198	ProSerIleThrIleAspProProGlnSerGlnGlyProArgThrProProSerProGly	2217	QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	6814	CCAGTATCTCTATAGACCCCGGAGACGAGGCTCTCGGCCCCCATGCGTCTCTGGT	6873	DB	474	GATGACTTTCATCTTTGCTGCTGGAATGGTGGTGAAGATGGTGGCCCTGGGC	533
QY	2218	IleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro	2237	QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
DB	6874	GTCCTGCTCAGGAGGAGCGCGCCAGTGACTCTAAGGATCCCTCGGCTCTCCAGCCCC	6933	DB	534	ATCTTTGGGAAGAAATGTTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTC	593
QY	2238	ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu	2257	QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	6934	CTTGACAGCAGCGCTGCCTCACCCCTCCCAAGAAAGACACGCTGAGTCTCTCTGTTTG	6993	DB	594	ATTGAGGGATGCTGAGTATTTCGTGGACCTGCAGAACGTGAGCTTCTCCGAGTCAGG	653
QY	2258	SerSerAspProAlaAspLeuAspPro	2266	QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	6994	TCTTCTGACCAACACAGATGGACCCC	7020	DB	654	ACAGTCCGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTCCCGAGATGGCATCTTC	713
RESULT 8							
US-10-377-139-7							
; Sequence 7, Application US/10377139							
; Publication No. US2004017561A1							
; GENERAL INFORMATION:							
; APPLICANT: Mackinnon, Roderick							
; APPLICANT: Jiang, Youxing							
; APPLICANT: Lee Mackinnon, Alice							
; APPLICANT: Lee Mackinnon, Alice							
; APPLICANT: Ruta, Vanessa							
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins							
; TITLE OF INVENTION: Uses thereof							
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9							
; CURRENT APPLICATION NUMBER: US/10/377,139							
; CURRENT FILING DATE: 2003-03-01							
; NUMBER OF SEQ ID NOS: 21							
; SOFTWARE: PatentIn version 3.1							
; SEQ ID NO 7							
; LENGTH: 6942							
; TYPE: DNA							
; ORGANISM: Rattus norvegicus							
US-10-377-139-7							
Alignment Scores:							
Pred. No.:	0	Length:	6942	QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
Score:	10945.00	Matches:	2107	DB	1074	ACCACTGCTCTCGGGCGGAGCACAACCCCTTCAGAGGCGCCATCAACTTTGACAACATT	1133
Percent Similarity:	94.0%	Conservative:	34	QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Best Local Similarity:	92.5%	Mismatches:	101	DB	1134	GGCTATGCTGGATGCCATCTTCCAGGTTCATCACACTGGAGGGCTGGGTCGACATCATG	1193
Query Match:	91.9%	Indels:	36	QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB:	9	Gaps:	6	DB	1194	TACTTCGTAAATGAGCGCTCACTCTCTTCAAACTTCACTTACTTCTTCTTCATCATC	1253
US-09-611-257A-37 (1-2266) x US-10-377-139-7 (1-6942)							
QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20	QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
DB	114	ATGGACGAGGAGGAGGATGAGCGGGCGCGGAGGTCGGAGAGTCCCGTAGCTTCACG	173	DB	1254	GTGGGCTCTTCTTCATGATCACTGTGCTGGTGGTGTGGCAGCGAGTTCCTCCGAG	1313
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40	QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	174	CAGCTCAACGACCTGTCCGGGGCGGGGGCGCGAGGGCGGGGTCGACGGAAGGAC	233	DB	1314	ACCAAAACAGCGGAGAGTCAGTGCATCGGGAGCAGCGTGTACGATTCTCTGTCCAATGCT	1373
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60	QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
DB	234	CCGGGACGCGGAGTCTCGAGCGGAGGGGTGCGGTACCGCGCGCTAGCCCCGGTGT	293	DB	1374	AGCACCTGGCAGCTTCTCTGAGCCAGGAGCTGCTATGAGGAGCTACTCAAGTACCTG	1433
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80	QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	294	TTCCTTACTTACTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACAGCTCTGTAA	353	QY			

[illegible]

QY	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198	QY	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaAraArgArgGluGluLys	1558
DB	3585	CAGGTCCGGGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCCTCTGAGCACCAAGAC	3644	DB	4665	AACTTCCATAAGTGCAGACAGACCAGGAGGAGGCGCGGCTGAGGAGAAG	4724
QY	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaAraArgAlaLeuArgProAspSerPro	1218	QY	1559	ArgLeuArgArgLeuGluLysLysArg-----LysAlaGln	1571
DB	3645	TGTAATGGCAAGTCGGCTTCAGGGCGTTTGGCGCGCACCTGAGGACTGATACCCCAA	3704	DB	4725	CGACTACGGAGGCTCGAGAAAAGAGAGGAGTAAGGAGAAGCAGATGCCCGAAGCCAG	4784
QY	1219	LeuAspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238	QY	1572	CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr	1591
DB	3705	CTGGATGGGATGATGACAAATGATGAGGAAATCTGAGCAAGGGGAAACGATACAGCC	3764	DB	4785	TGCAAGCCCTACTACTCTGACTACTCGAGATTCCGGCTCTTGTCCACCACCTGTGTACC	4844
QY	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluAraAspSerTrpSerAlaTyrIle	1258	QY	1592	SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla	1611
DB	3765	TGGGTGAGATCCCGGCTTCTGCTGCTTGCAGAGAGCGAGATTCTTGGTCGGCTATATC	3824	DB	4845	AGCCACTACTCGACCTCTTTCATCTACTGTGTCTATCCGGCTGAACTGTCTACTATGGCC	4904
QY	1259	PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278	QY	1612	MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle	1631
DB	3825	TTTCTCTCAGTCAAGGTTTCGTCTCTGTGTGCACCGGATCATCCCCACAAAGATGTTT	3884	DB	4905	ATGGAACAATTACAGCAGCCCCAGATCTCTGGAGAGGCTCTGAAGATCTGCAATTACATC	4964
QY	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298	QY	1632	PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg	1651
DB	3885	GACCATGTGCTCTGTCATCATCTTCTCACTGTATCACTATCGTATGGAGCGCCCC	3944	DB	4965	TTTACCGTCACTCTTGTCTTTGAGTCAGTTTCAAACCTTGTGGCCTTTGGCTTCCGCCGT	5024
QY	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318	QY	1652	PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly	1671
DB	3945	AAAATTGACCCCCACAGCGCTGAGCGCATCTTCTGACCCCTCTCCAACCTACATCTTCAG	4004	DB	5025	TTCTTCCAGACAGGTGGAAACAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGC	5084
QY	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu	1338	QY	1672	IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg	1691
DB	4005	GCAGTCTTTCTAGCTGAATGACAGTGAAGGTGGTGGCACTGGGCTGCTTTGGGAG	4064	DB	5085	ATCACACTGAGGAGATTGAGGTCAATCTGTGCTGCCCATCAACCCCACTCATCCGT	5144
QY	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358	QY	1692	IleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMet	1711
DB	4065	CAGCCTTACTGTGGCAGCAGCTGGAATGTCTGGACGGCTTGTGTGTCATCTCCGTC	4124	DB	5145	ATCATGAGGTGCTCCGCAATGCTCGAGTTCTGAAGCTGTGTGAAGATGGCTGTGGGCATG	5204
QY	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378	QY	1712	ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu	1731
DB	4125	ATCGACATCTGGTCTCATGGTCTCCGACAGCGGCACCAAGATCTTGGCATGCTGAGG	4184	DB	5205	CGGGCACTGCTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTC	5264
QY	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398	QY	1732	PheMetLeuLeuPhePheIlePheAlaLeuLeuGlyValGluLeuPheGlyAspLeuGlu	1751
DB	4185	GTGCTGGGTGCTGCGGACCTCGCTCCACTAGGGTCAATCAGCGGGCCACAGGACTG	4244	DB	5265	TTCATGTATTGTGTTTTCATCTTTGCAGCTCTGGGCTGGAGCTCTTTGGAGACCTGGAG	5324
QY	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418	QY	1752	CysAspGluThrHisProCysGluGlyLeuGlyValArgHisAlaThrPheArgAsnPheGly	1771
DB	4245	AAGCTGGGTAGAGACTCTGAATGTCATCCCTCAAAACCCATTGGCAACATTGTGTGTCAT	4304	DB	5325	TGTGATGAGACACACCCCTTGTGAGGGCTTGGGTGGGCATGCCACCTTTAGAACTTTGCT	5384
QY	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438	QY	1772	MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys	1791
DB	4305	TGCTGTGCTTCTTCATCAATTTTGGAAATTCGCGGTGTCAGCTCTTCAAAGGGAAGTTC	4364	DB	5385	ATGGCCTTTCTGACCTCTTCCAGTCTCCACTGGTGACAACTGGAATGCTATTATGAAG	5444
QY	1439	PheValCysGlnGlyLeuAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458	QY	1792	AspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIle	1811
DB	4365	TTCTGTGTTCAGGTGAGGACACAGGAAACATCACTAACAAATCCGACTGGCTGAGGCC	4424	DB	5445	GACACCTCCGGACTGTGACCAGGATCCACCTGCTTACAACACTGTCTCATCTCCCTCATC	5504
QY	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478	QY	1812	TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaVal	1831
DB	4425	AGCTACCGATGGGTCCGGCACAAGTACAACTTTGACAACTGGGCCAGGCTCTGATGTCC	4484	DB	5505	TACTTTGTGCTCTCGTGTGACGGCCAGTTTGTGCTGGTCAAGCTGTGTATAGCTGTG	5564
QY	1479	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498	QY	1832	LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAla	1851
DB	4485	CTGTTTGTGCTGGCTCCCAAGATGTTGGTGTGACATCATGTATGATGGCTGGATGCT	4544	DB	5565	CTGATGAAGCACCTGGNAGAAAGCAACAAGAGGCCAAGGAGGAGGCCAGCTCGAGGCC	5624
QY	1499	ValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518	QY	1852	GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro	1871
DB	4545	GTGGGTGTGGATCAGACGCCCATCATGAACCAACCAACCCCTGGATGCTGCTACTTCTATC	4604	DB	5625	GAGCTGAGCTGGAGATGAAGACGCTCAGCCCGCAGCGCCCACTCCCGCTGGGAGCCCC	5684
QY	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538	QY	1872	PheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyValAlaLeu	1891
DB	4605	TCCTTCTCTCTCATCGTGGCTCTTCTTGTCTCTGAACATGTTTGTGGGCTGGTGGAG	4664	DB	5685	TTCTCTGGGCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTTAAGCTCTGGGCTCCA	5744
				QY	1892	HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln	1911

```
Db 5745 CACACACTGCCACATTTGGAGCAGCTTCGGGCTTCTCCCTTGGAGACCCACGATGGTA 5804
Qy 1912 ProHisProThrGluLeuPro-----GlyProAspLeuThrValArgLysSer 1928
Db 5805 CCCCACCCGAGAGGTGCGAGTCCCTTAGGACACAGACTGCTGAGTGTGAGGAAGTCT 5864
Qy 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
Db 5865 GGTGTGAGCGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCCAATGGGACACT 5924
Qy 1949 AlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerVal 1968
Db 5925 GCTGAGAGATCCCTAGGACACAGGGGCTGGGGCTCCCCAAAGCCAGCTCAGCTCCATC 5984
Qy 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988
Db 5985 TTGTCTGTTCACTCCCAACGACGACACACAGCTGCTATCAGCTTCCCAAGATGTG 6044
Qy 1989 ProHisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLeuProPro 2008
Db 6045 CACTATCTCTCAGGCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCA 6104
Qy 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp 2028
Db 6105 CCTGGCGCTCCCTCTGGCTCAGAGGCTCTCAGGCGCAGGCGAGCAATAAGGACTGAC 6164
Qy 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGlnValSerGlyPro 2048
Db 6165 TCCTGGATGTGAGGGCTGGGTAGCCGGGAAGACCTGTGTGAGAGTGTAGTGGCCC 6224
Qy 2049 SerProProLeuAlaArgAlaTyrSerPheThrTyrGlyGlnSerSerThrGlnAlaGlnGln 2068
Db 6225 TCCTGCGCTCTGACCGGTCCTCATCTTCTGGGGCGGTTCGAGCATCCAGGTGCAGCAG 6284
Qy 2069 HisSerArgSerHisSerLysLysSerLysHisMetThrProProAlaProCysProGly 2088
Db 6285 CGTTCGGCATCCAGAGCAAGTCTCCAAGCACATCCGCTGCCAGCCCTTGGCCAGGC 6344
Qy 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108
Db 6345 CTGGAACCCAGCTGGGCCAAGACCTCCAGAGACCAAGAGCAGCTTAGAGCTGGACAG 6404
Qy 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProSer 2128
Db 6405 GAGCTGAGTGTGATTTCAGAGACCTCCTT---CCAGCAGCCAGGAAGACCCCTGTTC 6461
Qy 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148
Db 6462 CCACGGGACCTGAAGAAGTGTCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGG 6521
Qy 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168
Db 6522 TTCTGGCTAGATGAACAGCGGAGACACTCATTTGTCTGCTGCTGCTGAGAGCGGCTCC 6581
Qy 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGly 2188
Db 6582 CAACCCCGCTATGTCCAAGCCCTCAAGCCTCGGGGCCAACCTCTTGGGGGTCTCTGG 6641
Qy 2189 SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGlnSerGln 2208
Db 6642 AGCCGGCCTTAAGAAAAAATCAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAG 6701
Qy 2209 GlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAsp 2228
Db 6702 GGCTCTGGCCCCCATGCACTCTGTGTCTGCCCTCAGGAGGAGGCGCGCCGCTAGTGAC 6761
Qy 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248
Db 6762 TCTAAGGATCCCTCGGTCTCCAGCCCCCTTTGACAGCAGCGGTGCTCACCTCCCCAAG 6821
Qy 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
|||||
|||||
```

Db 6822 AAAGACACGCTGAGTCTCTCTGTTGTCTTCTGTGACCCCAACAGACATGACCCC 6875

RESULT 9

```
US-10-930-301-51
; Sequence 51, Application US/10930301
; Publication No. US20050026207A1
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHUI590
; CURRENT APPLICATION NUMBER: US/10/930,301
; PRIOR FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/398,522
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
; NAME/KEY: CDS
; LOCATION: (373)...(3993)
US-10-930-301-51
```

Alignment Scores:

```
Pred. No.: 0 Length: 3993
Score: 6315.50 Matches: 1207
Percent Similarity: 98.1% Conservative: 0
Best Local Similarity: 98.1% Mismatches: 0
Query Match: 53.1% Indels: 23
DB: 9 Gaps: 1
```

US-09-611-257A-37 (1-2266) x US-10-930-301-51 (1-3993)

```
Qy 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGGACGAGGAGGAGGATGGAGCGGCGCGGAGGAGTGGGACACGCCCGGAGCTTCATG 432
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACACACTCTCGGGGCGCGGGCGCGGGCGGGGTGACAGAAAAGGAC 492
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 493 CCGGCGCGCGGACTCCGAGCGGAGGGGCTGCCGTATCCCGCGCGCTGGCCCGGTGTT 552
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 553 TTCCTTCTACTTGAGCGAGACAGCCCGCGGAGCTGGTGTCTCGCACGGTCTGTAAAC 612
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 613 CCCTGGTTTGAGCGCATCAGCATGTGTGTCATCTTCTCAACTGCGTGACCTGGGCATG 672
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 673 TTCGGGCGCATCGAGGACATCGCTGTGACTCCCGAGCGCTGCCGATCCTGCAGGCCCTTT 732
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 733 GATGACTTCACTTTTCCTTCTTCCCTGGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC 792
Qy 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160
Db 793 ATCTTTGGAAAAAAGTGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTTCATCGTC 852
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 853 ATCGAGGGATGCTGGAGTACTCGCTGGACCTGCAACGCTCAGCTTCTCAGCTCTCAGG 912
```

QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200	QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	913	ACAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGCATCCTT	972	Db	1993	GCCCTCTCCGGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC	2052
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220	QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	973	GTCAAGTTCTCTGTGGATACGCTGCCCATGTCTGGGCAACGTCCTGTCTGTCTGTCTTC	1032	Db	2053	TGCCACTTAGAGCCAGTCCGCTGCCAGGGCCCCCTCCAGGTCCCATCTGAGGCATCC	2112
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuLeuTrpAlaGlyLeuLeuArgAsnArg	240	QY	581	GlyArgThrValGlySerGlyIysValTyrProThrValHisThrSerProProProGlu	600
Db	1033	GTCTTCTTTCATCTTCGGCATCTGTGGCGTCCAGCTGTGGCAGGGCTGCTTCGGAAACGA	1092	Db	2113	GGCAGCACTGTGGGAGCGGGAGAGTGTATCCACCGTGCAACACAGCCCTCCACGGAG	2172
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln	260	QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1093	TGCTTCTACCTAGAGAAATTCAGCCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAG	1152	Db	2173	ACGCTGAAGGAAGACACTAGTAGGTGGTGCAGCTCTGGGGCCCCCAACCTCACC	2232
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280	QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	1153	ACAGAGAACGAGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACGCGATGGCG	1212	Db	2233	AGCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAT	2292
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProCysGlyLeu	300	QY	641	ThrGlyAlaCysGlnSerSerCysIysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	1213	TCTCGAAGAGCGTCCCACTGCGGGGACGGGGCGGTGGCCACCTTGGCGTCTG	1272	Db	2293	ACAGGTGCTGCAAAAGCTCTTGCAAGATCTCCAGCCCTTGTGTGAAAGCAGACAGTGA	2352
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320	QY	661	AlaCysGlyProAspSerCysProTyrCysAlaAaGAlaGlyAlaGlyGluValGluLeu	680
Db	1273	GACTATGAGGCCFACAAACAGCTCCAGCAACACCACCTGTCTCAACTGGAACCACTACTAC	1332	Db	2353	GCCGTGTGTTCCAGACAGCTGCCCTACTGTGCGGGCCGGGCGAGGGGTGGAGCTC	2412
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsnIle	340	QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
Db	1333	ACCAACTGCTCAGCGGGGAGCAACCCCTTCAAGGGGCGCCATCAACTTTGACAACAT	1392	Db	2413	GCGCACCGTGAATGCTGACTCAGACAGCAGGCGAGTTTATGAGTTTCAACAGGATGCC	2472
QY	341	GlyTyrAlaIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360	QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
Db	1393	GGCTATGCCGTGATCGCCATCTTCCAGTCAATCAGCTGGAGGGCTGGGTCCGACATCA	1452	Db	2473	CAGCACAGCGACCTCCGGGACCCCAACAGCGGGCAACGGAGCCCTGGGCCCAAGTGA	2532
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPhelIleTyrPheIleLeuLeuIle	380	QY	721	GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgIysIleVal	740
Db	1453	TACTTTGTGATGATGCTCATCTCTCTACAATTTTCATCTTCTATCTCTCTCTCATCATC	1512	Db	2533	GAGCCACAGCTCTGTGCTGSCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG	2592
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu	400	QY	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	1513	GTGGGCTCTCTTTCATGATCAACCTGTGCTGTGTGTGATGCCAGCAGTCTTCAGAG	1572	Db	2593	GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTCTGTGTCACACACTCAGCATG	2652
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420	QY	761	GlyIleGluTyrHisGlnGlnProGluGluThrAsnAlaLeuGluIleSerAsnIle	780
Db	1573	ACCAAGCAGCGGGNAACCAAGCTGATCGGGGAGCAGCGTGTGCGGTTCCTGTCCAAGCC	1632	Db	2653	GGCATCGAATACACACAGCAGCCCGAGGAGCTTACCACCGCCCTAGAAATCAGCAACATC	2712
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440	QY	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe	800
Db	1633	AGCACCTGTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTGCTCAAGTACCTG	1692	Db	2713	GTCTTTCACNAGCCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGTTCCCTTT	2772
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460	QY	801	GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp	820
Db	1693	GTGTACATCTCTCGTAAGGAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG	1752	Db	2773	GGCTACATCAAGAAATCCCTACAAACATCTTCGATGGTGTCTATGTTGGTCAACAGCGTGG	2832
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480	QY	821	GluIleValGlyGlnGlnGlyGlyLeuSerValLeuLeuArgThrPheArgLeuMetArg	840
Db	1753	CGGGTTGGGCTGCTCAGCAGCCCAAGCACCCCTCGGGGCCAGGAGACCCAGCCAGCAGC	1812	Db	2833	GAGATCGTGGGCGAGCAGGGGGCGGCGCTGTGCGTGTGCGGACCTTCCCGCTGATCGGT	2892
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis	500	QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	1813	AGCTGCTCTCGCTCCCAACCGCGCTATCCGCTCCACCACCTCTGTTGTCACCAACCA	1872	Db	2893	GTGCTGAAGCTGGTGGCTTCTCTGCCGCGCTGCAGCGCAGCTGGTGGTGTCTCATGAAG	2952
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520	QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
Db	1873	CATCACCACCACTACCACTCGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGGCCGAG	1932	Db	2953	ACCATGACAACGTTGGCCACCTTCTGCATGCTGCTTATGCTTCTCATCTTCTCATCTCAGC	3012
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540	QY	881	IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu	900
Db	1933	ATCCAGGACAGGGATGCCAATGGGTCCCGCCGGCTCATGCTGCCACCACCCCTCGACGCT	1992	Db	3013	ATCTGGGCGATGCATCTCTTCGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCCCTG	3072
QY				QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920

```
Db 3073 CCAGACGGGAAGAAATTTGACTCTTGCCTCGGGCCATCGTCACTCTCTTCAGATCCCTG 3132
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db 3133 ACCCAGGAGACTGGAAACAAAGTCTCTACATGGTATGGCTCCACGTCGCTCTGGGG 3192
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 3193 GCCCTTTATTTCAATGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTC 3252
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
Db 3253 GCCATTCTGTGTGAGGGCTTCAGGGCGGAG----- 3282
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyValAspAlaAsnLysSerGlu 1000
Db 3283 -----GGAGATGCCAACAAAGTCCGAA 3303
QY 1001 SerGluProAspPheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3304 TCAGAGCCCGAATTTCTTCTCACCCAGCTGGATGGTATGGGACAGGAAGAGTCTTGT 3363
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
Db 3364 GCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTCGGAAGAGCCTGCTGCGCCTCTCATC 3423
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3424 ATCCACACGGCCGCCACACCATGTCGTCGCCAAGAGCACACAGCGGGCCTGGGGCAG 3483
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3484 CGCCTGGGCCCTCGCTCGCGCGCACACAGCAGCAGCGGGTGGCAGAGCTGGGGCGGC 3543
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3544 CACGAGATGAAGTCAACCGCCAGCGCCAGCTCTCCGCACACAGCCCTCGAGCGCTGCA 3603
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3604 AGCAGCTGGACCAAGAGCGCTCCAGCCGGAACAGAGCTGGCGCTGCACCCAGCTGAAG 3663
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGln 1140
Db 3664 CGGAGAAGCCCAAGTGGAGAGCGCGCTCCCTGTTGTCGGGAGAGGCCAGGAGCCAG 3723
QY 1141 AspGluGluLysSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3724 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGGCCAGCCCTCGCGGCAGTGACCATGCCAC 3783
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3784 AGGGGTCTCCTGGAGCGGAGGCGCAAGATTCTTTGACCTGCCAGACACTGCAAGGTG 3843
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3844 CCAGGGCTCGATCGCACTGCCAGTGGCCGAGGCTGCTGCTTCGAGCACCCAGGACTGCAAT 3903
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3904 GGCAAGTCGGCTTCAGGGCGCTTGGCCCGGGCCCTCGCGCCTGATGACCCCACTGGAT 3963
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeu 1230
Db 3964 GGGGATGACCCGATGACGAGGGCAACCTTG 3993
```

RESULT 10

US-10-483-467-3

; Sequence 3, Application US/10483467

; Publication No. US20050164161A1

; GENERAL INFORMATION:

; APPLICANT: Kath, Gary S.

```
; APPLICANT: McManus, Owen
; APPLICANT: Galyantes, Tina
; APPLICANT: Bennett, Paul B., Jr.
; APPLICANT: Imredy, John P.
; APPLICANT: Augustine, Paul R.
; APPLICANT: Bugianesi, Randal M.
; TITLE OF INVENTION: ELECTRICAL FIELD STIMULATION OF
; FILE REFERENCE: EUKARYOTIC CELLS
; CURRENT APPLICATION NUMBER: US/10/483,467
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: PCT/US02/22161
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,955
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7898
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-483-467-3
```

Alignment Scores:

```
Pred. No.: 0 Length: 7898
Score: 6215.50 Matches: 1368
Percent Similarity: 65.3% Conservative: 212
Best Local Similarity: 56.5% Mismatches: 518
Query Match: 52.2% Indels: 322
DB: 10 Gaps: 60
```

US-09-611-257A-37 (1-2266) x US-10-483-467-3 (1-7898)

```
QY 7 GlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMetArgLeuAsnAspLeuSer 26
Db 317 GCGCTGTGTGGGGCGTCCCCGGAGAGCCCCGG----- 349
QY 27 GlyAlaGlyGlyArgProGlyPro-GlySer----- 36
Db 350 GCGCGCGGACGCGAGGGGCGGCGGGTCCGAGCTCGCGGTGTACCCCTCCGAGAGCCC 409
QY 37 -----AlaGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAl 55
Db 410 GCGCGCGGAGCGCGCGCGGAGCTGGGTGTCGAGCAGCAGCAGCGCGCTCCGCTACCGCGC 469
QY 55 aLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLe 75
Db 470 CTGGCGGCCACCGGCTCTTCTTGCTCGTCGTCAGACCACCGCGCGCGCGAGCTGGTGCC 529
QY 75 uArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCy 95
Db 530 CCGGCTGTGTCTCAACCCCATGTTTCGAGCACGTGAGCATGCTGGTAAATCATGCTCAACTG 589
QY 95 sValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysAr 115
Db 590 CGTGACCTTCGGGCATGTTCCGCGCCTGTGAGGACGTTGAGTGGCGCTCCGAGCGCTGCAA 649
QY 115 gIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValGluMetValVally 135
Db 650 CATCTGTGAGGCGCTTTGAGCGCTTCATTTTCGCCCTTTTTCGGGTGAGATGTCATCAA 709
QY 135 sMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLe 155
Db 710 GATGTGGCTTGGGGCTGTTTCGGGCAGAAAGTGTACCTGGGTGACACGCTGGAACAGGCT 769
QY 155 uAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSe 175
Db 770 GGATTTCTTCATCGTCGTGGCGGCATGATGAGTACTCGTTGGACGGACACAACGTGAG 829
QY 175 rPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPr 195
Db 830 CCTCTCGGCTATCAGGACCGTCCGGGTGCTCGGGCCCTCCCGGCCCATCACCGGTGCC 889
```


195 oSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLe 215
Db
890 TAGCATGCGGATCCTGGTCACTCTGCTGTGATACGCTGCCATGCTCGGAAAGTCTCT 949
Qy
215 uLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGl 235
Db
950 TCTGCTGTGCTTCTTCTCTCTTCTTCTTCTGCAATCGTTGGCTCCAGCTCTGGGCTGG 1009
Qy
235 vLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAsp-- 254
Db
1010 CTTCTCTGCGGAACCGCTGCTTCTTGACAGTGCCTTTGTCAGGAACAACCTGACCTT 1069
Qy
255 -LeuGluArgTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnPr 274
Db
1070 CTTGCGGCGCTACTACAGAGGAGGAGGCGGAGGAGAACCCGCTTCTATCTGCTCTCTCAGC 1129
Qy
274 oArgGluAsnGlyMetArgSerCysArgSerValPro-----ThrLeuArgGlyAs 291
Db
1130 CCAGACAACGGCATCGAAGAGTCTCGCACATCTCCCGCGCGCGGAGCTGCGC----- 1184
Qy
291 pGlyGlyGlyProProCysGlyLeuAspTyrGluAlaTyrAsn----- 306
Db
1185 -----ATGCCCTGCACCTGGCTGGAGGCTACACGAGCGCGAGCCCGA 1231
Qy
307 -----SerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSe 324
Db
1232 GGGGGTGGGCGTGCAGCAACGCTGCATCAACTGGAACCACTACTACAACGTGTGCCG 1291
Qy
324 rAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTr 344
Db
1292 CTGGGTGACTCAACACCCCAACCGTGCATCAACTTCGACAACATCGGCTACGCTG 1351
Qy
344 pIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMe 364
Db
1352 GATTGCCATCTTTCAGGTGATACGCTGGAGAGCTGGTGGACATCATGTACTACGTCA 1411
Qy
364 tAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPh 384
Db
1412 GGAGCGCACTATTCTACAACCTCATCTATTTTCATCTCTCATCTGCTGGGCTCCTT 1471
Qy
384 ePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrIysGlnAr 404
Db
1472 CTTTCATGATCAACCTGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1531
Qy
404 gGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl 424
Db
1532 GGAGAGTCAGTGTATGCGGGAGCAGCGGCGCACGCCACCTGTCCAAACAGACAGCGCTGGC 1591
Qy
424 aSerPheSerGluProGlySerCysTyrGluGluLeuLeuIysTyrLeuValTyrIleLe 444
Db
1592 CAGCTTCTCGAGCTGGCAGCTGCTACGAAGAGCTGCTGAAGTACGTGGGCGCACATATT 1651
Qy
444 uArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLe 464
Db
1652 CCGCAAGGTCAAGCGGCGCAGCTTGGCGCTCTACCGCGCTGGCGAGCGCTGGCGCAA 1711
Qy
464 uLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSerCysSerAr 484
Db
1712 GAAGGTGGACCCAGTGTGTGCAAGGCCAG-----GGTCCCGGACCGCCAGCGCGC 1765
Qy
484 gSerHisArgArg---LeuSerValHisHisLeuVal---HisHisHisHisHisHis 502
Db
1766 GCGAGGAGGACACAGCCTCGGTGCACACCTGCTGTACCAACCACTACCAACCA 1825
Qy
502 sHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleGl 522
Db
1826 CCACCATACCATTTTCAGCCATGGCAGCCCCCGAGCGCCCCCGCCGAGCCAGCGGCGCTG 1885
Qy
522 nAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProAlaLe 542
Db
1886 CGAC-----ACCAGGCTGGTCCGAGCTGGCGCGCCCCCTCGCCACCTTC 1930
Qy
542 uSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHi 562

1931 CCCAGCGCGGACCCCGGACGAGAGTCTGTGCACAGCATCTACCATGCCAGCTGCCA 1990
Db
562 sLeuGlu-----ProValArgCysGlnAlaProProArgSerProSerGluAlase 580
Qy
1991 CATAGAGGCGCGAGGAGGCGCGGTGGACATGCCGAGCACTGCCGCTGCCAG 2050
Db
580 rGlyArg---ThrValGlySerGlyIysVal---TyrProThrVal----- 593
Db
2051 CCTCAGGCTGGCCACAGGCTGGGCAACCATGAACATCCCAAGATCCCGCATCCTCCCTCAGGGGT 2110
Qy
594 -----HisThrSerPro----- 599
Db
2111 GGGAGCGGCAAGGAGCAGCACGCCCGGAGCCCAAGGGAAGTGGCGCGTGGACCGC 2170
Qy
599 oGluThrLeuIysGlyLeuValAlaLeuValGluValAlaLeuSerSerGlyProProThrLe 619
Db
2171 AGGCACC-----GGGGGCGACGCGCGTGTAGCTT 2200
Qy
619 uThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGl 639
Db
2201 GAACAGC-----CCTGATCCCTACGAGAAGATCCCGCATGTGTGGGAGCA 2248
Qy
639 nSerThrGlyAlaCysGlnSer-----SerCysLysIleSerSe 652
Db
2249 TGGAGTGGGCGAGGCGGCTGGCCATCTGTGGGCTCAGTGTGCCCTGCCCTGCCAG 2308
Qy
652 rProCysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaAr 672
Db
2309 CCCC-----CCAGCGGCGACACTGACCTGTAGCTGAAGAGTGGCGCTACTGCAACCG 2362
Qy
672 gAla-----GlyAlaGlyGluValGluLeuAlaaspArgGluMetProAspSerAspSerGl 691
Db
2363 TGCCCTGGAGGACCGCGAGGTGAGCTCAGCGCTCGGAAAGTGGAGACTCAGATGGCCG 2422
Qy
691 uAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro----- 708
Db
2423 TGCGGCTATGAATTACGCGAGGACGTCGCGCACGCTGACCGCTGGGACCCCGCGAC 2482
Qy
709 -----HisSerArgArgGlnArgSe 715
Db
2483 ACCCGCTGCGACGACACACAGCGCCAGCGCCAGCGCGCGCGGCGGACGCA 2542
Qy
715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspTh 735
Db
2543 GAGGCGAGCGCGCGGCGAGCGCTGGATGGGCGCGCTCTGGTGTACTTACCTTCAGCGCAA 2602
Qy
735 rPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuVa 755
Db
2603 GCTCGCGCGCATCGTGGACAGCAAGTACTTTCAGCGCTGGCATCATGATGGCATCTTGT 2662
Qy
755 lAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLe 775
Db
2663 CAACACGCTGAGCATGGGCGTGGAGTACCATGAGCAGCGCGGAGGAGTGAATGTCT 2722
Qy
775 uGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLe 795
Db
2723 GGAGATCAGCAACATCGTGTTCACCATGTTTTCCTCGGATGTTGAGATGCTGTGAAGCTGT 2782
Qy
795 uValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVa 815
Db
2783 GGCCTGGCGGCTCTGGCTACATCCGGAACCGGTACAACATCTTCAGCGCATCATCGT 2842
Qy
815 lValIleSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgTh 835
Db
2843 GGTATCAGCGCTCTGGAGATCGTGGGCGAGCGGCGGCTGGCTGTGTGTGCTGCGGAC 2902
Qy
835 rPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgIle 855
Db
2903 CTTCCGCGCTGTGCTGTGAAGCTGTGGCTTTCTGCGACGCTTCTGCGCGCGCGCT 2962
Qy
855 uValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPh 875

Db 2963 CGTGGTGGTGAAGACCAATGACAAACGTGGGTACCTTCGACACGCTCATGCTCTT 3022
Qy 875 eilePheilePheSerileLeuGlyMethHisLeuPheGlyCysLysPheAlaSerGluAr 895
Db 3023 CATTTTCATCTTCAGCATCTCGGSCATGCACCTTTTCGGTGTCAAGTTCAGCCTGAAGAC 3082
Qy 895 gAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleVa 914
Db 3083 AGACACGGAGACACCGTGCCTGACAGGAAGAACTTCGATCCCTCGTGTGGGCCATCGT 3142
Qy 914 lThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAl 934
Db 3143 CACCGTGTCCAGATCTGTACCCAGGAGGACTGGAACGTGGTCTCTGTACACGGCATGGC 3202
Qy 934 aSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVa 954
Db 3203 CTCACACTCTCTCGGGCGCCCTCTACTTCGTGGGCCCTCATGACCTTCGGCAACTATGT 3262
Qy 954 lLeuPheAsnLeuLeuValAlaIleLeuValGlnGluGlyPheGlnAlaGluGluIleSerLy 974
Db 3263 GCTCTTCAACCTGCTGTGGCCATCTCTGTGGAGGGCTTCAGGCGGAG----- 3311
Qy 974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGl 994
Db 3312 -----GG 3313
Qy 994 yAspAlaAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAsp-- 1013
Db 3314 CGATGCCAACAGATCCGACACGGACGAGGACAGAGCGTGGTCCACTTCGAGGAGACTT 3373
Qy 1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerLe 1025
Db 3374 CCACAAGCTCAGAGAATCCAGACACAGAGCTGAAGATGTGTCCCTGGCGCGTACCC 3433
Qy 1025 uGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAl 1045
Db 3434 CAACGGGCACCTGGAGGACGAGGAGCGCTGTCCCTCCCTCATCATGTGCACAGCTGC 3493
Qy 1045 aThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAl 1065
Db 3494 CAGCCCATGCCTACCCCAAGAGCTCACCATTCCTGGATGCAGCCCGCCAGCTCCGAGA 3553
Qy 1065 aSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGlyMetLysSe 1085
Db 3554 CTCCTCGCGCTGGCAGCAGCAGCTCCGGGACCCGCGCA-----CTGGGAGACGAGAAGCC 3607
Qy 1085 rProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105
Db 3608 TCCGGCCAGCCTCCGAAGTTCTCCCTGTGCCCCCTGGGCCCCCAGTGGCGCTGGAGCAG 3667
Qy 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1125
Db 3668 CCGCGCTCCAGTGGAGCAGCTGGGCGCTGCCCTCAGCCCTCAAGCGCGCGCCAGTG 3727
Qy 1125 rGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSe 1145
Db 3728 TGGGGAACCTGATGCTCTGTCTGGCGAGGCAAGGCGAGCAGCCGACGAGCA----- 3782
Qy 1145 rSerGluGluGluArgAlaSerProAla-----GlySerAspHisArgHisArgGlySe 1163
Db 3783 -GCTGAGGACGGCAGGGCGCGCGCGCGCGCTGCACCCCACTCGCGCGCGCGCGAGTC 3841
Qy 1163 rLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu----- 1178
Db 3842 CTGGACCCACGGCCCTCGGCGCGCGCGCTCCCGCTACCAAGTGGCGCGATCGCA 3901
Qy 1179 -----GlnValProGlyLeuHis-----ArgThrAlaSerGlyArgGlySe 1192
Db 3902 CGGGCAGGTGGTGGCCCTGCCACGAGCTTCTTCTCTGCGCATCGACAGCCACCGTGAGGA 3961
Qy 1192 rAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLe 1212
Db 3962 TGCAGCCGAGCTTGACGACGACTCGGAGGACAGCTGCTGCCCTCCGCGCTCATAAAGTGCT 4021

Qy 1212 uArgProAspAspProLeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLy 1232
Db 4022 GGAGCCCTCAAGCCC----- 4037
Qy 1232 sGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAs 1252
Db 4038 -----CAGTGGTGGCGGAG-----CQCGA 4057
Qy 1252 pSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCysHisArgIl 1272
Db 4058 GGCTGGGCGCTCTACTCTTCTCCCAACAAACCGGTTCCGGGTCTCTTCGCAGAAAGT 4117
Qy 1272 eileThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleTh 1292
Db 4118 CATCACACAAAGATGTTTGATCACGTGTCCTCGTCTTCATCTTCTCAACTGCGTCAC 4177
Qy 1292 rIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLe 1312
Db 4178 CATCGCCCTGGAGAGCGCTGACATTGACCCCGGACGAGCGGGTCTTCCTCAGCGT 4237
Qy 1312 uSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLe 1332
Db 4238 CTCCTAATTCATCTTCACGGCCATCTTCGTGGCGGAGATGATGTTGAAGTGTGGCCCT 4297
Qy 1332 uGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLe 1352
Db 4298 GGGGCTGCTGTCCGGCGACACGCTACCTGCAGAGCAGCTGGAACCTGCTGGATGGCT 4357
Qy 1352 uLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLy 1372
Db 4358 GCTGTGTGTGTGTCCTCGTGGACATTGCTGGCCATGCGCTCGGCTGGTGGCGCAA 4417
Qy 1372 rIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIl 1392
Db 4418 GATCTCTGGGTGTCTGCGGCTGTGCTGTGCGGACCCCTGCGCGCTCTAAAGGTGCAT 4477
Qy 1392 eSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIl 1412
Db 4478 CAGCGGGCCCCGGGCCCTCAAGCTGGTGGAGAGCGCTGATATCTGCTCAGGCCAT 4537
Qy 1412 eGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGl 1432
Db 4538 TGGGAACATCGTCTCATCTGCTGCGCTTCTTCATCATTTTTTGGCATCTTGGGTGTGA 4597
Qy 1432 nLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLy 1452
Db 4598 GCTCTTCAAGGGAAGTTCTACTTGCAGGGGCCCCGACACGAGGAACATCTCCACCAA 4657
Qy 1452 sSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLe 1472
Db 4658 GGCACAGTGGCGGGCGGCCCTACCGCTGGGTGGCGACCGCAAGTACAACCTTCGACAACCT 4717
Qy 1472 uGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe 1492
Db 4718 GGGCCAGGCGCTGATGCTGCTGTGCTGTCTCAAGGATGGATGGGTGAACATCAT 4777
Qy 1492 tTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTr 1512
Db 4778 GTACAGCGGCTGGATGCGGTGGGTGTCACGAGAGCTGTGCAGAAACACCAACCCCTG 4837
Qy 1512 pMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPh 1532
Db 4838 GATGCTGCTGTACTTCT 4897
Qy 1532 eValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAl 1552
Db 4898 CGTGGCGCTGCTGGTGCAGAACTTCCAAAGTCCGCGGACGACCCAGGAGCGGAGGAGC 4957
Qy 1552 aArgArgGluGluLysArgLeuArgLeuGluLysLysLysArgArg----- 1568
Db 4958 GCGCGCGGAGAGGAGAACGCGCTCGCGCGCTTAGAGAGGAGCGGAGGACACTTTTCCC 5017

[illegible]

5972	Db	CAGGATGCCCAACCTGGTT---GCAGCAAGGTGTCGGTGTCCAGGATGCTCTCGCT	6020
1936	Qy	uProAsnAspSerTyMetCysArgHisGlySerThrAlaGluGlyPro-----	1952
6029	Db	GCCCAACAGACAGTACATTTCAGGCCCGTGTGCTGCTCGGCCGCCACCCCGGCC	6088
1953	Qy	-----LeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySe	1967
6089	Db	GCTCAGGAGGTGGAGAGACCTATGGGCCGCCACCCCC-----TTGGGCTC	6139
1967	Qy	rValLeuSerValHisSerGlnProAlaAspThrSerTyriIleLeuGlnLeuProLysAs	1987
6140	Db	CGTTGGCTCTGTGCACCTCCGCCCGCAGAGTCTCTGTGCTCCCTCCAGATCCCA	6194
1987	Qy	pAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuPr	2007
6195	Db	-----CTGGCTGTGTCGTCCCCAGCCAGGAGCGCGAGCCCTCCACGCCCTGTG	6244
2007	Qy	oProProGly-----ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIai	2025
6245	Db	CCCTCGGGGCACAGCCCGCTCCCCAGTCTCAGCCGGTGTCTCGCAGACAGAGGCTGT	6304
2025	Qy	eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu-----	2043
6305	Db	GCACCCGATTCCTTGAAGGGAAG---ATTGACAGCCCTAGGACACCCCTGGATCTGC	6361
2043	Qy	gLuValSerGlyProSerPro-----ProLeuAlaArgAlaTySerPheTrpGly--	2060
6362	Db	AGAGCCTGTGAGAAACCCCGGTGAGCGCGTGATCCAGGGGGGTCTCCCTGCAGTCCC	6421
2061	Qy	----GlnSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHi	2079
6422	Db	ACCACGCTCCCCAGGCCCGCCAGCGTCCGCATCTGTAAGCAATACC---TTGGACAGCA	6478
2079	Qy	sMetThrProProAlaPro--CysProGlyProGluProAsnTrpGlyLysGlyProPr	2098
6479	Db	CTCGTCTCAGCGCGCGCGCCCGCCAGCGGAGAG-----6515	6515
2098	Qy	oGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2118
6516	Db	-GAGCCGAGGCTCGGACCCAGCCGACGAGGAGGTGAGCCATCATCACCAGCTCCGCTG	6574
2118	Qy	uPro-----ProGlyGlyGlnGluProPro-----SerPr	2129
6575	Db	CCCTTGCGACCCACAGCCGAGCCCATGTCGCCGAGCGCTCTCCGTGGCGGGCGGA	6634
2129	Qy	oArgAspLeuLysLysCysTySerValGluAlaGlnSerCysGlnArgArgProThrSe	2144
6635	Db	GCGGGACCTCGCAGAGGCTTACAGCTGGAGCGTTCAGGGTCTCTGGACAGAGCC--	6699
2149	Qy	rTrpLeuAspGluGlnArgHisSerIleAlaValSerCysLeuAspSerGlySerGl	2166
6692	Db	CCGGCCAGACGACAGTGGCGGCCCTCGCGGAGCTGGCGACGGGAGACCTGGGGAGGC	6755
2169	Qy	nProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySe	2188
6752	Db	GAAGGCTGGGGCCCTGAG-----GCCGAGGCC-----GCTCTGGGTGC	6799
2189	Qy	rArgProLysLysLysSerProProSerIleThrIleAspProPro---GluSerGl	2208
6791	Db	GCGCAGAAAGAAGATGAGCCCCCTGCATCTCGGTGGAAACCCCTCGCGAGGACGA	6855
2208	Qy	nglyProArgThrProProSerPro-----GlyIleCysLeuArgArgAlaPr	2221
6851	Db	GGGCTCTCGGGCCCTCCGGCGGACGGGCGGACACCACACTAGGCGCGAGACCCC	6911
2225	Qy	oSer-----SerAspSerLysAspProLeu-----AlaSe	2233
6911	Db	GTCTGTGAGGCCACGCTCACAGGAGCTCCCTGGAGCCCAAGAGGGCTCAGGCGCGG	6971
2235	Qy	rGlyProProAspSerMetAla-----AlaSerProSerProLysLysAspValle	2255

```
Db 6971 GGGGGACCTGTCAGCAAGGGGAGCGCTGGGCGCAGGCGCTCTGCGCGGCTGAGCACCT 7030
Qy 2252 uSerLeuSerGlyLeuSerSerAspProAlaAspLeu-----AspPro 2266
Db 7031 GACCGTCCACAGCTTTGGCTTGAGCGCGCTGGACCTCGGGGTCCCGAGTGAGACCT 7088

RESULT 11
US-10-377-139-8
; Sequence 8, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-8

Alignment Scores:
Pred. No.: 0 Length: 6990
Score: 5496.50 Matches: 1244
Percent Similarity: 60.3% Conservative: 216
Best Local Similarity: 51.4% Mismatches: 525
Query Match: 46.2% Indels: 437
DB: 9 Gaps: 60

US-09-611-257A-37 (1-2266) x US-10-377-139-8 (1-6990)
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 73 CAGCCGGACCCCGGAGCCCCCATCTCCCGCCAGGCGCTGGAGAGCGCTCTGGATGGA 132
Qy 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
Db 133 GCTGATCCTCATGTCACACACCAGACCTGGCGCTATTGCTTCTTCTGCTGCGACAG 192
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 193 ACCACCAGCCCCCGGAACCTGGTGCAATCAAGATGGTGTGCAACCCCGTGGTGAATGTGC 252
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 253 ACATGCTGGTGATCTGCTGAACTCGTGACACTTGGCATGTACCGCCGCTGGCAGCAG 312
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAla 126
Db 313 ATGGACTGCTGTGCGACCGCTGCAAGATCCTGCGAGGTCTTGTGACTTCATCTTATC 372
Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys 146
Db 373 TTCTTTGCCATGGAGATGGTGTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAAGTGC 432
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 433 TACCTCGGGACACATGGAAACCGCTGGATTCTTCATCGTCATGGCAGGATGGTCGAG 492
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 493 TACTCCTCGGACCTTCAGAAACATCAACCTGTCCAGCCATCCGACCGTGCCTGAGG 552
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAsp 206
Db 553 CCCCTCAAAGCCATCAACCGCGTGCAGTATGCGGATCTTGGTGAACCTGCTCTCTGGAC 612
```

```
Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuCysPhePheValPhePheIlePheGly 226
Db 613 ACATGCCCCATGCTGGGAATGTCCTGCTGCTCTGCTCTTCTTCTTCTTCTTCTTGGC 672
Qy 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 673 ATCATAGGTGTGAGCTCTGGCGGGCGCTGCTGCGTAACCGCTGCTCTCTGGAGAGAAC 732
Qy 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db 733 TTCACCATACAAGGGATGTGGCTTGCCCCCATACTACAGCCGAGAGGATGATGAG 792
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 793 ATGCCCTTCATCTGCTCCCTGCGGGCAACATGGGATAATGGGCTGCCATGAGATCCCC 852
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 853 CCGCTCAAGGAGCAG-----GGCCGTGAGTGTCTGCTGTCTCAAGGACGACGTCTAC 903
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
Db 904 GACTTTGGGCGGGCGCGCAGGACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGT 963
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheGlyGlyAlaIleAsnPheAsp 338
Db 964 TACTACATGTGTGCGCGCAGCGCGCCACCCCAACAGGGTGCATCAACTTTGAC 1023
Qy 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
Db 1024 AACATCGGTATGCTTGGATTGTCATCTTCCAGGTGATCACTCTGGAAGGCTGGTGGAG 1083
Qy 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db 1084 ATCATGTACTACGTGATGATGCTCACTCCTTCTCACTTCACTTCTTCTTCTTCTTCTT 1143
Qy 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
Db 1144 ATCATAGTGGGCTCTCTTCTTATCATCACTGTGCTGCTGCTCATAGGACCCAGTTTC 1203
Qy 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1204 TCGGAGACCAAGCAACGCGGAGCAGCGGTGATGCTGGAGCAGCGGAGCGCTACCTGTCC 1263
Qy 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys 438
Db 1264 ---TCCAGCACGCTGCCAGCTACGCCGAGCCTGGCGACTGTCTACGAGGAGATCTTCCAG 1320
Qy 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
Db 1321 TATGCTGCCACATCTCTGGCAAGGCCAAGCGC-----CGGCGCCTG 1362
Qy 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
Db 1363 GGCCTCTACAGGCCCTGCAGAGCGCGCCAGGCGCTGGGCGCGGAGGCCCGGCCCGCCC 1422
Qy 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHis 498
Db 1423 GCCAAACCT-----GGGCCCCAC 1440
Qy 499 HisHisHisHisHisHisHis-----LeuGlyAsnGlyThrLeuArgAlaPro 515
Db 1441 GCCAAGGAGCCCCGCGCACTTACCATGGGAAGACTAAGGTCAGGGA----- 1485
Qy 516 ArgAlaSerProGluIleGlnAspArgAspAlaAsn---GlySerArgArgLeuMet--- 533
Db 1486 -----GATGAAGGGAGACATCTCGGAAGCGCGGATTTGCCAGACT 1524
Qy 534 LeuProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerVal 553
Db 1525 TTGCATGGCGCTGCCTCCCT-----GGAAATGATCATCTCGGGAAGAGAG----- 1569
```

QY 554 HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPro 573
DB 1570 -----CTGTGC-----CCGCAA 1581
QY 574 ArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVal 593
DB 1582 CATAGCCCCCTGATGCGACGCCACACCCCTG----- 1614
QY 594 HisThrSerProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSer 613
DB 1615 ----GTGACCCCATCCCCCAGCGTG----- 1638
QY 614 SerGlyProProThrLeuThrSerLeuAenIleProProGlyProTyrSerSerMetHis 633
DB 1638 ----- 1638
QY 634 LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerPro 653
DB 1638 ----- 1638
QY 654 CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg--- 672
DB 1639 -----GCTTCGATCCCGCCAGCTGCCCTTGCTGCCAGCATGAG 1677
QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAsp 687
DB 1678 GACGGCGCGCGCCCTCGGGCCTGGCGACACCGAC---TCGGGCCAGGAGGCGCTCGGC 1734
QY 688 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 707
DB 1735 TCCGGAGCTCCGCTGGTGGCGAG-----GACGAGCGGATGGGACGGGCCCCGAGC 1788
QY 708 ProHisSerArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeu--- 726
DB 1789 AGCAGACGGAGCCTCTCAGAACTGGGAAAGAGGAGGAGGAGGAGGAGCGGAT 1848
QY 727 -----AlaPheTyrArgLeuIleCysAspThrPheArgLysIle 739
DB 1849 GGGCGGTCTGCTGCGGGGATGTGTGGCGGAGACGGCAGCAAGCTGCGCGGCATC 1908
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAenThrLeuSer 759
DB 1909 GTGACAGCAAGTACTTCAACCGGGGCATCATGTGCCATCTCTGTTCACACCGTCAGC 1968
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
DB 1969 ATGGGCATCGAGCACACAGCAGCAGCGGAGGAGCTGACCAACATCTCTGGAGATCTGCAAT 2028
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
DB 2029 GTGCTCTTCCACGACATGTTTGGCCTGGAGATGATCTCTGAAGCTGGCTGCAATTTGGGCTC 2088
QY 800 PheGlyTyrIleLysAenProTyrAsnIlePheAspGlyValIleValIleSerVal 819
DB 2089 TTCGACTACTGCTGATAACCCCTCAACATCTTTCAGACATCATGTTCATCATCAGCATC 2148
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
DB 2149 TGGAGATCTGGGGCAGCGGACGCTGGGCTGTCTGGTGTCTGGACCTTCCGGCTCTGTG 2208
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
DB 2209 CGCGTGTGAACTGGTGGCTTCATGCTCCCTGGCGGCCAGCTCGTGTGCTCATG 2268
QY 860 LysThrMetAspAenValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879
DB 2269 AAGACCATGGACAACGTCGCCACCTTCGCAATGCTGTCTCATGCTTCATCTTCATCTTC 2328
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAsp 898
DB 2329 AGCATCTTGGATGCATATTTTGGCTGCAAGTTCAGCCTCCGACCGACACTGGAGAC 2388
QY 899 ThrLeuProAspArgLysAenPheAspSerLeuLeuTrpAlaIleValThrValPheGln 918

DB 2389 ACGGTGCCCGCAGCAGAGAACTTCACATCCCTGCTGTGGCCATCGTCACTGTGTCTCCAG 2448
QY 919 IleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSer 938
DB 2449 ATCTCTACCCAGGAGACTGGAACTGCTCTTCTACAATGGCATGGCCTTCCATCTTCCC 2508
QY 939 TrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeu 958
DB 2509 TGGGCTCTCCCTACTTGTTCGCCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTG 2568
QY 959 LeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAla 978
DB 2569 CTGTGGCCATCTCTGTGGAGGGCTTCAGGGCGAG----- 2604
QY 979 SerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLys 998
DB 2605 -----GGTAGCCCAATCGC 2619
QY 999 SerGluSerGluProAspPheSerProSer----- 1009
DB 2620 TCCTACTCGGACGAGGACCAGAGCTCATCCACATAGAAGATTTGATAGCTCCAGGAA 2679
QY 1010 ---LeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHis 1028
DB 2680 GCGCTGGACAGCAGCGGAGATCCCAAGCTTGCCCAATCCCATGACCCCAATGGGCAC 2739
QY 1029 ProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPromet 1048
DB 2740 -----CTGGACCCC----- 2748
QY 1049 SerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArg 1068
DB 2749 AGTCTCCCATGCTGGTGGCACCCTAGGTCTCTGTGGGCTGCGGAGCTGCCCCGACTC 2808
QY 1069 Thr-----SerSerSerGlySerAla 1075
DB 2809 TCATCTGACCGGACCCCATGTGTGGCTGGCTCCCGAAAGACAGTGTCTGTCT 2868
QY 1076 GluProGlyAlaAlaHisGluMetLysSerProSerProSerAlaArgSerProHisSer 1095
DB 2869 CTAGGGAGGATGAGTATGACACAGCGCTCCCTCTCCAGCTCCCGGAGCTCTACTACGG 2928
QY 1096 ProTyrSerAlaAlaSerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArg 1115
DB 2929 CCATGGGCGCGCAGCGGCTGGCCAGCGCTGCTCCAGCTGGAAC----- 2976
QY 1116 AlaProSerLeuLysArgArgSerProSerGlyLysArgSerLeuLeuSerGlyGlu 1135
DB 2977 -----AGCCTCAAGCACACAGCGCTGCGGAGCATGAGTCCCTGCTCTCTGCGGAG 3030
QY 1136 ---GlyGlnGluSerGlnAspGluGluGluSerSerGluGlu-----GluArgAlaSer 1152
DB 3031 CGCGGCGCGCGCGCGGCTGCGAGGTTGCGCGGACGAGGGGCGCGCGCGCGCGCGCA 3090
QY 1153 ProAlaGlySerAspHis----- 1158
DB 3091 CCCTGTGCACACCCACACGCCCCACCATTCATCAGCGGCCCATCTTGGCGCACCGCCAC 3150
QY 1159 ---ArgHisArgGlySerLeuGluArgGluAlaLysSerPheAspLeuProAspThr 1177
DB 3151 CGCCACACCGCGGACGCTGCTCCTCGACACAGGAGACTCGGTGGACCTGCGCGGAGCTG 3210
QY 1178 LeuGlnValProGlyLeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGlu 1195
DB 3211 GTGCGCGCGGTGGCGGCCACCCCGCGGCGGCGGAGGGCGGCGGCGGCGGCGGCGG 3270
QY 1196 HisGlnAspCysAenGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAsp 1215
DB 3271 CATGAGCATGCAATGGCAGGAT-GCCAGCATGCG---CAAGACGCTTTCACCAAGAT 3326
QY 1216 AspProLeu-AspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArg 1235

Db 3327 GGGCGACCGGGGATCGCGGGAGGATGAGGAGGAAATCGATACACCCCTGTGCTTCG 3386
Qy 1235 gValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSe 1255
Db 3387 CGTCCGCAAGATCATCGAGCTATTAAGCCGAGCTGGTGGAGGTCCGGAGAGCTGGTC 3446
Qy 1255 rLatyrIlePheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHi 1275
Db 3447 TGTCTACCTCTCTCTCCGAGAACAGGTTCGGGTCTGTGTGCAGACCATATTATGCCCA 3506
Qy 1275 sIysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMe 1295
Db 3507 CAAACTCTTCGATACGTCTGCTCGCCCTTCATCTTCTCAACTGTCATCACCATCGCCCT 3566
Qy 1295 tGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTy 1315
Db 3567 GGAGCGGCTCAGATCGAGCGCGGACGACCGAGCGCATCTTCTCACCGTGTCCAACTA 3626
Qy 1315 rIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCy 1335
Db 3627 CATCTTCAGCGGCATCTCTGTGGCGGAGATGACATTTGAAGGTAGTCTCGCTGGCCCTGA 3686
Qy 1335 sPheGlyGluGlnAlaTyrLeuArgSerTrpAsnValLeuAspGlyLeuLeuValLe 1355
Db 3687 CTTGGCGGAGCGGCTACTACGACGACGCTGGAACGCTGCTGGATGGCTTCTTGTCTT 3746
Qy 1355 uIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGl 1375
Db 3747 CGTGTCATCATCGACATGTGTGTCTCTGGCTCAGCGGGGAGCCAGACATCTTGGG 3806
Qy 1375 yMetLeuArgValLeuLeuArgLeuArgThrLeuArgProLeuArgValIleSerArgAl 1395
Db 3807 GGTCTCTCCGAGTCTTCCGCTCTCTGGCCACCTTACGCCCTCTGCTGTCTATCAGCGG 3866
Qy 1395 agGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnI 1415
Db 3867 GCGGGCGCTGAAGCTGGTGGAGACATCATCTCTCCCTCAAGCCCATCGGCAACAT 3926
Qy 1415 eValValIleCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLy 1435
Db 3927 CGTGCTCATCTGCTGTGCTCTTTCATCATCTTGGCATCTCTGGAGTGCAGCTTTCAA 3986
Qy 1435 sGlyLysPheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCy 1455
Db 3987 GGGCAAGTTCTACCACTGTCTGGCGTGACACCCGCAACATCACCACCGCTCGGACTG 4046
Qy 1455 sAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAl 1475
Db 4047 CATGGCGGCAACTACCGCTGGGTCCATCACAATAACAATTCGACAACTGGGCGGAGC 4106
Qy 1475 aLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGl 1495
Db 4107 TCTGATGTCTCTTGTCTGGCATCCAAAGATGTTGGTGGTGAACATCATGTACATGG 4166
Qy 1495 yLeuAspAlaValGlyValAspGlnProIleMetAsnHisAsnProTrpMetLeuLe 1515
Db 4167 ACTGGATGTGTGTGTGGACGAGCGCTGTGACCAACCAACACCCCTGGATGTGCT 4226
Qy 1515 uTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyVa 1535
Db 4227 GTACTTTCATCTCTCTCTCATCTGCTGAGTCTTGTGTGCTCAACATGTTGTGGGTGT 4286
Qy 1535 lValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgAr 1555
Db 4287 CGTGGTGGAGAACTTCCAAAGTGGCGGACGACACGAGGAGGTGAAGAGCGACGCGGCG 4346
Qy 1555 gGluGluLysArgLeuArgLeuGluLysLysArgArgLysAlaGlnCysLysProTy 1575
Db 4347 TGAGGAGAGAGCGGCTCGCGGCTCTGAGAGAAGCGCCGGAAGGCCCGAGCGGCTGCCCTA 4406
Qy 1575 rTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLe 1595
Db 4407 CTATGCCACCTATTGTTCACACCGGCTGTCTCATCTCCATCTCCATGTGTGACACGACCTACCT 4466

Qy 1595 uAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisty 1615
Db 4467 GGACATCTTCATCACCTTCATCTCCCTCAACGTGGTGCACCATGCTCCCTGGAGCACTA 4526
Qy 1615 rGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI 1635
Db 4527 CAATCAGCCACAGTCCCTCGAGACAGCCCTCAAGTACTCAACTATATGTTCACCACTGT 4586
Qy 1635 ePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgPhePheGlnAs 1655
Db 4587 CTTTGTGTGGAGGCTGTCTGAAGCTGTGGCATTTGTCTCTGAGCGCTTCTTCAAGGA 4646
Qy 1655 pArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGl 1675
Db 4647 CCGATGGAACACAGCTGGACCTGGCCATTTGTCTACTGTCTCAGTCATCGGCATCACCTGGA 4706
Qy 1675 uGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgVa 1695
Db 4707 GGAGATCGAGATCAATTCGCGCCCTGCCCATCAATCCACCATCATCCGATCATGAGGT 4766
Qy 1695 lLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLe 1715
Db 4767 TCTGGCATTTGCCGAGTGTCTGAAGCTGTGAAGATGGCCACAGGAATCGGGCCCTGCT 4826
Qy 1715 uAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLe 1735
Db 4827 GGACACGGTGTGCAAGCTTTGCCCCAGGTGGCAACCTGGGCCCTCTCTTTCATGCTGCT 4886
Qy 1735 uPhePheIlePheAlaLeuLeuGlyValGluIlePheGlyAspLeuGlyCysAspGluTh 1755
Db 4887 CTTCTTCATCTATGTCTCTCGGGGTGGAGCTCTTTGGGAAGCTGTGTGCAACGACGA 4946
Qy 1755 rHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLe 1775
Db 4947 GAACCGCTGCGAGGGATGAGCGGCATGCCACTTCGAGAACTTCGGGATGGCTTCCT 5006
Qy 1775 uThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuAr 1795
Db 5007 CACACTTTCAGGCTCTCCACGGGTGACAACTGGAACGGGATCATGAAGACACGCTGCG 5066
Qy 1795 gAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTy 1812
Db 5067 GGACTGCAACCCACGACGAGCGAGCTGCTCGAGACGCTGACAGTTGTGTGCGCGCTGA 5126
Qy 1812 rPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLe 1832
Db 5127 CTTCTGTAGCTTCTGTCTCACCAGGAGTTCTGTCTCATCAAGTGTGTGTGTGTGCT 5186
Qy 1832 uMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGl 1852
Db 5187 CATGAAGCACCTGGAGCAGACCAACAGGAGCGCAGGAGGACGCCGAGATGGATGCCGA 5246
Qy 1852 uLeuGluLeuGluMet---LysThrLeuSerProGlnProHisSerProLeuGlySerPr 1871
Db 5247 GCTCAGCTGGAGATGGCCATGGCTTGGGCCCTTGCCCGAGGCTGCTTACCGGCTCCCC 5306
Qy 1871 oPheLeuTrpProGlyValGluGlyProAsp----- 1881
Db 5307 GGGCGCC---CCTGGC---CGAGGGCGGGAGGGCGGGCGGGCGGCGACACCGAGGG 5360
Qy 1882 -----SerPro----- 1883
Db 5361 CGGCTGTGGCGGCTGCTACTCGCTGCCCGAGGAGAACCTGTGGCTGGACAGCGCTC 5420
Qy 1884 -----AspSerProLysProGl 1889
Db 5421 TTTAATCATCAAGGACTCCTTGGAGGGGAGCTGACCATCATCGACAACTGTGCGGCTC 5480
Qy 1889 yAlaLeuHis-----ProAlaAla----- 1895
Db 5481 CATCTTCCACCACTACTCTCTCGCTCGCGGTGCAAGAGTGTCAACCAAGCAAGA 5540


```
QY 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys 146
Db 373 TTCTTTGCCATGGAGATGGTGCTCAAGATGGTGGCCCTGGGGATTTTGGCAAGAGTGC 432
QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 433 TACTCTGGGACACATGGAACCCGCTGGATTCTTCATCGTCATCGGAGGATGGTCGAG 492
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 493 TACTCTCCGTGACCTTCAGAACATCAACCTGTGAGCCATCCGACCGTGGCGCTCTGAGG 552
QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
Db 553 CCCCTCAAGCCATCAACCGCGTCCAGATGCGGATCTGTGTGAACCTGCTCTCTGGAC 612
QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheGly 226
Db 613 ACATGCGCCATGCTGGGGAATGCTGCTGCTCTGCTCTCTGCTCTCTCTCTCTCTCTG 672
QY 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 673 ATCATAGTGTGAGCTCTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db 733 TTCACCATCAAGGGATGTGGCTTGGCCCTATCTACCATCCGCGGAGGATGATGAG 792
QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 793 ATGCCCTTCACTGCTGCTGCTGCGGCGCAATGGGTAATGGGCTGCCATGATGATCCCC 852
QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 853 CCCTCAAGAGCAG-----GGCGGTGAGTGTGCTCTGCCAAGGACGCTCTAC 903
QY 301 AspTyrGluAlaTyrAsnSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
Db 904 GACTTTGGGCGGGCGCCAGGACCTCAATGCCAGCGGCTCTGTGTCACTTGAACCGT 963
QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 964 TACTACAAATGTGTGCGCGACGGCGCGCCCAACCCCAAGGGTGCATCAACTTGTGAC 1023
QY 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
Db 1024 AACATCGTTATGCTTGGATTGTTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAG 1083
QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db 1084 ATCATGTACTACGTGATGATGCTCACTCTTCTACAACTTCATCTACTTCTCTGCTT 1143
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPhe 398
Db 1144 ATCATAGTGGCTCTCTTTCATGATCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1203
QY 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1204 TCGGAGACCAAGCAAGGGAGCACCGGCTGATCTGAGGAGCGGCGGCTACCTGTGTC 1263
QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys 438
Db 1264 ---TCCAGCAGGTGGCCAGCTACCGCGAGCTTGGGAGCTTCCAGGAGATCTCCAG 1320
QY 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaAla 458
Db 1321 TATGTCTGCCACATCTCTGCGCAAGGCCAAGCGC-----CGCGCCCTG 1362
QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThrGlnPro 478
Db 1363 GGCCTCTACAGGCCCTGCAAGAGCGCGCGCCAGGCCCTGGGCGCGGAGGCCCGGCCCC 1422
```

```
QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHis 498
Db 1423 GCCAAACCT-----LeuGlyAsnGlyThrLeuArgAlaPro 515
QY 499 HisHisHisHisHisHisHis-----LeuGlyAsnGlyThrLeuArgAlaPro 515
Db 1441 GCCAAGAGCCCGCGGACCTACCATGGGAAGACTTAAGGTGTCAGGA----- 1485
QY 516 ArgAlaSerProGluIleGlnAspArgAspAlaAsn---GlySerArgArgLeuMet--- 533
Db 1486 -----GATGAAGGAGACATCTCGGAAGCCGCGCATTCGCAGACT 1524
QY 534 LeuProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerVal 553
Db 1525 TTGCATGGGCTTCCCTCCCT-----GGAATGATCACTCGGGAAGAGAG----- 1569
QY 554 HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPro 573
Db 1570 -----CTGTGC-----CCGCAA 1581
QY 574 ArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVal 593
Db 1582 CATAGCCCCCTGATGCGAGCCCCACACCTG----- 1614
QY 594 HisThrSerProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSer 613
Db 1615 ---GTGAGGCCCATCCCGCCACGCTG----- 1638
QY 614 SerGlyProProProThrLeuThrSerLeuAsnIleProGlyProTyrSerSerMetHis 633
Db 1638 ----- 1638
QY 634 LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerPro 653
Db 1638 ----- 1638
QY 654 CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg--- 672
Db 1639 -----GCTTCGATCCCGCCAGCTGCTGCTGCTGCCAGCATGAG 1677
QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAsp 687
Db 1678 GACGGCGCGCGCTCGGGCTGGGCGAGCAGCCGAC---TCGGGCGCAGAGGGCTCGGGC 1734
QY 688 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 707
Db 1735 TCCGGAGCTCCCTGCTGTCGAG-----GACGAGCGGATGGGACGCGGCGCGGAGC 1788
QY 708 ProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeu--- 726
Db 1789 AGCGAGGACGGACCTCTCAGAACTGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1848
QY 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 1849 GGGCGGCTCTGGCTGTGCGGGATGTGTGCGGGAGACGCGAGCCCAAGCTGCGCGGATC 1908
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 1909 GTGACACGCAAGTACTTCAACCGGGCATCATGATGGCCATCTCTGTCAACACCGTCAGC 1968
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 1969 ATGGGATCGAGCACCGAGCAGCGGAGGAGCTGACCAACATCTCTGGAGATCTGCAAT 2028
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799
Db 2029 GTGGTCTTCAACGACATGTTGCCCTGGAGATGATCTTGAAGCTGCTGATTTGGGCTC 2088
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2089 TTGACTACTGCGTAACCCCTCAACATCTTCAGACGATCATTTGTCATCATCAGCATC 2148
QY 820 TrpGluIleValGlyGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
```

Db	2149	TGGGAGATCTGGGGCAGCGGACGGTGGGCTGTGGTCTCGGACCTTCGGCTGCTG	3091	CCCCGTGCACACCCACACGCGCCACACATTCATCAGCGGCCCATCTTGGCGCACCGCCAC
Qy	840	ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet	1159	---ArgHisArgGlySerLeuGluArgGluAlaLysSerPheAspLeuProAspThr
Db	2209	CGGCTGCTGAACCTGGTGGCTTCATGCTGCTGCTGCGGGCCAGCTCGTGGTGTCTCATG	3151	CGCCACACCGCGGACGCTGTCCCTCGACAAAGGAGCTCGGTGGACCTGCGCGAGCTG
Qy	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe	1178	LeuGlnValProGlyLeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGlu
Db	2269	ARGACCATGACAACTGGCCACTTCTGTCATGCTGCTCATGCTTCTTCATCTTCATCTTC	3211	GTGCGCGGTGGGCCCCACCGCGGCGCTGGAGGCGCGAGGCCCGCCCGCGG
Qy	880	SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAsp	1196	HisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAsp
Db	2329	AGCATCTTTGGGATGCATATTTTGGCTGCAAGTTTTCAGCTTCGCGCATCGGACATGGAG	3271	CATGAGGACTGCAATGGCAGGAT-GCCAGCATCGC---CAAAGACGCTTTCACCAAGAT
Qy	899	ThrLeuProAspArgLysAsnPheAspSerLeuLeuTIPAlaIleValThrValPheGln	1216	AspProProLeu-AspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluAr
Db	2389	ACGGTGGCCGACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGTCACTGTGTCCAG	3327	GGCGGACCGCGGGATCGCGGGGAGGATGAGGAGGAAATCGATACACCTGTGCTCCG
Qy	919	IleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSer	1235	gValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSe
Db	2449	ATCTCACCCAGGAGGACTGGAAGCTGCTTCTTACAATGGCATGGCTCCACTTCTCC	3387	CGTCCGCAAGATCATCGACTCTATAAGCCCGACTGTGTGCGAGGTCCGCGAAGACTGGTC
Qy	939	TrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeu	1255	rAlaTyrIlePheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHi
Db	2509	TGGGCTCTCCCTACTTTGTGCGCCTCATGACCTTGGCAACTATGTGCTTTCACACCTG	3447	TGTCTACTCTCTCTCCCGAGAACAGGTTCCGGGTCTGTGTGCAGACCATTAATGCCCA
Qy	959	LeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAla	1275	slsMetPheAspHisValLeuValIleIlePheLeuAsnCysIleThrIleAlaMe
Db	2569	CTGGTGCCATCTCTGGTGAGGGCTTCCAGCGGAG-----GGTGACGCCAATCGC	3507	CAAACCTTTTCGACTAGCTGCTGCGCTTCACTTTCTCACTGCATACCATCGCCCT
Qy	979	SerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLys	1295	tGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTy
Db	2605	-----GGTGACGCCAATCGC	3567	GGAGCGGCTTCAGATCGAGCCCGGACCGCAACGCACTTTCTCACCGTGTCCAACCTA
Qy	999	SerGluSerGluProAspPhePheSerProSer-----	1315	rIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCy
Db	2620	TCCTACTCGGACGAGGACCGAGCTCATCCAACATAGAAGAGTTTGATAAGCTCCAGAA	3627	CATCTTCACGGCCATCTTCGTGGCGAGATGACATTAAGGTAGTCTTCGTGGGCGCTGTA
Qy	1010	---LeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHis	1335	spheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLe
Db	2680	GGCTGGACACGCGGAGATCCCAAGCTGTGCCAATCCCATGACCCCAATGGGCAC	3687	CTTCGGGAGACGGCGTACCTACGACAGCTGGAAGCTGTGGATGGCTTTCTTGCTTT
Qy	1029	ProGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMet	1355	uIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGl
Db	2740	-----CTGACCCC-----	3747	CGTGTCTCATTCGACATCGTGTGCTCCCTGGCTCAGCCGGGAGCCCAAGATCTTGGG
Qy	1049	SerLeuProLysSerThrSerThrGlyLeuGluAlaLeuGlyProAlaSerArgArg	1375	yMetLeuArgValLeuArgLeuArgThrLeuArgProLeuArgValIleSerArgAl
Db	2749	AGTCTCCCACTGGGTGGGCACCTAGTCTCTGCTGGGGCTGGGGACCTGCCCGGACTC	3806	GGTCTCCGAGTCTTGGGCTCTTCGCGACCCCTACGCGCCCTGCGTGTCAACCGCGGC
Qy	1069	Thr-----SerSerSerGlySerAla	1395	aGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIl
Db	2809	TCACTGACCGGACCCCATGCTGTGTGGCCCTGGGCTCCCGAAGAGAGTGTATGTCT	3867	GCCGGGCTGAAGCTGTGGTGGAGACATCATCTCTCTCCCTCAAGCCCATCGGCAACAT
Qy	1076	GluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSer	1415	eValIleCysCysAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLy
Db	2869	CTAGGAGGATGAGTATGACACGAGGCTCCCTGCTCCAGCTCCCGAGCTCTACTACGGG	3927	CGTGCTCATCTGCTGTGCTCTTCATCATCTTTGGCATCTCTGGAGTGCAGCTCTTCAA
Qy	1096	ProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArg	1435	sGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCy
Db	2929	CCATGGGCGCGGCGGCTGGGCCAGCGCTCGCTCCAGCTGGAAC-----	1455	GGGCAAGTTTACCACCTGTCTGGGCTGGACACCGCAACATCACCAACCGCTGGAGCTG
Qy	1116	AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu	1475	sAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAl
Db	2977	-----AGCCTCAACACAAAGCCCGTGGCGGAGCATGACTCCTCTCTCTCGGAG	4046	CATGGCGCCCAACTACCGCTGGGTCCATCAAAATACAACTTCGAAACCTTGGGCCAGGC
Qy	1136	---GlyGlnGluSerGlnAspGluGluSerSerGluGlu-----GluArgAlaSer	4106	aLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGl
Db	3031	CGCGCGCGGCGCGGCTGTGCGAGGTTCGCGGAGGTTCGCGGACGAGGGCGCGCGCGCGCA	1495	TCTGATGTCCTCTTTGCTCTGGCATCCAGGATGGTTGGGTGAACATCATGTCAATGG
Qy	1153	ProAlaGlySerAspHis-----	4166	yLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLe
			1515	ACTGGATGCTGTGTGTGGACGAGCTGTGTGACCAACCAACCCCTGGATGCTGCT

Db	6234	GGGCTGCGGGCG-	:::		-----CATCAGCGCAG	6257
Qy	2156	gHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPr				2176
Db	6258	CCACGAGCGGGGGTCC---ACCACCGGGGTGCACCCACCACTCCATGACCC				6314
Qy	2176	oSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLy				2193
Db	6315	CTGGACAGGAGGGCCGCGTGGCGGGCGGGGGCGGGCAGCAGCACTCGGA				6374
Qy	2193	sLysLeuSerProProSerIleThr-----IleAspProProGluSerGlnGlyPr				2210
Db	6375	GACCCCTCAGCAGCCCTCTCGCTCACTCCCTCTTCTGCCCGCGGCC-				6420
Qy	2210	oArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer--				2229
Db	6421	---CCGCCCGCACCCCGCGCTCACGCCCGCCAGGAAGTTACAGACACCCAGCAGCCT				6476
Qy	2230	-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSe				2246
Db	6477	GGCGCGCCCGCGCGCCACGCGCGCGCCCTGGCCCCACGGCTGSCCGGAGCCCTC				6536
Qy	2246	rProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPr				2266
Db	6537	GTGGGCGCGGAC-----CGCAGCAAGACCCCGCCCGCGGGCACC				6578
Qy	2266	o 2266				
Db	6579	G 6579				

```

RESULT 13
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

```

Alignment Scores:	
Pred. No.:	0
Score:	5492.50
Percent Similarity:	60.3%
Best Local Similarity:	51.4%
Query Match:	46.1%
DB:	3
Length:	6816
Matches:	1236
Conservative:	213
Mismatches:	506
Indels:	449
Gaps:	55

US-09-611-257A-37 (1-2266) x US-09-935-541-1 (1-6816)

Qy 31 A t g p r G l y p r o C l y s e r l a g l u l y s a s p r o g l y s e r a l a n s p s e r c l u a l a g l u g l y 50
::: ||||| |
Db 264 C a g c c g g a c c c c g g a c c c c c a t c c t c c c c g c a g g c c t g g a g a g c c t c t g a i g a 323
::: ||||| |
Qy 51 -----LeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGln 66
324 G T G A T C C T C A T G C C C A C C C A G A C C T G G G C C T A T T G C C T T C T G C C T G G A C A G 383
::: ||||| |

Qy	67	AspSerArgProArgSerTrpCysIeuAurGthrValCysAsnProTrpPheGluArgile	86
Db	384	ACACAGCCCCCGGAACCTGGTGCATCAAGATGGTGTGCAACCCGGTGTGAATGTGTC	443
Qy	87	SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp	106
Db	444	AGCATGCTGGTGATCTGCTGAACCTGCGTGACACCTGGCATGTACACCGCTGGACGAC	503
Qy	107	IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla	126
Db	504	ATGGACTGCTGTCGACACCGCTGCAAGATCCTGCAAGTCTTTGTAGACTTCATCTTTATC	563
Qy	127	PhePheAlaValGluMetValValIysMetValAlaLeuGlyIlePheGlyLysCys	146
Db	564	TTCTTTGGCATGAGATGGTGTCAAGATGGTGGCCCTGGGATTTTGGCAAGAAGTGC	623
Qy	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu	166
Db	624	TACTCTGGGACACATGGAACCGCTGGATTTCTTCATCGTCATGGCAGGATGTCGAG	683
Qy	167	TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValIeuAurG	186
Db	684	TACTCCCTGGACCTTCAGAACATCAACCTGTGAGCATCCGACCGTGGCGTCTCTGAGG	743
Qy	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206
Db	744	CCCTCAAGCCCATCAACCGGTGCCAGTATCGGATCTCGTGAACCTGCTCTGGAC	803
Qy	207	ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly	226
Db	804	ACACTGCCCATGCTGGGAATGTCCTGCTGCTGCTGCTTCTTGTCTTCTTCATCTTTGGC	863
Qy	227	IleValGlyValGlnIleThrPAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn	246
Db	864	ATCATAGTGTGAGCTGTGGGGCGGCTGCTGCGTAAACCGCTGCTCTCTGGAGGAGAAC	923
Qy	247	PheSerLeuProLeuSerValAspLeuGluAurGlyTyrTyrGlnThrGluAsnGluAspGlu	266
Db	924	TTCACCATACAGGGATGTGGCTTGCCCCCATACTACCGCGGAGGAGGATGATGAG	983
Qy	267	SerProPheIleCysSerGlnProArgIleAsnGlyMetArgSerCysArgSerValPro	286
Db	984	ATGCCCTTCATCTGCTCCCTGTCGGGCGACAAATGGGATAATGGGCTGCCATGAGATCCCC	1043
Qy	287	ThrLeuArgGlyAspGlyGlyGlyProCysGlyLeu	300
Db	1044	CCGCTTCAAGGAGCAG-----GGCGGTGAGTGTGCTGCTCCAGGACGACGTCTAC	1094
Qy	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln	318
Db	1095	GACTTTGGGCGGGCGCCAGGACCTCAATGCCAGCGGCTCTGTGTCAACTGGAAACCGT	1154
Qy	319	TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp	338
Db	1155	TACTACAATGTGTCGCGCAGCGGCGAGCCCAACCCCAACAGGGTGCATCAACTTTCGAC	1214
Qy	339	AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAsp	358
Db	1215	AACATCGGTTATGCTGGATTGTCACTTCCAGGTGATCACTCTGGNAGGCTGGGTGGAG	1274
Qy	359	IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu	378
Db	1275	ATCATGTACTACGTGATGGATGCTCACTCTCTTCAACCTTCATCTACTTCACTCTGCTT	1334
Qy	379	IleIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPhe	398
Db	1335	ATCATAGTGGGCTCCTTCTTCATGATCAACCTGTGCGCTCGTTGTATAGCGACCCAGTTC	1394
Qy	399	SerGluThrLysGlnArgGluSerClnIleuMetArgGluGlnArgValArgPheLeuSer	418
Db	1395	TCGGAGACCAAGCAACGGGAGCAGCGGTGATGTGTGGACGACGGCGACGCTACTCTGCC	1454

Db	3030	GCGGCCTGGCCAGCGCTCGCTCCAGCTGGAAC-----AGCCTCAAG	3071	Qy	1460	rArgTrpValArgHisLysTyrAsnPheAspHisLeuGlyGlnAlaLeuMetSerLeuPh	1480
Qy	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer	1139	Db	4148	CGCGTGGGTCCTATCAAAATACAACTTCGACAACTCGGCGCCAGGCTCTGATGTCCTCTT	4207
Db	3072	CACAAGCCGCGTCGGGAGCATAGTCTCTCTCTCGGAGCGCGCGCGCGCC	3131	Qy	1480	eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValG1	1500
Qy	1140	GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp	1157	Db	4208	TGTCCTGGCATCAAGGATGGTGGTGAAACATCATGTACAAATGGAGCTGGATCTGTTC	4267
Db	3132	CGGGTCTCGAGGTTGCGCGGAGCGAGGGCGCGCGCGCGCATGCCCTGCACACCCCA	3191	Qy	1500	yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh	1520
Qy	1158	His-----ArgHisArgGly	1162	Db	4268	TGTGGACACGACGCTGTGACCAACCAACCCCTGGATGCTGCTACTTCTATCTCCTT	4327
Db	3192	CACGCCACACCATTTATCATCGGCGCCCATCTGCGCGCACCGCCACCCACCGCGCG	3251	Qy	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh	1540
Qy	1163	SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly	1182	Db	4328	CCTGCTCATGCTCAGCTCTTTGCTCAACATGTTTGGGGTCTGTTGGTGAGAACCTT	4387
Db	3252	ACGCTGTCCTCCACAACAGGACTCGTGCAGCTGCGCGAGCTGGTGGCGCGGTGGC	3311	Qy	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe	1560
Qy	1183	LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn	1200	Db	4388	CCACAAGTCCGCGACGACCCAGGAGGCTGAAGAGGCACGCGCGCTGAGGAGAAGCGCT	4447
Db	3312	CCCCACCCCGCGCTGGAGGGCGGAGGGCGCGCGCGCGCGCATGAGGACTGCAAT	3371	Qy	1560	uArgArgLeuGluLysArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe	1580
Qy	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeu-As	1220	Db	4448	GCGCGCTCGAAGAACGCGGAGGCGCGCGCTGCCCTACTATGCCACCTATTG	4507
Db	3372	GGCAGGAT-GCCCCAGCATCGC---CAAAGACGCTCTTCAACAAGATGGCGACCGCGGGA	3427	Qy	1580	rArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh	1600
Qy	1220	pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpI1	1240	Db	4508	TCACACCGCGCTGCTCATCCACTCCATGTCACCGAGGAGGAGGAGGAGGAGGAGG	4567
Db	3428	TCGCGGGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3487	Qy	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI1	1620
Qy	1240	eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr	1260	Db	4568	CTTCATCATCTGCTCAACGCTGCTCACCCTGCTGCTGCTGCTGCTGCTGCTGCTG	4627
Db	3488	CGACGCTATAAGCCCGACTGCTGCGAGGTCGCGGAGAGCTGCTGCTGCTGCTGCTC	3547	Qy	1620	eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe	1640
Qy	1260	oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi	1280	Db	4628	CCTGGAGACAGCCCTCAAGTACTGCAACTATATGTCACCACTGCTTGTGTGGAGGC	4687
Db	3548	TCCCGAGAACAGGTTCCGGGTCCTGTGTGACAGCATATTATGCCACCAACTCTTCGACTA	3607	Qy	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe	1660
Qy	1280	sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI1	1300	Db	4688	TGTCCTGAAGCTGGTGGCATTTGCTGAGGCGCTTCTTCAAGGACCGATGGAACCACT	4747
Db	3608	CGTGTCTGCGCTTCACTTCTTCACTGATCACCATCGCCCTCGGAGCGCGCTCAGAT	3667	Qy	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
Qy	1300	eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa	1320	Db	4748	GGACTTGGCCATTTGCTACTGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC	4807
Db	3668	CGAGSCCGGACGACCGCAACGCATCTTCTCACCGTGTCCAACATACATCTTCACGGCCAT	3727	Qy	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
Qy	1320	lPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl	1340	Db	4808	TGCGCGCTGCGCCATCAATCCCATCATCCGATCATGAGGGTTCTGCGCATTTGCCG	4867
Db	3728	CTTCGTGGCGAGATGATGAAGGTAGTCTCGCTGGGCTGTACTTTCGGCGAGCGGC	3787	Qy	1700	gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl	1720
Qy	1340	aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs	1360	Db	4868	AGTGTGAAGCTGTTGAAGATGGCCACAGGAATCGGGGCCCTGCTGGACACGGTGTGCA	4927
Db	3788	GTACCTAGCAGCAGCTGGAAGCTGCTGGATGGCTTTCTGTCTTCGTGCTCATCGA	3847	Qy	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl	1740
Qy	1360	pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValIe	1380	Db	4928	AGCTTGGCCCCAGGTGGGCAACCTGGGCTCTCTCTCATGTGCTCTTCTTCTCATATGC	4987
Db	3848	CATCGTGTGCTTCCCTGAGCGCTCAGCGGGGAGCAAGATCTTGGGGGTCTCCGAGTCTT	3907	Qy	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1	1760
Qy	1380	uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe	1400	Db	4988	TGCTCTCGGGTGGAGCTCTTTGGGAAGCTGCTGCAACGACGAGACCCCGTGGAGGG	5047
Db	3908	GCGGCTCTGCGACCCCTACGCGCCCTCGGTGTATCATGCGCGGGCGCGGGCTGAGCT	3967	Qy	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
Qy	1400	uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy	1420	Db	5048	CATGACCGCGGATGCCCTTCGAGAACTTCGGCATGGCTTCTTCTTCTTCTTCTTCTT	5107
Db	3968	GGTGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGCTG	4027	Qy	1780	lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspGl	1799
Qy	1420	sAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa	1440	Db	5108	CTTCCACGGGTGACAACTGGAAACGGGATCATGAAGACACGCTGCGGGAGCTGACCCACA	5167
Db	4028	TGCTTCTTTCATCATCTTTGGCATCTGGGAGTGCAGCTCTTCAAGGGCAAGTCTTACCA	4087	Qy	1799	nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa	1817
Qy	1440	lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy	1460	Db	5168	CGAGCGCAGCTGCTGAGCAGCCTCGAGCTTGTGTGCGCGCTGTACTTCTGTAGCTTCTG	5227
Db	4088	CTGTCTGGGCGGTGGACACCCCGCAACATCACCAACCGCTCGGACTGATGCGCCCACTA	4147				

```
QY 1817 lLeuThrAlaGlnPheValLeuValAenValValIleAlaValLeuMetLysHisLeuGl 1837
Db 5228 GCTCACCGCCAGTTCGTGCTCATACAGTGGTGGTGTCTCATGAACACCTGGA 5287
QY 1837 uGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeu 1857
Db 5288 CGACAGCAACAGAGCGCAGGAGGACGCCGAGATGGATGCCAGCTCGAGCTGGAGAT 5347
QY 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGl 1876
Db 5348 GGCCCATGGCTTGGGCCCTTGGCCGAGGCTGCTACCGGCTCCCGGGCGCC---CCTGG 5404
QY 1876 yValGluGlyProAspSerProAsp----- 1884
Db 5405 C---CGAGGGCCGGGAGGGCGGGCGGGCGGGCGACACACAGGGCGGCTTGTGCCGGCG 5461
QY 1885 -----SerProLysProGlyAlaLeu----- 1891
Db 5462 CTGCTACTCCCTGGCCAGGACTCTTGGAGGGGGAGCTGACCATCATCGAACCTGTG 5521
QY 1892 -----HisProAlaAlaHisAla----- 1897
Db 5522 GGGCTCATCTTCCACCACTACTCTCTCGCTCGCGCTGCGAGAGTGTACACACGACAA 5581
QY 1898 -----ArgSerAlaLe 1901
Db 5582 GCAAGAGGTGCAGCTGGCTGAGACGGAGGCTTCTCCTCGAACTCAGACAGGTCTCTGTC 5641
QY 1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
Db 5642 CATCTGTGGGTGACGACTGAGTCTCGAGGACCCACAGACCTGCCACCTGGCCGCA 5701
QY 1913 ---HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929
Db 5702 GGACACAAGGGTGAGCTGGACCACTGAGCCCATGCGCCATGCTGTGGAGACCTGGCGCAATG 5761
QY 1930 -----ValSerArgThrHisSerLeuProAsn---AspSerTyMetCysArgHi 1945
Db 5762 CTTCCTTCCCTTGTCTCTACGGCGCTCTCGCGGATGCTCCAGCCCTCTCTGCGCCATGCC 5821
QY 1945 sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe 1965
Db 5822 GGAGGAGATCCCATCAACCTCTG-----CGGTCTGTG-----CTGAACATCATGACAG 5869
QY 1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyTrpIleLeuGlnLeuPr 1985
Db 5870 CAGTCAAGCACCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCTGCGCCATGCC 5929
QY 1985 oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999
Db 5930 AGCCGAGTCTTCCACCTGTCAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGG 5989
QY 1999 rTrpGlyThrIleProLysLeuProProProGly-----ArgSerProLe 2014
Db 5990 CACTGGAACCTTCCCAAGATTCGGTGCAGGGCTCTCTGGGCATCTCTGCGGTCACCAAG 6049
QY 2014 uAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGl 2034
Db 6050 GGTCACACTGTACCTCTCCGGCAGGCCACCGGGAGGACACGCTCGCTGGAC----- 6101
QY 2034 yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaAr 2054
Db 6102 -----GCCAGCCCCAGCAGCTCCCGGGCGAG 6127
QY 2054 gAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSe 2074
Db 6128 CTGCGACACCACTCGAGACAGCTGACCTCTGAGCGACAGCCCGCCCGGCGTGC----- 6182
QY 2074 rLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGl 2094
Db 6183 -----CTGGGGCCGCGCGCTCTCTCAGGACCCCGGGCGGCGCTGTGC 6226
QY 2094 yLysGlyProProGluThrArgSerSerLeuGluLeuAspThrThrLeuSerTrpIleSe 2114
```

```
Db 6227 C-----CCGCGCGCTCGCCCGCGCTCGACGCTG----- 6254
QY 2114 rGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLy 2134
Db 6255 -----CGCGGCCCGGGCGCTCTTCAG 6274
QY 2134 sCysTySerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGl 2154
Db 6275 CCTGCGGGGCTCGGGCG-----CATCA 6298
QY 2154 nArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisIleuGlyTh 2174
Db 6299 GCGCACCCACAGCAGCGGGGCTCC---ACCAGCCCGGCTGCACCCACCGACTCCAT 6355
QY 2174 rAspProSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgPr 2191
Db 6356 GGACCCCTCGAGCAGAGGGCGCGGTGGCGGGCGGGCGGGCGGGCGGGCGGACGCA 6415
QY 2191 oLysLysLysLeuSerProProSerIleThr-----IleAspProProGluSerGl 2208
Db 6416 CTGGAGACCTTCAGCAGGCTCTCGCTCACCTCTCTTCTGCGCGCGCC----- 6467
QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6468 -----CGCGCCAGCCCGCGCGCTCACGCCCGCAGGAAGTTCAGCAGCACCGAG 6517
QY 2228 pSer-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSe 2244
Db 6518 CAGCCTGGCGCGCCCGCGCGCCCGCCAGCGCGCGCGCTGCGCCCGCGCGCGAG 6577
QY 2244 rProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264
Db 6578 CCGCTCTGGCGCGCGGAC-----CGCAGCAAGGACCCCGCGCGCGG 6619
QY 2264 uAspPro 2266
Db 6620 GGCACCG 6626

RESULT 14
US-10-425-800-1
; Sequence 1, Application US/10425800
; Publication No. US20030180896A1
; GENERAL INFORMATION:
; APPLICANT: McGiven, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-10-425-800-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.3% Conservative: 213
Best Local Similarity: 51.4% Mismatches: 506
Query Match: 46.1% Indels: 449
DB: 7 Gaps: 55

US-09-611-257A-37 (1-2266) x US-10-425-800-1 (1-6816)
```


QY	31	ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly	50	QY	379	IleIleValGlySerPheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe	398
Db	264	CAGCCCGGACCCCGGAGCCCCCATCTCCCGCCAGGCTGGAGGAGCCCTCGGATGA	323	Db	1335	ATCATAGTGGGCTCCTTTCATGATCAACCTGTGCTGTGCTCATAGCGACCCAGTTC	1394
QY	51	-----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln	66	QY	399	SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer	418
Db	324	GCTGATCCTCATGTCCACACCCAGACCTGGCGCCTATTGCCTTCTTCTGCTGCGACAG	383	Db	1395	TCGGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAGCGGAGCTACCTGTGTC	1454
QY	67	AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle	86	QY	419	AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys	438
Db	384	ACCACAGCCCCCGGAACCTGGTCATCAAGATGGTGTGCACCCCGGTGGTTGATGTGC	443	Db	1455	---TCCAGCAGCGTGGCCAGCTACGCGAGCCCTGGCGACTGTACACGAGGATCTTCCAC	1511
QY	87	SerMetLeuValIleLeuLeuAnCysValThrLeuGlyMetPheArgProCysGluAsp	106	QY	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAa	458
Db	444	AGCATGCTGTGATCCTGCTGAACCTGCGTGACACTTGGCATGTACACGCGGTGGACGAC	503	Db	1512	TATGCTGCACATCTCTGCGAAGGCCAAGCGC-----CGCGCCCTG	1553
QY	107	IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAla	126	QY	459	GlyValArgValGlyLeuLeuSerProAlaProLeuGlyGlyGlnGluThrGlnPro	478
Db	504	ATGGACTGCTGTCGACCCGCTGCAAGATCCTGCAGGCTTTTGATGACTTTCATCTTATC	563	Db	1554	GGCTCTACCGAGCCCTGCAGAGCCGCGCGCCAGCTGGCC-----1595	
QY	127	PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys	146	QY	479	SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis	498
Db	564	TTCTTTGCCATGAGATGGTGCTCAAGATGGTGCCCTGGGATTTTGGCAAGAGTGC	623	Db	1595	-----1595	
QY	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGlu	166	QY	499	HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer	518
Db	624	TACTCGGGACACATGAACCGCTCGAATTTCTTCATCGTCATGGCAGGATGTCGAG	683	Db	1595	-----1595	
QY	167	TyrSerLeuAspLeuGlnAnValSerPheSerAlaValArgThrValArgValLeuArg	186	QY	519	ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer	538
Db	684	TACTCCTGGACCTTCAAGACATCAACCTGTCAACCATCCGACCGTGGCGCTCTGAGG	743	Db	1596	-----CCGGAG	1601
QY	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206	QY	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis	558
Db	744	CCCCCAAGGCATCAACCGGCTGCCAGTATGGCGATCTGTGTGAACCTGCTCCTGGAC	803	Db	1602	GCCTCGGCC-----CCCGCAAACTGGGCC-----CAC	1631
QY	207	ThrLeuProMetLeuGlyAsnValLeuLeuCysPhePheValPheIlePheGly	226	QY	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu	578
Db	804	ACACTGCCATGCTGGGGAATGCTCTGCTGCTGCTCTTCTTCTTCTTCTTCTTCTT	863	Db	1632	GCCAAG-----GAGCCCCGGCACTACAGCTGTGCCCGCAACATAGCCCCCTGAT	1682
QY	227	IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAn	246	QY	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro	598
Db	864	ATCATAGTGTGCAGCTCTGGCGGGCTGCTGCGTAACCGCTCTCTCTCTCTCTCTCT	923	Db	1683	GCGACGCCACACCCCTG-----GTCCAGCCCATC	1712
QY	247	PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu	266	QY	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr	618
Db	924	TTACCATACAGGGATGGGCTTGGCCCATCTACCGCCGAGGAGGATGATGAG	983	Db	1713	CCCCCACGCTG-----1724	
QY	267	SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro	286	QY	619	LeuThrSerLeuAnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr	638
Db	984	ATGCCCTTCATCTGCTCCCTGTCGGGCGACAATGGATAATGGGTGCTGCATGATCCCC	1043	Db	1724	-----1724	
QY	287	ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu-----300		QY	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658
Db	1044	CCGCTCAAGAGGACGAG-----GGCGTGAGTGCTGCTGTCCAAGGACGAGCTTAC	1094	Db	1724	-----1724	
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln	318	QY	659	SerGlyAlaCysGlyProAspSerSerCysProTyrCysAlaArg-----672	
Db	1095	GACTTTGGGGGGGGCCGACGAGACCTCAATGCCAGCGCCTCTGTGTCAACTGGAAACCGT	1154	Db	1725	-----GCTTCCGATCCCGCCAGCTGCCCTTGTGCCAGCATGAGGAGCGCGCGCGCC	1778
QY	319	TyrTyrThrAsnCysSerAlaGlyLysHisAsnProPheLysGlyAlaIleAsnPheAsp	338	QY	673	AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla	692
Db	1155	TACTACAATGTGTGCGCAGCGGACGCGCAACCCCAAGGGTGCCATCAACTTTGAC	1214	Db	1779	TCGGGCTGGGACACCGAC---TCGGCCAGGAGGCGCTCGGGCTCCGGAGCTCCGCT	1835
QY	339	AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp	358	QY	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712
Db	1215	AACATCGGTATGCTTGATTTGATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAG	1274	Db	1836	GCTGGCGAG-----GACGAGCGGATGGGACGGGCGCGCGAGCAGCAGCAGCAGC	1889
QY	359	IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu	378	QY	713	GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-----726	
Db	1275	ATCATGTACTACGTGATGATGCTCACTCTTCTTACAACTTCACTTCACTCTTCACTCT	1334	Db	1890	TCCTCAGAACCTGGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1949
				QY	727	-----AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr	744

Db 1950 TCGGGGATGTGGCGGAGACGCGAGCCAAGCTGCGCGCATCGTGGACAGCAAGTAC 2009
QY PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
Db 2010 TTCAACCGGGCATCATGAGCATCTCTGTCAACACCGTCAGCATGGGCATCGAGCAC 2069
QY HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
Db 2070 CACGAGCAGCGGAGGAGCTGACCAACATCTGGAGATCTGCAATGTGGTCTTCAACGAGC 2129
QY LeuPheAlaLeuMetLeuLeuLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTTCCCTCGAGATGATCTCTGAAGCTGGCTGCAATTTGGGCTCTTCGACTACCTGCGT 2189
QY AsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGluIleValGly 824
Db 2190 AACCCCTACCAACATCTTCGACAGCATCTGTATCATCATCAATCTGGAGATCGTGGGG 2249
QY GlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
Db 2250 CAGCGGACGGTGGGCTGTGGGTGTCGGACCTTTCGGGCTGCTGGCGTGTGAAACTG 2309
QY ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
Db 2310 GTGCGCTTCACTGCTGCTGCGCGCCAGCTGCTGTGTCTCATGAAGACCATGGACAAC 2369
QY ValAlaThrPheCysMetLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet 884
Db 2370 GTGGCCACCTTCGATGCTGCTATCTCTTCATCTTCATCTTCAGCATCTTGGGATG 2429
QY HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGCTGCAAGTTTCAGCTCCGCGACGACACTGGAGACACGGTGGCCGACAGG 2489
QY LysAsnPheAspSerLeuThrAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
Db 2490 AAGAATCTCACTCCCTGCTGTGGGCACTGCTGCTGTGTTCAGATCTCTCAACCCAGGAG 2549
QY AspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerThrAlaAlaLeuTyr 943
Db 2550 GATCGNACGCTGTTCTCAATATGATGGCTGCTCACTTCTCCCTGGGCTCCCTCTAC 2609
QY PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963
Db 2610 TTTGTGCGCTCATGACCTTCGCAACTATGTGCTCTTCAACCTGCTGTGGTGGCCATCTG 2669
QY ValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
Db 2670 GTGGAGGGCTTCCAGCGGAG----- 2690
QY CysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTGACGCCAATCGCTCTACTCGGACGAG 2720
QY AspPhePheProSer-----LeuAspGlyAsp 1013
Db 2721 GACCAGAGCTCATCAACATAGAAGATTGATAAGCTCCAGGAGCGCTGGACAGCAGC 2780
QY GlyAspArgLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGCAC----- 2825
QY SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
Db 2826 -----CTGACCC-----AGTCTCCCATCGGCT 2849
QY ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgThr----- 1069
Db 2850 GGGCACCTAGTCTGTGGGGTGGGGACCTGCCCCGCTCTCACTGACGACGGAC 2909
QY -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 1070 ----- 1100

Db 2910 CCATGCTGTGCTGGCTCCCGAAAGAGCAGTGTCTATGTCTCTAGGAGGATGAGC 2969
QY HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla 1100
Db 2970 TATGACAGCGCTCCCTGTCTCAGCTCCGAGAGTCTTACTACGGGCATGGGCGGAGC 3029
QY SerSerTyrThrSerArgArgSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 GCGGCTGGGCCAGCGTCTCGCTGGAAC-----AGCTCAAG 3071
QY ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139
Db 3072 CACAACCGCGCTCGCGGAGCATGATCTCTCTCTCGAGCGCGCGCGCGCGCC 3131
QY GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGGTCTGAGGTTGCGCGGAGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 3191
QY His-----ArgHisArgGly 1162
Db 3192 CACGCCACCATTCATCAGCGGCCCATCTGGCGCACCGCCACCGCACCGCCCGG 3251
QY SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACCTGTCTCTCGACCAACAGGGACTCGGTGGACCTGGCCGAGCTGGTGGCGGTGGC 3311
QY LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCACCGCGCGCGCTGGAGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 3371
QY GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspPheProLeu-As 1220
Db 3372 GGCAGGAT-GCCAGCATCGC---CAAAGACGCTTCCACCAAGATGGCGCACCGCGGGA 3427
QY pGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyValArgValArgAlaTyrIle 1240
Db 3428 TCGCGGGAGGATGAGAGGAAATCGACTACACCTGTGCTTCGCGTCCGCAAGATGAT 3487
QY eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTyrSerAlaTyrIlePhePr 1260
Db 3488 CGAGCTCTATAGCCCGACTGGTGGAGGTCCGCGAAGACTGGTCTGTCTACCTTCTC 3547
QY oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAAGACAGGTTCCGGTCTGTGTGTCAGACCATATTATTGCCACAAACTCTCGACTA 3607
QY sValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3608 CGTGTCTTGGGCTTCTCTTCAACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3657
QY eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 3658 CGAGCGCGGAGCAGCAGAACGCATCTTCTCACCGTGTCCACTACATCTTACGGCCAT 3727
QY lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAl 1340
Db 3728 CTTCTGGGCGAGATCACATTGAAGTAGTCTCGTGGGCTGTCTACTTCCGCGAGCAGGC 3787
QY aTyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 3788 GTACCTACGACGAGCTGGAACGTGTGGATGGCTTCTTGTCTTGTGTCTTCAATCAATCA 3847
QY pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
Db 3848 CATCTGGTGTCTCTGGCTCAGCGGGGAGCAAGATCTTGGGGGTCTCTCGAGTCTT 3907
QY uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGGCTCTCGCACCTACGCCCTGTGTGTGTATCAGCGGGCGCGCGGCTGAAGCT 3967
QY uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 3968 GGTGGTGGAGACACTCTCTCTCCCTCAAGCCCATCGGCAACATCGTCTCATCTGCTG 4027

QY	1420	sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLeGlyLysPhePheVa	1440	QY	1780	lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---	AspG1	1799
Db	4028	TGCCTTCTTCATCATCTTTGGCATCTCTGGGAGTGCAGCTCTTCAAGGGCAAGTTCTACCA	4087	Db	5108	CTCCACGGGTGAACACTGGAACCGGATCATGAAGGACACGCTCGGAGACTGCACCCACGA	5167	
QY	1440	lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy	1460	QY	1799	nGluSerThrCysTyAsnThrVal-----IleSerProIleTyPheValSerPheVa	1817	
Db	4088	CTGTCTGGGGGTGGACACCGCAACATCAACCAACCGCTCGGACTGGATGGCCGCCCACTA	4147	Db	5168	CGAGCGCAGTGCCTGAGCAGCCTGCAGTTGTGTGTCGCGCTACTCTCTGAGCTTCGT	5227	
QY	1460	rArgTtpValArgHisLysTyAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh	1480	QY	1817	lleuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG1	1837	
Db	4148	CCCTGGGTCCATCAACAATACAACTTCGACACCTTGGGCAGGCTCTGATGTCCTCTT	4207	Db	5228	GCTCACGGCGCATTCGTCTCATCAACGTGTGGTGTGCTCATGAAGCACCTTGGGA	5287	
QY	1480	eValLeuAlaSerLysAspGlyTrpValAspIleMetTyAspGlyLeuAspAlaValG1	1500	QY	1837	uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMe	1857	
Db	4208	TGTCCTGGCATCCAAGGATGTTGGGTGAACATCATGTACAATGGACTGGATGCTGTTGC	4267	Db	5288	CGACACAACAGAGGCGCAGGAGCAGCCGAGATGGATGCCGAGCTCGAGCTCGAGTGGAGAT	5347	
QY	1500	yValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyPheIleSerPh	1520	QY	1857	t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG1	1876	
Db	4268	TGTGGACCAAGCGCTGTGACCAACCAACCCCTGGATGCTGTGTACTTTCATCTTCCTT	4327	Db	5348	GGCCCATGGCTGGGCCCTGGCCCGAGGCTGCCTACCGGCTCCCGGGCGCC---CCTGG	5404	
QY	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh	1540	QY	1876	yValGluGlyProAspSerProAsp-----	1894	
Db	4328	CTGTCTCATCTGTAGCTTCTTTGTGCTCAACATGTTTGTGGTGTCTGTGTGGAGAACTT	4387	Db	5405	C---CGAGGGCGGGAGGGCGGGCGGGCGGCGACACCGAGGGGGCTTGTGCCGGCG	5461	
QY	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe	1560	QY	1885	-----SerProLysProGlyAlaLeu-----	1891	
Db	4388	CCACAAGTGGCGGAGCACCAGGAGGCTGAAGAGGCACGGCGGCTGAGGAGAAGCGGCT	4447	Db	5462	CTGCTACTCCCTGCCCGAGGACTCTTGGAGGGGAGCTGACCATCATGCACAACCTGTC	5521	
QY	1560	uArgArgLeuGluLysArgArgLysAlaGlnCysLysProTyTrpSerAspTyRSe	1580	QY	1892	-----HisProAlaAlaHisAla-----	1897	
Db	4448	CGCGCGCTGGAGAAGAAGCGCGGAAGGCCAGCGGCTGCGCTTATGCCACTATTG	4507	Db	5522	GGGCTCATCTTCCACCCTACTCTCTGCTGCGGCTGCAAGAAGTGTCAACACGACAA	5581	
QY	1580	rArgPheArgLeuValHisHisLeuCysThrSerHisTyTrpLeuAspPheIleTh	1600	QY	1898	-----ArgSerAlaSe	1901	
Db	4508	TCACACCGGCTGCTATCCACTCCATGTGCACACGACCTACTCTGACATCTTCATCAC	4567	Db	5582	GCAAGAGTGCAGTGGCTGAGCGGAGGCTTCTCCCTGAATCAGACAGGTCTCTCGTC	5641	
QY	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyTrpGlnGlnProGlnI1	1620	QY	1901	r-----HisPheSerLeuGluHisProThrMetGlnPro-----	1912	
Db	4568	CTTCATCATCTGCTCAACGTGGTCAACATGCTCCCTGGAGCACTACAATCAGCCACGCTC	4627	Db	5642	CATCTCTCTGGGTGACACCTGTAGTCTCGAGGACCCACAGCCTGCCACCTGGCCGCAA	5701	
QY	1620	eLeuAspGluAlaLeuLysIleCysAsnTyTrpIlePheThrValIlePheValLeuGluSe	1640	QY	1913	-----HisProThrGluLeuProGlyProAspLeuThrValArgLysSerGly-----	1929	
Db	4628	CCTGGAGACACCCCTCAAGTACTGCAACTATATGTTCAACACTGCTTTGTGTGGAGGC	4687	Db	5702	GGACAGCAAGGTGAGTGGACCCACCTGAGCCCATGCTGTGGAGACCTGGGCGAATG	5761	
QY	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe	1660	QY	1930	-----ValSerArgThrHisSerLeuProAsn---AspSerTyMetCysArgHi	1945	
Db	4688	TGTCTGNAGCTGTGGCATTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACCACTG	4747	Db	5762	CTTCTTCCCTTGTCTCTACGGCCGCTCGCGGATCCAGAGAACTTCTGTGTGAGAT	5821	
QY	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAs	1680	QY	1945	sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyTrpGlyLeuProLysAlaGlnSe	1965	
Db	4748	GGACTGGCCATTGTCTACTGTGAGTCAATGGCATCAACCTGGAGGAGATCGAGATCAA	4807	Db	5822	GGAGGATCCCATTCACCTGTC-----CGGTCTCTGG-----CTGAAACATGACAG	5869	
QY	1680	nAlaSerLeuProIleAsnProThrIleArgIleMetArgValLeuArgIleAlaAr	1700	QY	1965	rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyTrpIleLeuGlnLeuPr	1985	
Db	4808	TGCGGCCCTGGCCATCAATCCACCATCATCCGATCATGAGGGTTCTGCCATTTGCCG	4867	Db	5870	CAGTCAAGCACCCCAAGTCTCTCCCGGATCGCTCCAGCCCTCTCTCTGCCCATGCC	5929	
QY	1700	gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG1	1720	QY	1985	oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh	1999	
Db	4868	AGTCTGAAGCTGTGAAGATGGCCACAGGAATGGGGCCCTGCTGGACACGGTGGTGCA	4927	Db	5930	AGCCGAGTCTTTCACCTCGAGTGTGTGCCAGCCAGAAAGGCCAGAAAGGGCAGCTGG	5989	
QY	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl	1740	QY	1999	rTrpGlyThrIleProLysLeuProProProGly-----ArgSerProLe	2014	
Db	4928	AGCTTTGCCAGGTGGGCAACCTGGGCTCTCTTTCATGTGCTCTTCTTCATCTATGC	4987	Db	5990	CACTGGAACTCTCCCAAGATTGGCTGCGAGGGCTCTGGGCATCTCTGTGGTACCAAG	6049	
QY	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1	1760	QY	2014	uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG1	2034	
Db	4988	TGCTCTCGGGGTGGAGCTCTTTGGGAAGCTGCTGCAACGACGAGAAACCCGTGGCAGGG	5047	Db	6050	GGTCAACTGTACTCTCTCCGCGAGGCCACCGGAGCGACACGTCTGCTGGAC-----	6101	
QY	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780	QY	2034	yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaAr	2054	
Db	5048	CATGAGCCGGCATGCCACTTCGAGAACTTCGGCATGGCTTCTCTCACACTCTTCCAGGT	5107	Db	6102	-----GCCAGCCACGACGTCTCGCGGGCAG	6127	
				QY	2054	gAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSerHisSe	2074	

QY	339	AsnIleGlyTyrAlaTirPileAlaIlePheGlnValIleThrIleuGluGlyTirPValAsp	358	Db	1836	GTTGGCGAG-----GACGAGCGGATGGGACGGGCCCGGAGCAGCAGCAGCAGCGGCC	1889
Db	1215	ACATCGGTATGCTGGATGTCATCTTCCAGTGATCATTCTGGAAGGCTGGGTGGAG	1274	QY	713	GlnArgSerIleuGlyProAspAlaGluProSerSerValLeu-----	726
QY	359	IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleIleuLeu	378	Db	1890	TCCTCAGAACTGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1949
Db	1275	ATCATGTACTACGTGATGATGCTACTCTCTTACAACCTTCACTACTTCACTTCGCTT	1334	QY	727	-----AlaPheTirPArgIleuIleCysAspThrPheArgLysIleValAspSerLysTyr	744
QY	379	IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe	398	Db	1950	TGCGGGGATGTGTGGCGGAGAGCGGAGCAAGCTCGCGGCATCTGTGACACCAAGTAC	2009
Db	1335	ATCATAGTGGCTTCCTTTCATGATCAACCTGTGCTCTGTGTCATAGGACCCAGTTTC	1394	QY	745	PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr	764
QY	399	SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer	418	Db	2010	TTCAACCGGGCATCATGATGGCCATCTTGCTCAACACCGTCAGCATGGGATCGGACAC	2069
Db	1395	TCCGAGNCCCAAGCAACGGGAGCACCGGCTGATCTGAGCAGCGGAGCGCTACCTGTCC	1454	QY	765	HisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer	784
QY	419	AsnAlaSerThrIleuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys	438	Db	2070	CACGAGCAGCGGAGGAGCTGACCAACATCTGGAGATCTGCAATGTGTCTTCACACGC	2129
Db	1455	---TCCAGCACGGTGGCCAGCTACGCCGAGCCCTGGCGACTGTACGAGGAGATCTTCCAC	1511	QY	785	LeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLys	804
QY	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla	458	Db	2130	ATGTTTGGCTGGAGATGATCTCTGAAGCTGGCTGCATTTGGGCTCTTCGACTACCTGCGT	2189
Db	1512	TATGTCTGCACATCTCTGCGAAGGCCAAGCGC-----CGGCGCCTG	1553	QY	805	AsnProTyrAsnIlePheAspGlyValIleValIleSerValTirPValIleValGly	824
QY	459	GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnPro	478	Db	2190	AACCCCTACAAACATCTTCGACAGCATGTGTATCATCAGCATCTGGGAGATCGTGGG	2249
Db	1554	GGCTCTACACGGCCCTGCAGAGCGCGCGCCAGCCCTGGGC-----	1595	QY	825	GlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu	844
QY	479	SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHis	498	Db	2250	CAGCGGAGCGTGGGCTGTGGTGTGCGGACCTTCGGGCTGTGCGGCTGTGCGGAACTG	2309
Db	1595	-----	1595	QY	845	ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn	864
QY	499	HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer	518	Db	2310	GTGCGCTTCATGCTGCCCTGCGGCGCCAGCTGTGTGTCTCATGAACACCATGGACAAC	2369
Db	1595	-----	1595	QY	865	ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet	884
QY	519	ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer	538	Db	2370	GTGGCCACCTTCGTCATGCTGCTCATCTCTTCATCTTCATCTTCAGCATCTCTGGGATG	2429
Db	1596	-----CCGGAG	1601	QY	885	HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg	903
QY	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis	558	Db	2430	CATATTTTGGCTCAAAGTTTCAGCTCCGCACGACACGTGGAGACACGGTCCCGACAGG	2489
Db	1602	GCCCGGGC-----CCGCGCAACCTGGGGCC-----CAC	1631	QY	904	LysAsnPheAspSerLeuLeuTirPAlaIleValThrValPheGlnIleLeuThrGlnGlu	923
QY	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu	578	Db	2490	AAGAACTTCGACTCCCTGCTGGGCCATCTGCTACTGTGTTCAGATCTCTCACCAGAG	2549
Db	1632	GCCAAG-----GAGCCCGGCACCTACAGCTGTCCCGCAACATAGCCCCCTGGAT	1682	QY	924	AspTirPAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTirPAlaAlaLeuTyr	943
QY	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerPro	598	Db	2550	GACTGGAAACGTGCTTCTCAATGGCATGGCCCTCCACTTCTCCCTGGGCTCCCTCTAC	2609
Db	1683	GCGAGCCCCACACCTG-----GTGCGAGCCCATC	1712	QY	944	PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu	963
QY	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProThr	618	Db	2610	TTTGTGCGCCCTCATGACCTTCGCAACTATGTGTCTTCAACCTGCTGGTGCCCATCTG	2669
Db	1713	CCCGCCAGCGCTG-----	1724	QY	964	ValGluGlyPheGlnAlaGluLysSerLysArgGluAspAlaSerGlyGlnLeuSer	983
QY	619	LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuThr	638	Db	2670	GTGGAGGGCTTCCAGGGCGAG-----	2690
Db	1724	-----	1724	QY	984	CysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPro	1003
QY	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658	Db	2691	-----GGTGAGCCCAATCGCTCTCTACTCTCGGACGAG	2720
Db	1724	-----	1724	QY	1004	AspPhePheSerProSer-----LeuAspGlyAsp	1013
QY	659	SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg-----	672	Db	2721	GACCAGAGCTCATCCAACATAGAGAGTTTGATAAGCTCCAGAAAGCCCTGGACAGCAGC	2780
Db	1725	-----GCTTCGCATCCCCCAGCTGCCCTTCTGCTCCAGCATGAGACGGCGCGGGCCC	1778	QY	1014	GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys	1033
QY	673	AlaGlyAlaGlyLeuValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla	692	Db	2781	GGAGATCCCAAGCTCTGCCCAATCCCAATGACCCCAATGGGCAC-----	2825
Db	1779	TGGGCTCGGGCAGCACCCAC---TCGGGCCAGGAGGGCTCGGGCTCCGGGAGCTCCGCT	1835	QY	1034	SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer	1053
QY	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712				

Db 2826 -----CTGGACCCC-----AGTCTCCCACTGGGT 2849
Qy 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGCACCTAGTCTCTGTGGGGTCTGGGACCTGCCCCGACTCTCACTGCAGCCGAC 2909
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGGTGGCCCTGGGCTCCGAAAGAGCAGTGTCTCTPAGGAGGATGAGC 2969
Qy 1081 HisGluMetLysSerProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATGACACCGCTCCCTGTCTCAGCTCCGGAGCTCTACTACGGCCCTGGGCGCGAGC 3029
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 CGGCGCTGGGCCAGCGCTGCTCCAGCTGGAAC-----AGCCTCAAG 3071
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu-----GlyGlnGluSer 1139
Db 3072 CACAAGCCGCTGGCGGAGCATGAGTCCCTGTCTCTCGGAGCGCGCGCGGCC 3131
Qy 1140 GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGCTGTCAGGTTGCTCCGCGACGAGGCGCGCGCGCGCGCGCGCGCGCGCGCC 3191
Qy 1158 His-----ArgHisArgGly 1162
Db 3192 CACGCCACACCATTCATCAGCGGCCCTCTGGCGCACCGCCACCGCCACCGCCG 3251
Qy 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACCTGTCTCCACACAGGAGCTCGTGGACCTGGCCGAGCTGTGTGGTGGTGGTGGTGG 3311
Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCACCCCGCGCGCTGGAGGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3371
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspSerProProLeu-As 1220
Db 3372 GGCAGGAT-GCCCAGCATCGC---CAAAGACGCTTCACCAAGATGGCGACCGCGGGA 3427
Qy 1220 pGlyAspAlaAspAspGluGlyLeuSerLysGlyGluArgValArgAlaTrpIl 1240
Db 3428 TCGCGGGAGGATGAGGAGGAAATCGACTACACCTGTGTCTCCGGCTCGCGAAGATGAT 3487
Qy 1240 eArgAlaArgLeuProAlaCysTyrlLeuGluArgAspSerTrpSerAlaTyrlPhePr 1260
Db 3488 CGACGTCTATAGCCCGACTGGTGGAGGTCCCGAAGACTGTGTCTTACCTCTCTC 3547
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAGAACAGGTTCGGGTCTGTGTACAGACCATATTGCCCCACAACTCTTCACATA 3607
Qy 1280 sValValLeuValIlePheLeuLeuAsnCysIleThrIleAlaMetGluArgProLysIl 1300
Db 3608 CGTGTCTGGCTTTCATCTTCTCACTCACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3667
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrlPheThrAlaVal 1320
Db 3668 CGAGCGCGGAGCAGCAGACGATCTTCTCACCGGTGTCACACTATCATCTTCACGGCCAT 3727
Qy 1320 lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
Db 3728 CTTCTGGGCGAGATGACATTGAAGGTAGTCTCGCTGGGCTGTACTTTCGGCGAGCAGGC 3787
Qy 1340 aTyrlLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLeuSerValIleAs 1360
Db 3788 GTACCTACGAGCAGCTGGAACGCTGTGGATGCTTCTGTCTGTGTCTTCATCATCGA 3847
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValIle 1380
Db 3848 CATCGTGGTGTCTCTGGCTCAGCGGGGAGCAAGATCTTGGGGGTCTCTCGAGTCTT 3907

Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGGCTCTCTGGCACCTACGCCCCCTGCGTGTGCATCAGCGCGCGCGCGCTGAAGCT 3967
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCy 1420
Db 3968 GGTGGTGGAGACACTCATCTCTCCCTCAAGCCCATCGCAACATCGTGTCTCATCTGCTG 4027
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysPhePheVal 1440
Db 4028 TGCCTTCTTCATCATCTTTGGCATCTTGGAGTGCAGCTCTTCAAGGCGAAGTTCATCCA 4087
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGGCGTGGACACCGCCCAACATCACCAACCGCTCGACTGCATGCCCGCAACTA 4147
Qy 1460 rArgTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGCTGGTCCATCACAAATACAACTTCGACAACTGGGCGAGGCTCTGATGTCCTCTT 4207
Qy 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrlAspGlyLeuAspAlaValGl 1500
Db 4208 TGTCTCTGGCATCCAAAGATGGTTGGGTGAACATCATGTACATGGACTGGATGCTGTGTG 4267
Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrlPheIleSerPh 1520
Db 4268 TGTGGACAGCAGCTGTGACCAACCAACCCCTGGATGCTGCTGTCTTCTATCTCTT 4327
Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
Db 4328 CTTGTCTCATCTGCTCAGCTTCTTTGTGTCAACATGTGTGGTGTGCTGTGGAGAACTT 4387
Qy 1540 eHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCAAAAGTCCGCGACACCCAGGAGGCTGAAGAGGACCGCGCGGTGAGGAGAGCGGCT 4447
Qy 1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrlTyrlSerAspTyrlSe 1580
Db 4448 GCGGCGCTGGAGAGAACGCGCGGAAGCCCGAGCGCTGCCCCCTACTATGCCACCTATTG 4507
Qy 1580 rArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrlLeuAspLeuPheIleTh 1600
Db 4508 TCACACCGGCTGCTCATCTCACTTCCATGTGTGCACAGCAGCTACCTGAGACATCTTCATC 4567
Qy 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrlGlnGlnProGlnIl 1620
Db 4568 CTTTCATCTCTGCTCAACGTGTGTACCATGTCCCTGGAGCATACAAATCAGGCCACGTC 4627
Qy 1620 eLeuAspGluAlaLeuLysIleCysAsnTyrlPheThrValIlePheValLeuGluSe 1640
Db 4628 CTTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCCACCACCTGTCTTTGTGTGGAGGC 4687
Qy 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660
Db 4688 TGTGTGTAAGCTGTGTGGCTTGTGTGAGGGCTTCTTCAAGGACCGATGGAACAGCT 4747
Qy 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
Db 4748 GGACCTGGCCATGTGTCTACTGTACATGGGACATCCCTGGAGGAGATCGAGATCAA 4807
Qy 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TGGCGGCTGCCCATCAATCCCAACCATCATCCGCATCATGAGGGTCTTCGCGCATTCGCCG 4867
Qy 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720
Db 4868 AGTGTGAAGCTGTGAAGATGGCCACAGAAATGCGGGGCTCTGCTGACACGCGTGTGCA 4927
Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl 1740
Db 4928 AGCTTTGGCCCCAGGTGGGCAACCTGGGCGCTCTCTTCTTCTGCTGCTCTCTTCTATCTATGC 4987

QY	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlu	1760	Db	6050	TCGGTGCAGGGCTCTCTGGGCATCTCTGGGTCACCAAGGTCACCTGTACCTCTCCG	6109
Db	4988	TGCTCTCGGGTGGAGCTCTTTGGGAAGCTGTCTGCAACGACGAGAACCCGTGCGAGG	5047	QY	2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe	2041
QY	1760	yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780	Db	6110	GCAGGCCACCGGAGGACACACGTCGCTGCAC	6140
Db	5048	CATGAGCCGCGATGCGACCTTCAGAACTTCGCGATGCGCTTCTCACACTCTTCAGGT	5107	QY	2041	uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyG	2061
QY	1780	lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---	1799	Db	6141	-----GCCAGCCCCAGCAGCTCCCGGGCAGCCCTGCAGACACCGCTCAGGA	6187
Db	5108	CTCCACGGGTGCAACTGGAAACGGGATCATGAAGGACACGCTCGGAGACTGCACCCACGA	5167	QY	2061	nSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMetTh	2081
QY	1799	nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa	1817	Db	6188	CAGCTGACCTGAGCGACAGCCCCCGGCGTGC	6226
Db	5168	CGAGCGAGCTGCTGAGCAGCTGCGAGTTGTGTCGCGCTGTACTTCTGAGCTTCGT	5227	QY	2081	rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr	2101
QY	1817	lLeuThrAlaGlnPheValLeuValIleAlaValLeuMetLysHisLeuG	1937	Db	6227	GCAGCCCGCGCTGCTCAGGACCCCGGCGGCTGTC	6277
Db	5228	GCTCAGCGCGAGTTCGTGCTCATCAACGTGTGTGTGCTGCTCATGAAGCACCTGGA	5287	QY	2101	gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProG	2121
QY	1837	uGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluMe	1857	Db	6278	CCGCCGCTGAGCTG	6293
Db	5288	CGACAGCAACAGAGCGGAGGAGCGCGGAGATGGATGCCGAGCTCGAGCTGAGAT	5347	QY	2121	yGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaG	2141
QY	1857	t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG	1876	Db	6294	-----CGCGCGCGGCGCTTTCAGCTCGGGGGCTCGGGCG	6332
Db	5348	GGCCATGGCTTGGCCCTGCGCGAGGCTGCTACCGGCTCCCGGGCGCC---CCTGG	5404	QY	2141	nSerCysGlnArgArgProThrTrpLeuAspGluGlnArgArgHisSerIleAlaVa	2161
QY	1876	yValGluGlyProAsp	1881	Db	6333	-----CATCAGCGCAGCCACAGCAGCGGGG	6358
Db	5405	C---CGAGGGCGGGAGGGCGGGCGGCGGCGACACCGAGGGCGGCTTGTGCGGGC	5461	QY	2161	lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn	2178
QY	1882	-----SerPro-----	1883	Db	6359	CTCC---ACCAGCCCGGCTGCACCCACACGACTCCATGAGCCCTCGGACGAGGAGG	6415
Db	5462	CTGCTACTCGCTCCCGAGGAGAACCTGTGGCTGAGCAGCGTCTCTTAATCATCAAGGA	5521	QY	2179	-LeuGlyGlnProLeuGlyGlyProGlySerArgTrpProLysLysLysLeuSerPro	2198
QY	1884	-----AspSerProLysProGlyAlaLeuHis-----	1892	Db	6416	CCGGGTGGCGGGCGGGCGGGCGGGCGGCGGAGCAGCCTCGGAGACCTCAGCAGCT	6475
Db	5522	CTCCTTGGAGGGGAGTGACCATCATCATCAACCTGTGGGGCTCCATCTCCACCACTA	5581	QY	2198	oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSe	2215
QY	1893	-----ProAlaAla-----	1895	Db	6476	CTCGCTCACCTCCCTCTTCTGCGCGCGCGC	6517
Db	5582	CTCCTCGCTCCCGCTGCAAGAGTGTACACAGCAAGAGAGGTGAGCTGGCTGA	5641	QY	2215	rProGlyIleCysLeuArgArgAlaProSerSerAspSer-----LysAs	2231
QY	1903	-----HisAlaArgSerAlaSer-----HisPh	1903	Db	6518	CCCCGGCTCAGCCCCCGGAGAGTTTCAGCAGCACCAGCAGCTGGCCGCCCGCGCGG	6577
Db	5642	GACGAGGCTTCTCCCTGAACCTCAGACAGTCTCTGCTCCATCTGCTGGGTGAGCAGCT	5701	QY	2231	pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa	2251
QY	1903	eSerLeuGluHisProThrMetGlnPro-----HisProThrGluLeuPr	1918	Db	6578	CCCCCAGCGCGCGCGCTGGCCACGCGCTGGCCCGGAGCCCTCTGTGGCGCGCGAGC	6635
Db	5702	GAGTCTCGAGGACCCACAGCCTGCCACCTGGCGCGCAAGACAGCAGGAGTGA	5761	QY	2251	lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
QY	1918	oGlyProAspLeuLeuThrValArgLysSerGly-----ValSerArgTh	1933	Db	6636	-----CGCAGCAAGGACCCCCCGCGCGCGCACCG	6665
Db	5762	CCCACCTGAGCCATCGGTGTGGAGACCTGGGCGAATGCTTCTCCCTTGTCTCTAC	5821	QY			
QY	1933	rHisSerLeuProAsn---AspSerTyrMetCysArgHisGlySerThrAlaGluGlyPr	1952	Db			
Db	5822	GGCGTCTCGCGGATCCAGAGAACTTCTGTGTGAGATGGAGGAGATCCCATCAACCC	5881	QY			
QY	1952	oLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi	1972	Db			
Db	5882	TGTC-----CGGTCTCG-----CTGAACATGACAGCAGTCAAGCACCCCAAGTCC	5929	QY			
QY	1972	sSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHis-----	1990	Db			
Db	5930	CTTCTCCCGGATCGCTCCAGCCCTCTCTGCGCCATGCCCGCGAGTCTTCCACCCCTGC	5989	QY			
QY	1991	-----LeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe	2006	Db			
Db	5990	AGTGCTGCCACCCAGAAAGGCCAGAAAGGGCAGTGGCACTGGAAACCTCCCAAGAT	6049	QY			
QY	2006	uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr	2021				

Search completed: July 10, 2006, 09:55:32
Job time : 5359.36 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 10, 2006, 06:41:43 ; Search time 516.109 Seconds
(without alignments)
8562.447 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904
Sequence: 1 MDEEDGAGAESGQPRSPM.....PKKDVLSGLSDPADLDP 2266

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 844069 seqs, 650066433 residues

Total number of hits satisfying chosen parameters: 1688138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/abes/ABSSWEB.spool/US09611257/runat_10072006_064129_7044/app_query.fasta_1
-DB=Published Applications_NA_New -QMI=fascap -Suffix=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=absos8
-USER=US09611257 @CGN 1.1.792 @runat_10072006_064129_7044 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YCAPEXT=0.5 -DSELP=6 -DELEXT=7

Database : Published Applications NA New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11684.5	98.2	7834	8	US-11-266-748A-31661 Sequence 31661, A
2	6230.5	52.3	8079	8	US-11-266-748A-56474 Sequence 56474, A
3	1786.5	15.0	7376	8	US-11-350-336-3 Sequence 3, Appl
4	1782.5	15.0	7364	8	US-11-350-336-5 Sequence 5, Appl
5	1776	14.9	7177	8	US-11-350-336-7 Sequence 7, Appl
6	1728.5	14.5	7011	8	US-11-350-336-9 Sequence 9, Appl
7	1678	14.1	6051	8	US-11-313-450-9 Sequence 9, Appl
8	1595.5	13.4	5934	8	US-11-313-450-13 Sequence 13, Appl

9	1595.5	13.4	6371	8	US-11-251-465-8	Sequence 8, Appl
10	1595.5	13.4	6371	8	US-11-266-748A-56579	Sequence 56579, A
11	1594	13.4	7193	8	US-11-266-748A-29006	Sequence 29006, A
12	1594	13.4	7193	8	US-11-266-748A-57267	Sequence 57267, A
13	1590.5	13.4	5943	8	US-11-313-450-11	Sequence 11, Appl
14	1590.5	13.4	7008	8	US-11-263-326-98	Sequence 98, Appl
15	1590.5	13.4	7008	8	US-11-263-326-104	Sequence 104, Appl
16	1579.5	13.3	5511	8	US-11-313-450-7	Sequence 7, Appl
17	1558.5	13.1	8292	6	US-10-501-814-2	Sequence 2, Appl
18	1557.5	13.1	6328	8	US-11-263-326-148	Sequence 148, Appl
19	1556.5	13.1	6328	8	US-11-263-326-147	Sequence 147, Appl
20	1555.5	13.1	6328	8	US-11-263-326-103	Sequence 103, Appl
21	1555.5	13.1	6328	8	US-11-263-326-149	Sequence 149, Appl
22	1555.5	13.1	6328	8	US-11-263-326-151	Sequence 151, Appl
23	1555.5	13.1	6600	6	US-10-473-173-94	Sequence 94, Appl
24	1553.5	13.1	6018	8	US-11-313-450-3	Sequence 3, Appl
25	1552.5	13.0	6328	8	US-11-263-326-102	Sequence 102, Appl
26	1551.5	13.0	6328	8	US-11-263-326-101	Sequence 101, Appl
27	1551.5	13.0	6328	8	US-11-263-326-146	Sequence 146, Appl
28	1551.5	13.0	6328	8	US-11-263-326-150	Sequence 150, Appl
29	1550.5	13.0	6328	8	US-11-263-326-152	Sequence 152, Appl
30	1550	13.0	6003	8	US-11-313-450-5	Sequence 5, Appl
31	1550	13.0	9123	8	US-11-266-748A-56739	Sequence 56739, A
32	1548.5	13.0	8381	8	US-11-263-326-5	Sequence 5, Appl
33	1548.5	13.0	8381	8	US-11-263-326-9	Sequence 9, Appl
34	1548	13.0	8377	8	US-11-263-326-95	Sequence 95, Appl
35	1546.5	13.0	8381	8	US-11-263-326-93	Sequence 93, Appl
36	1545.5	13.0	8370	8	US-11-263-326-90	Sequence 90, Appl
37	1544.5	13.0	8380	8	US-11-263-326-89	Sequence 89, Appl
38	1544.5	13.0	8381	8	US-11-263-326-8	Sequence 8, Appl
39	1544.5	13.0	8381	8	US-11-263-326-11	Sequence 11, Appl
40	1544.5	13.0	8381	8	US-11-263-326-92	Sequence 92, Appl
41	1544.5	13.0	8381	8	US-11-263-326-96	Sequence 96, Appl
42	1544.5	13.0	8381	8	US-11-263-326-97	Sequence 97, Appl
43	1544.5	13.0	8381	8	US-11-263-326-108	Sequence 108, Appl
44	1544.5	13.0	8381	8	US-11-263-326-138	Sequence 138, Appl
45	1544.5	13.0	8381	8	US-11-263-326-144	Sequence 144, Appl

ALIGNMENTS

RESULT 1
US-11-266-748A-31661
; Sequence 31661, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31661

```

; LENGTH: 7834
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-31661

Alignment Scores:
Pred. No.: 0 Length: 7834
Score: 11684.50 Matches: 2241
Percent Similarity: 94.8% Conservative: 1
Best Local Similarity: 94.7% Mismatches: 1
Query Match: 98.2% Indels: 123
DB: Gaps: 3

US-09-611-257A-37 (1-2266) x US-11-266-748A-31661 (1-7834)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGCAGGAGGAGGAGTGGAGCGGGCGCGAGAGTCCGGACAGCGCCCGAGCTTCATG 432
Qy 21 ArgLeuAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACGACCTGTCTGGGGGGCGGGGGCGGGGGCGGGGGTCCAGCAGAAAGGAC 492
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 493 CCGGGCAGCGGAGTCCGAGCGGGGGTCCGTTACCGGGCTGGCGCCGGTGGTT 552
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 553 TTCTTCTACTTGGACGAGGACAGCGCGCGGGAGCTGGTGTCTCCCGCAGGCTCTGAAC 612
Qy 81 ProTrpPheGluArgGlySerMetLeuValIleLeuLeuAenCysValThrLeuGlyMet 100
Db 613 CCCTGGTTTGAGGCATCAGCATGTTGGTCATCTCTCAACTCGGTGACCTGGCGCATG 672
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 673 TTCGGCCATCGAGACATCGCTGTACTCCAGCGCTCCCGAGCTCCCGAGGCTTT 732
Qy 121 AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 733 GATGACTTCATCTTTGGCCCTTTTTCGCCGTGGAGATGGTGTGAAGATGGTGGCTTGGC 792
Qy 141 IlePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 793 ATCTTTGGGAAAGTGTACCTGGAGACACTTGGAAACCGGCTTGACTTTTCATGCTC 852
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 853 ATCGCAGGAGTCTGGAGTACTCGCTGGACCTGCGAGAACGTCAGCTCTTCAGCTGTCAG 912
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 913 ACAGTCCGCTGCTCGACCGCTCAGGGCCATTACCCGGGTGCCAGCATGGCATCCTT 972
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 973 GTACGTTGCTCTGGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTCTGCTCTTC 1032
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1033 GTCTTCTTCATCTTGGCATCTGTCGGCTCCAGCTGTGGGCGGGGCTGCTTCGHAACCGA 1092
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln 260
Db 1093 TGTCTTCTACCTGAGAAATTCAGCTCCCGCTGAGCGTGGACCTGGAGCGCTATTACCA 1152
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1153 ACAGAAAGGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGGCG 1212
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProCysGlyLeu 300

```

Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2353 GCCTGTGGTCCAGACAGTGCCTTACTGTGCCCGGCGCGGAGGAGTGCAGTCC 2412
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2413 GCCGACCGTGAATGCTGTGACTCAGACAGCGAGGAGTATATAGTTTCAACAGAGTGC 2472
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2473 CAGCACAGGACCTCCGGGACCCCAACAGCGCGGCGCAACGGAGCCTGGGCCCCAGATGCA 2532
Qy 721 GluProSerSerValLeuAlaPheTrpArgLeulleCysAspThrPheArgLysIleVal 740
Db 2533 GAGCCACAGCTCTGTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2592
Qy 741 AspSerLysTyrPheGlyArgGlyLysMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2593 GACAGCAAGTACTTTGGCCGGGGAAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2652
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2653 GGCATCGAATACCACAGACGCGCGAGGAGCTTACCACGCGCTAGAAATCAGCAACATC 2712
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPhe 800
Db 2713 GTCTTCAACAGCCTCTTTGCGCTGGAGATGCTGTGAAGCTGCTTGTGTATGGTCCCTTT 2772
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820
Db 2773 GGCTACATCAAGAAATCCCTACAAACATCTTCGATGGTGTCAATGGTGCATCAGCGTGTG 2832
Qy 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2833 GAGATCGTGGCCAGCAGCGGGGGCGGCTCTCGGTGTGCGGACCTTCCGCTGTATGCGT 2892
Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2893 GTGCTGAAGCTGTGTGCGCTTCTCGCGCGCTGCAGCGGAGCTGGTGTGCTCATGAAG 2952
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheSer 880
Db 2953 ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTATGTCTTCACTTTCATCTTCAGC 3012
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3013 ATCTTGGGCATGATCTCTTTCGCTGCAAGTTTGCCTCTGAGCGGGATGGGGACACCTTG 3072
Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3073 CCAGACCGGAAGAAATTTGACTCCTTGTCTGGGCCATGCTCACTGTCTTTCAGATCCTTG 3132
Qy 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db 3133 ACCCAGAGAGACTGGAAACAAAGTCCCTACAATGGTATGGCCCTCCACGTCGCTCGGGCG 3192
Qy 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 3193 GCCTTTATTTCAATGGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGGTC 3252
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluLysLeuSerLysArgGluAspAlaSerGly 980
Db 3253 GCCATTCTGGTGGAGGGCTTCCAGGCGGAG----- 3282
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
Db 3283 -----GCAGATGCGCAACAAAGTCCGAA 3303
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3304 TCAGAGCCCGATTTCTTCTCACCAGCCTGGATGGTGGGACAGGAAGAAGTGTCTTG 3363

Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
Db 3364 GCCTTGTGTCTTGGGAGAGACCCCGAGCTGCGGAAGAGCCTGTCTGCCCTCTCATC 3423
Qy 1041 IleHisThrAlaIleThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3424 ATCCACACGGCGCCACACCCATGTCTGCTGCCAAGAGACACAGACGGGCTTGGGCGAG 3483
Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3484 CGCTGGGCGCTTGGTCTGCCCGCCAGCAGCAGCGGCTCGGAGAGCCTGGGCGGCGCC 3543
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3544 CACGAGATGAAGTCAACCGCCAGCGCCGAGCTCTCCGACACAGCCCTCGAGGCGCTGCA 3603
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3604 AGCAGCTGGACACAGCAGCGCTCCAGCCGGAACAGCCTCGGCGGTGACCCAGCCTGAAG 3663
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGluGlyGlnGluSerGln 1140
Db 3664 CGAGAAAGCCCAAGTGGAGAGCGCGGTCTCTGTTGCGAGAGAGCCAGAGAGCGAG 3723
Qy 1141 AspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3724 GATGAAGAGAGAGCTCAGAAAGAGGAGCGGCGCAGCCCTCGGCGCAGTACCACATCGCAC 3783
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3784 AGGGGTGCTCTGAGCGGGAGGCGCAAGAGTCTCTTGACCTGCCAGACACACTGCAGGTG 3843
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3844 CCAGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACACAGGACTGCAAT 3903
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProProLeuAsp 1220
Db 3904 GGCAAGTCCGCTTTCAGGGCGCTTGGCGCGGCTGCGGCTGATGATACCCCGCCTGGAT 3963
Qy 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 3964 GGGGATGAGCCCATGACAGGGCAACCTGAGCAAGGGGAAACGGGTCCGCGGTGGATC 4023
Qy 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 4024 CGAGCCGACTCCTCGCTGCTGCTCGCTCGAGGAGACTCTCGTTCAGCCTACATCTTCCCT 4083
Qy 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 4084 CCTCAGTCCAGGTTCGCGCTCTCTGTGTACCGGATCATCACCAAGATGTTTCGACCAAC 4143
Qy 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 4144 GTGGTCTTGTTCATCTCTTCTTAACTGCATCACCATCGCCATGGAGCGCCCGCAAAATT 4203
Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 4204 GACCCCAACAGCGCTGAAAGCATCTTCTCGTACCCCTCTCCAAATTAATCTTTCACCGCAGTC 4263
Qy 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
Db 4264 TTTCTGGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTGTCTCGGGGAGCAGCGG 4323
Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4324 TACCTCGGAGCAGTGGAAACGTGGAGCGGCTGTGTGTCTCATCTCTCCGTCATCGAC 4383
Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4384 ATTCTGGTGCATGTCTCTGACAGCGGCACCAAGATCTCTGGGCATCTGTAGGGGTGCTG 4443
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400

5524	TTGTTGTTTTTCATCTCTTTGGCGGTGGAGCTCTTTTGGAGACCTTGGAGTGTGAC	5583
1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
5584	GAGACACACCCCTGTGAGGGCCTGGCGCTCATGCCACCTTTGCGAACTTTGGCATGGCC	5643
1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
5644	TTCTTAACCCCTCTTCCGAGTCTCCACAGGTGACAAATTTGSAATGGCATTTATGAAGGACACC	5703
1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
5704	CTCGGGGACTGTGACCCAGGAGTCCACCTGTCTAACACAGCGTCATCTCGCCTACTACTTT	5763
1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
5764	GTGTCTTCTGTCTGACGGCCCCAGTTCGTCTAGTCAACGTGTGTGATCGCGCTCTGATG	5823
1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeu	1853
5824	AAGACCTGGAGGAGCAACAAGAGGCCAAGGAGGAGCGCGAGCTAGAGGCTGAGCGTG	5883
1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
5884	GAGCTGGAGATGAAGACCTTCAGCCCCCAGCCCCCAGAGCCCCAAGCTGGGGCTCTGCACCCA	5943
1874	TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHiPro	1893
5944	TGGCTTGGGTGGAGGCCCCGACAGCCCCCAGAGCCCCCAGAGCCCCCAGAGCAGCGAGCTG	6003
1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThr	1909
6004	GGCGCCACGCGAGATGAGCTCCACCTTTTCCCTGGAGCACCCACAGCAGGAGCGAGCTG	6063
1909	-----	1909
6064	TTTGACACCATATCCCTGCTGATCAGGGCTCCCTGGAGTGGGAGCTGAAGCTGATGGAC	6123
1909	-----	1909
6124	GAGCTGGCAGGCCAGGGGGCCAGCCCTCTGCCTTCCCTTCTGCCCCCAGCCTGGGAGGC	6183
1909	-----	1909
6184	TCCGACCCACAGATCCCTCTAGCTGAGATGGAGGCTCTGTCTCTGACCTCAGAGATTGTG	6243
1909	-----	1909
6244	TCTGAACCTCTGCTCTTAGCTCTGACGGATGACTCTTTGCCCTGATGACATGCACACA	6303
1910	-----MetGlnProHisProThrGluLeuProGlyPro	1920
6304	CTCTTACTTAGTCCCTGGAGAGCAATATGCAGCCCCCAGCAGGAGCTGCAGAGCCA	6363
1921	AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer	1940
6364	GACTTACTGCTGTGGGAAGTCTGGGGTCAGCGCAACGACCTCTCTGCCCAATGACAGC	6423
1941	TyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeu	1960
6424	TACATGTGTGGCATGGGAGCACTGCCGAGGGGGCCCTGGGACACAGGGGGCTGGGGGCTC	6483
1961	ProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyr	1980
6484	CCCAAGCTCAGTCAGGCTCCGTCTTGTTCGTCTACTCCAGCCAGCAGATACCAGCTAC	6543
1981	IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrp	2000
6544	ATCCTGAGCTTCCCAAAAGATGACCTCATCTCTCCAGCCCCCAGCAGCCCCAACCTGG	6603
2001	GlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArg	2020
6604	GGCACCATCCCCAACTGCCCCCCACAGGACGGCCCTCTTGGCTCAGAGGCCACTCAGG	6663

```
Qy 2021 ArgGlnAlaIleAlaArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040
Db 6664 CGCCAGGAGCAATAGAGACTGACTCTCTGGACGTTTCAGGGCTTGGGCAAGAC 6723
Qy 2041 LeuLeuAlaGluValSerGlyProSerProLeuAlaAlaArgAlaTyrSerPheTrpGly 2060
Db 6724 CTGCTGGCAGAGTGAAGTGGGCTCTCCCGCCCTGGCCGCGGCTACTCTTTCTGGGGC 6783
Qy 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080
Db 6784 CAGTCAGTACCCAGGACAGCAGCACTCCCGCAGCCACAGCAGATCTCCAGCACATG 6843
Qy 2081 ThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThr 2100
Db 6844 ACCCGGCAGCCCTTCCCGCAGGCCAGAACCTGGGGCAAGGCCCTCCAGAGACC 6903
Qy 2101 ArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProPro 2120
Db 6904 AGAAGCAGCTTAGAGATTGGACACGAGCTGAGCTGGATTTCAGGAGACCTCTCCGCCCT 6963
Qy 2121 GlyGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAla 2140
Db 6964 GCGGCCAGAGGAGGCCCTCCACCGGACCTGAAGAAGTCTACAGCGTGGAGGCC 7023
Qy 2141 GlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAla 2160
Db 7024 CAGAGCTGCCAGCGCGGCTACGCTCTGGCTGGATGAGCAGAGAGACACTCTATCGCC 7083
Qy 2161 ValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGly 2180
Db 7084 GTCAGCTGCCCTGGACAGCGGCTCCCAACCCACCTGGGSCACAGACCCCTTAACCTTGGG 7143
Qy 2181 GlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIle 2200
Db 7144 GGCAGGCTCTTGGGGGCTTGGAGCGCGGCCCAAGAAAACTCAGCCCGCTTAGTATC 7203
Qy 2201 ThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyLysCysLeu 2220
Db 7204 ACCATAGACCCCGCAGAGACCAAGGTCTTCGACCCCGCCGCTGGTATCTGCCTC 7263
Qy 2221 ArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSer 2240
Db 7264 CGAGAGAGGCTCCGTCACGCACTCCAGGATCCCTTGGCCCTTGGCCCGCCCTGACAGC 7323
Qy 2241 MetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAsp 2260
Db 7324 ATGGCTGCCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTATCTCTGAC 7383
Qy 2261 ProAlaAspLeuAspPro 2266
Db 7384 CCAGCAGACCTGGACCCC 7401
```

RESULT 2

```
US-11-266-748A-56474
; Sequence 56474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; METHODS OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIORITY FILING DATE: 2005-11-03
; PRIORITY APPLICATION NUMBER: EP 04105479.2
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105482.6
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105483.4
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY APPLICATION NUMBER: EP 04105507.0
```

```

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 56474
; LENGTH: 8079
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56474

Alignment Scores:
Pred. No.: 2,89e-269 Length: 8079
Score: 6230.50 Matches: 1367
Percent Similarity: 65.5% Conservative: 213
Best Local Similarity: 56.7% Mismatches: 519
Query Match: 52.3% Indels: 314
DB: 8 Gaps: 57

US-09-611-257A-37 (1-2266) x US-11-266-748A-56474 (1-8079)
Qy 7 GlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMetArgLeuAsnAspLeuSer 26
Db 317 GCGCTGGTGGGGGGCTCCCGGAGAGCCCCGG----- 349
Qy 27 GlyAlaGlyGlyArgProGlyPro-GlySer----- 36
Db 350 GCGCGCGGACGCGAGCGGCGGCGGGGTCCGAGCTCGGGGTGTCACCTCCGAGAGCCCC 409
Qy 37 ----AlaGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTrpAl 55
Db 410 GCGCGCGGACGCGGCGGCGGAGCTGGGTGCGCAGCAGAGAGCAGCGCTCCGTACCCGCGC 469
Qy 55 aLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLe 75
Db 470 CTTGGCGGCCACCGCTCTTCTTCGCTCGGTAGACACCGCGCGCGGAGCTGGTGCCT 529
Qy 75 uArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCy 95
Db 530 CCGGCTGGTCTGCAACCCATGTTTCGAGCAGCAGTCTGGTAAATCATGCTCAACTG 589
Qy 95 sValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysAr 115
Db 590 CGTGACCTGGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGGCGCTCCGAGCGCTCAA 649
Qy 115 gIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetValVal 135
Db 650 CATCTGGAGGCCCTTTGACGCCCTTCATTTTCGCTTTTTCGGGTGGAGATGGTCACTAA 709
Qy 135 sMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLe 155
Db 710 GATGGTGGCTTGGGGCTGTTCCGGCAGAGAAGTGTACCTGGGTGACACGTGGAAACAGCT 769
Qy 155 uAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSe 175
Db 770 GGATTTCTTCATCGTCGCGGCGCATGATGGAGTACTCGTTTGGACGACACACCGTGAG 829
Qy 175 rPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPr 195
Db 830 CCTCTCGGCTATCAGACCGCTGGGGTGTGCGGCCCTCCCGGCCCATCAACCGCGTGCC 889
Qy 195 oSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLe 215
Db 890 TAGCATGCGGATCCTGCTGCTCACTCTGCTGGTATACGCTGCCCATGCTCGGAAACGCTCT 949
Qy 215 uLeuLeuCysPhePheValPhePheIleValGlyIleValGlyValGlnLeuTrpAlaGl 235
```


QY 895 gAsp---GlyAspThrLeuProAspArgLysAsnPhaAspSerLeuLeuTrpAlaIleVa 914
DB AGACCGGAGACACCGTCTGACAGAGAACTTCGACTCCCTGCTGGGCGATCGT 3142
QY 914 lThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAl 934
DB CACCGTGTTCAGATCTCTGACCCAGGAGGACTGGAACGTGCTGTACAAACGGCATGGC 3202
QY 934 aSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVa 954
DB CTCACCTCTCTGGGCGCCCTCTACTTCGTGGCCCTCATGACCTTCGGCAACTATGT 3262
QY 954 lLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLy 974
DB GCTCTTCAACCTGCTGGTGGCCATCTCTGAGGGCTTCAGGCGGAG----- 3311
QY 974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGl 994
DB 3312 -----GG 3313
QY 994 yAspAlaAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAsp-- 1013
DB 3314 CGATGCCAACAGATCCGACACGAGCAGGACAGACGTGGTCCACTTCGAGGAGGACTT 3373
QY 1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerLe 1025
DB 3374 CCAAGAGCTCAGAGAACTCCAGAGCACAGAGCTGAAGATGTTCCTGGCCGCTGACCCC 3433
QY 1025 uGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAl 1045
DB 3434 CAACGGGCACCTGGAGGAGCAGGACCTGTCCCTCCCTCATCATGTGCACAGCTGC 3493
QY 1045 aThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyAlaLeuGlyProAl 1065
DB 3494 CACGCCCATCCATCCCAAGAGCTCACCATCTTCGATGCAGCCCCCAGCCTCCAGA 3553
QY 1065 aSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSe 1085
DB 3554 CTCCTCGGCTGGCAGCAGCAGCTCCGGGGACCCGCCA-----CTGGGAGCACCAGAGCC 3607
QY 1085 rProProSerAlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105
DB 3608 TCGGGCCAGCTCCGAAGATTCTCCCTGTGCCCCCTGGGGCCCCAGTGGCGCCCTGGAGCAG 3667
QY 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1125
DB 3668 CCGGCGCTCAGCTGGAGCAGCTGGGCGCTGCCCCAGCCTCAAGCGCCGCGGCAGTG 3727
QY 1125 rGlyGluArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSe 1145
DB 3728 TGGGGAACGTGAGTCTCTGTCTGGCGAGGGCAAGGGCAGCAGCCGACGACGAA----- 3782
QY 1145 rSerGluGluGluArgAlaSerProAla-----GlySerAspHisArgHisArgGlySe 1163
DB 3783 -GCTGAGGACGGCAGGGCCCGCCCGGGCCCCGTGCCACCCCTGCGCGGGCCCGAGTC 3841
QY 1163 rLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu----- 1178
DB 3842 CCTGGACCCACGCCCCCTGGCGCGCGCCGCTCCCGCTCCCAAGTGGCGCGCATCGCGA 3901
QY 1179 ----GlnValProGlyLeuHis-----ArgThrAlaSerGlyArgGlySe 1192
DB 3902 CGGGCAGGTGGTGGCCCTGCCACGACGACTTCTTCCTGCGCATCGACAGCCACCGCTGAGGA 3961
QY 1192 rAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLe 1212
DB 3962 TGCAGCCGAGCTTGACAGCAGCTCGGAGGACACTGCTGCTCCGCTCGCATAAAGTGCT 4021
QY 1212 uArgProAspProProLeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLy 1232
DB 4022 GGAGCCCTACAGCCC----- 4037
QY 1232 sGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAs 1252

DB 4038 -----CAGTGGTCCCGGAGC-----CGCGA 4057
QY 1252 pSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeuCysHisArgIle 1272
DB 4058 GGCTTGGCCCTTACTCTTCTCCACAGAACCGGTTCGGGTCTCTCTGCGCAAGGT 4117
QY 1272 eIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleTh 1292
DB 4118 CATCACACAAGATGTTTGATCAGCTGGTCTCTCTTCTTCTTCTCAACTGCGTCAC 4177
QY 1292 rIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLe 1312
DB 4178 CATCGCCCTGGAGAGCCTGACATTGATCCCGCAGCAGCAGCGGTCTCTCTCAGCGT 4237
QY 1312 uSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLe 1332
DB 4238 CTCCAATTATCATCTTCAGGCCATCTTCGTGGCGGAGATGATGTAAGGTGGTGGCCCT 4297
QY 1332 uGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLe 1352
DB 4298 GGGGCTGCTGTCCGCGCAGCAGCCTACCTGCAGAGCAGCTGGAACTGCTGGATGGCT 4357
QY 1352 uLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLy 1372
DB 4358 GCTGGTGGTGTCTGCTGGACATTGCTGTGGCCATGGCCTCGGCTGGTGGCGCAA 4417
QY 1372 sIleLeuGlyMetLeuArgValLeuLeuLeuLeuArgThrLeuArgProLeuArgValIle 1392
DB 4418 GATCCTGGGTGTTTCTCGCGGTGCTGCTGTCTGCGGACCTCGGCTCTGAGGGTCAT 4477
QY 1392 eSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIle 1412
DB 4478 CAGCGGGCCCCGGGCTCAAGCTGTGTGGTGGAGACGCTGATATCATCATCAGGCCAT 4537
QY 1412 eGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGl 1432
DB 4538 TGGGAACATCGTCTCATCTGCTGCGCTTCTTTCATCATTTTGGCATTTTGGGTGTCGA 4597
QY 1432 nLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLy 1452
DB 4598 GCTCTTCAAGGGAAGTTCTACTACTGCGAGGCCCCGACACGAGGAACATCTCCACCAA 4657
QY 1452 sSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLe 1472
DB 4658 GGCACAGTCGCGGGCGCCACTACCGTGGTGGTGGCGCAGCGCAAGTACAACTTCGACAACT 4717
QY 1472 uGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe 1492
DB 4718 GGGCCAGGCCCTGATGCTGCTGTCTGCTGTCATCCAAGGATGGATGGGTGAACATCAT 4777
QY 1492 tTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTr 1512
DB 4778 GTACGACGGGCTGGATGGGCTGGGTGTCACGAGCAGCTGTGCAGAACCCACACCCCTG 4837
QY 1512 pMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPh 1532
DB 4838 GATGCTGCTGACTTCTCTCTCTGCTCATCGTCTGCTTCTCTGCTCAACATGTT 4897
QY 1532 eValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluAl 1552
DB 4898 CGTGGGCGTGGTGGTGGAGAACTTCCACAAGTCCCGCAGCAGCAGGAGCGGAGGAGGC 4957
QY 1552 aArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgLysAlaGlnCy 1572
DB 4958 GGGCGCGCAGAGGAGGAGCGGCTGCGGCCCTTAGAGAGCGGCGGAGGAGGCCCGCGC 5017
QY 1572 sLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysThrSe 1592
DB 5018 CCGGCCCTACTATGCGGACTACTCGCCACGCGCCCTCCATTCTCTGCTGTGCCAGCAG 5077
QY 1592 rHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMe 1612

Db	5078	CCATATCTCGACCTCTTCATCACCTTCATCTGTGTCAACGTCATCACCATGTCCAT	5137
Qy	1612	tGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePh	1632
Db	5138	GGAGCACTATAACCAACCAAGTCGCTGGACGAGCCCTCAAGTACTGCACTACGTC	5197
Qy	1632	eThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgPh	1652
Db	5198	CACCATCGTTTGTCTTCGAGCGTCACTGAAGCTGGTAGCATTTGGGTTCGTCG	5257
Qy	1652	ePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly	1672
Db	5258	CTTCAAGGACAGGTGAACACAGCTGGACCTGGCCATCGTCTGTCACTATGGCAT	5317
Qy	1672	eThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg	1692
Db	5318	CAGCTGGAGAGATAGATAGACCGCGCGCTGCCCATCAACCCACCATCATCGCAT	5377
Qy	1692	eMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMet	1712
Db	5378	CATGGCGCTCTTCGCATTCGCCGTGTCTGAAGCTGCTGAAGCTGCTACGAGCAT	5437
Qy	1712	gAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuPh	1732
Db	5438	CGCCCTGCTGGACACTGTGTGTGAAGCTCTCCCGAGGTGGGAACCTGGGCTTCT	5497
Qy	1732	eMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG	1752
Db	5498	CATGCTCCTGTTTTTATCTATGCTGCTGGGAGTGAGCTGTTCCGGAGGCTGGAG	5557
Qy	1752	sAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG	1772
Db	5558	CAGTGAAGACACCCCTGCGAGGCGCTGAGCAGGCACGCCACCTTCAGCAACT	5617
Qy	1772	tAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetL	1792
Db	5618	GGCCTCTCTCACGCTGTTCGCGTGTCCACGGGGGCAACTGGAAACGGGATCAT	5677
Qy	1792	pThrLeuArgAspCys-----AspGlnGluSerThrCysTyrAsnThrValIle	1809
Db	5678	CACCTGCGCGAGTGTCCCGTAGGACACAGCACTGCTGAGCTACCTGCGCGCTG	5737
Qy	1809	rProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVal	1829
Db	5738	GCCCGTCTACTTCTGACCTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5797
Qy	1829	eAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGlu	1849
Db	5798	GGCGGTGCTCATGAAGCACCTGGAGGAGAGCAACAAGGAGGACGCGGAGTGC	5857
Qy	1849	uGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProLeu	1869
Db	5858	GGAGCCGAGATCAGCTGGAGATG-----	5882
Qy	1869	ySerProPheLeuTrpProGlyValGluGlyProAspSerPro-----AspSer	1886
Db	5883	-----GCGCAGGCGCGCGGAGTGCACGCCGGTGGAGCGCGA	5920
Qy	1886	oLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSer	1906
Db	5921	CAGGCT-----	5927
Qy	1906	uHisProThrMetGlnProHisProThrGluLeuProGly-----ProAspLe	1922
Db	5928	-----CCTTGGCCCGAGAGAGTCCGGCGCGCCAGGGACGCCCAACCT	5971
Qy	1922	uLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer	1942
Db	5972	GTT---GCACGCAAGGTGTCGCTGCCAGGATGCTCTGCTGCTGCCCAACGAC	6028
Qy	1942	tCysArgHisGlySerThrAlaGluGlyPro-----Le	1953
Db	6029	GTTACAGCGCGGTGCTGCTGCTGCGGCGCCCAACCCCGCGCTGCGAGGAGTGC	6088
Qy	1953	uGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis	1973
Db	6089	GGAGACCTATGGCGCGGCACCC-----TTGGGCTCGTTCCTCTGTGCATC	6139
Qy	1973	rGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeu	1993
Db	6140	TCGCGCGGAGAGTCTGTGCTCCCTCCAGATCCA-----TTGGCTGT	6184
Qy	1993	nProHisSerAlaProThrTrpGlyThrIleProLysLeuProProProGly-----	2011
Db	6185	GTCTGCTCCCGCAGCAGGCGGCGGAGCCCTCCACGCGCTCTCCCTCGGGCAG	6244
Qy	2011	gSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAspSerLeuAs	2031
Db	6245	CTCCCCAGTCTCAGCGCGCTGCTGTGCAGACAGGAGGTGTGCACACGATTCCT	6304
Qy	2031	pValGlnGlyLeuGlySerArgGluAspLeuLeu-----AlaGluValSerGly	2049
Db	6305	AGGGAAG---ATTGACAGCCTAGGACACCTTGGATCCTGCAGAGCTTGGTGA	6361
Qy	2049	rPro-----ProLeuAlaArgAlaTyrSerPheTrpGly-----GlnSerSer	2065
Db	6362	CCCGGTGAGCGCGTGCACCGGGGCTCCTGCAGTCCCCACCGCTCCCGCAGCC	6421
Qy	2065	nAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrProAla	2085
Db	6422	CGCAGCGTCCGCACTCGTAAGCATACCTTCGACAGCGCTGCTCTCCAGCGCG	6481
Qy	2085	oCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrArgSerSer	2105
Db	6482	GGCCCGCAGGCGGAGAG-----GAGCGCGAGGCTCGGACCC	6517
Qy	2105	uLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro-----	2119
Db	6518	AGCCGACGAGGAGTGCAGCACATCACAGCTCGCGCTCGCGCGCCACACAGCC	6577
Qy	2120	-ProGlyGlyGlnGluProPro-----SerProArgAspLeuLysLysCysTy	2136
Db	6578	GCCTCATGGCGCGGAGCCTCTCGGTGGCGCGGCGGAGCGGAGCTGCGCGCT	6637
Qy	2136	rSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGln	2156
Db	6638	CAGCTGATGCTCAGCGCTTCTGGACAGCCG---GGCGGCGCAGCAGCAGTGG	6694
Qy	2156	gHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThr	2176
Db	6695	GCCCTCGCGAGCTGGCGGAGCGGAGCCTGGGGAGCGAGGCTGGGGCGCTGAG	6752
Qy	2176	oSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeu	2196
Db	6753	-----GCCAGCC-----GCTCTGGTGGCGCGGAGCGCGAGGCTGGGG	6793
Qy	2196	rProSerIleThrIleAspProPro---GluSerGlnGlyProArgThrProPro	2215
Db	6794	CCCCCTTGATCTCTCGGTGGAAACCTCTCGGAGGACGAGGCTCTGCGCGCT	6853
Qy	2215	rPro-----GlyIleCysLeuArgArgAlaProSer-----	2226
Db	6854	GGCAGAGGCGGACACACATGAGCGCGAGGACCCCGCTCTGTGAGGCCACCG	6913
Qy	2227	-SerAspSerLysAspProLeu-----AlaSerGlyProProAspSerMet	2242
Db	6914	CAGGACTCTCTGAGGCCACAGAGGGCTCAGGCGCGGGGGGAGCCCTGCAGC	6973
Qy	2242	a-----AlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSer	2259
Db	6974	GGAGCGCTGGGCGCAGGCTCTCTGCGGGCTCAGCACCTGACCGTCCCGAGCT	7033
Qy	2259	rAspProAlaAspLeu-----AspPro	2266
Db	7034	TGAGCGCTGACCTCTCGGGTCCCGCAGTGGAGACCT	7070

QY	537	ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe	556
DB	1465	-----	1465
QY	557	TyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerPro	576
DB	1465	-----	1465
QY	577	SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer	596
DB	1465	-----	1465
QY	597	ProProGluThrLeuLysGluTyrAlaLeuValGluValAlaAlaSerSerGlyPro	616
DB	1465	-----	1465
QY	617	ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeu	636
DB	1465	-----	1465
QY	637	GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLys	656
DB	1466	-----CTCTGCTGTTGGATCCCCCTTCGCCCGC	1495
QY	657	AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly	676
DB	1496	GCACGCTCAAGCGGAGACAGAGACTCGTCATCTCCGGAGG-----	1543
QY	677	GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe	696
DB	1544	-----AAGGAGAAGATGTTCCGGTTT	1564
QY	697	ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu	716
DB	1564	-----	1564
QY	717	GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe	736
DB	1565	-----TTTATC	1570
QY	737	ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn	756
DB	1571	CGCGCATGTGAAGGCTCAGAGCTTCTACTGGGTGTGTGTCGCTGGTGGCCCTCGAAC	1630
QY	757	ThrLeuSerMetGlyIleGluTyrHisGlnGluProGluGluLeuThrAsnAlaLeuGlu	776
DB	1631	ACACTGTGTGGCCATGGTGCAATCAACACGCGCGCGGTACACGACCCCTGTAT	1690
QY	777	IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuVal	796
DB	1691	TTTCGAGATTGTTTTCTGGGTCTCTCTCCACAGAGATGTCCTCGAAGATGATGGC	1750
QY	797	TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal	816
DB	1751	CTGGGGCCCAAGACTACTCCGGTCTCTTCAACTGCTTCGACTTTGGGGTCATCGTG	1810
QY	817	IleSerValTrpGluIleValGlyGln-----GlnGlyGlyGlyLeuSer	831
DB	1811	GGGAGCGTCTTTGAAGTGGTCTGGCGGCCCATCAAGCGGGAAGCTCCTTTGGATCAGT	1870
QY	832	ValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeu	851
DB	1871	GTGCTGCGGGCCCTCCGCTGCTGAGGATCTTCAAGTCAAGAGTACTGGAGCTCCCTG	1930
QY	852	GlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu	871
DB	1931	CGGAACCTGGTGTCCCTGCTGAATCCATGAAGTCCATCATCAGCCTGCTCTCTTG	1990
QY	872	LeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPhe	891
DB	1991	CTCTTCCTGTCATGTGGTCTTTCGCCCTGTGGGATGCAGCTGTTTGGGGACAGTTC	2050
QY	892	AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp	911

[illegible]

Db 3113 GAGGCTGTGGAGGAAGAGACACCGAGGAAGAGCGGCCAGGAGAGAGGCGCTGAGATAGT 3172
Qy ProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPhe 1172
Db GAAGCCGACAGGAAGAGGAGCTCGGAACACACCGCCCGGGAGCCACACTGTGACCTG 3232
Qy AspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySer 1192
Db GAGACCAAGTGGGACTGTGACTGTGGTCCCATGTGCACACACTGCCCGCAGCACTGTCTCCAG 3292
Qy AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeu 1212
Db AAGTGGAGAACCGCAGAGGATGAGACAATCAGCGGAACGTCATCGCATGGGCGAGT 3352
Qy ArgProAspAspPro-----ProLeuAsp 1220
Db CAGCCCGCAGCCGACACACTATTGTACATATCCCACTGATGCTGACGGGCCCTCTTGGG 3412
Qy GlyAspAlaAspAspGluGlyAsnLeu-----SerLysGlyGluArg 1235
Db GAAGCCACGCGTCTCCAGTGTGTAACGTGACCTGGAAAGCCCAAGCAGAGGGGAAGAAG 3472
Qy -----ValArgAlaTrpIleArgAlaArgLeuProAlaCysTyr 1248
Db GAGGTGGAACGGATGATGATGAGAGCGGCCCGCCCTATCGTCCCATACAGC--- 3529
Qy LeuGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeu 1268
Db -----TCCATGTTCTGTTTAAGCCCAACCACTGCTCCCGCGCTTC 3571
Qy CysHisArgIleLeuHisLysMetPheAspHisValValLeuValIlePheLeu 1288
Db TGGCACTACATCGTACCATGAGTACTCGAGGTGTCATCTCGTGGTCACTCGCCTG 3631
Qy AsnCysIleThrIleAlaMetGluArgProGlyIleAspProHisSerAlaGluArgIle 1308
Db AGCAGATCCCTGGCTGCTGAGGACCCA---GTGCGCACAGACTCGCCAGGAACAAC 3688
Qy PheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLys 1328
Db GCTTGAATACCTGGATTACATTTTACCTGGTGTCTTTACCTTTGAGATGGTGATAAG 3748
Qy ValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnVal 1348
Db ATGATGCATTTGGGACTGCTGCTTCACTCCCTGGAGCCTATTTCGGGACTTGTGGAACATT 3808
Qy LeuAspGlyLeuLeuValLeuIleSerValIleAspIle---LeuValSerMetValSer 1367
Db CTGGACTTCATTGTGTCAGTGGCGCCCTGGTGGCGTTCCTTCTCGAGCTTCGTGGGA 3868
Qy AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1387
Db GATCCAAAGGGAAGACATCAATACATCAAGTCTCTGAGAGTCTTCTGTCCTGTCGGG 3928
Qy ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1407
Db CCCTCAAGACCATCAACCGCTGCCCAAGCTCAAGGCTGTGTTCAGCTGTGTGGTGAAC 3988
Qy SerLeuLysProIleGlyAsnIleValIleValIleCysCysAlaPhePheIlePheGly 1427
Db TCCTGAAGAAATGCTCTCAACATCTTGAATGCTATACATGCTCTTCAATGTTTCATATTGGC 4048
Qy IleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGlu----- 1444
Db GTCAATTCGGGTGAGCTCTTCAAGGGAAGTCTTCTACTGCACATGATCCAAAGGAG 4108
Qy -----AspThrArgAsn-----IleThrAsnLysSerAspCysAlaGluAlaSer 1459
Db CTGGAGAGGAGTCAAGGGGTCAAGTATTGGAATATGAGAAGGAGGAAGTGAAGCTCAG 4168
Qy TyrArg---TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db ----- 4169
Qy CCCAGGACGTGGGAAGAAATACGACTTTTCACTACGACAAATGTGCTCTGGGCTCTGCTGACG 4228

Qy LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
Db CTGTTACAGTGTTCACGGGAGAGGCTGCCCATGTGTGTAACACTCCGTGGATGCC 4298
Qy ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db ACCTATGAGGAGCAGGAGTCCCAAGCCCTGGGTACCGATGAGAGTGTCCATCTTCTACGTG 4348
Qy SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu 1538
Db GTCTACTTTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4408
Qy AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys 1558
Db ACCTTC-----CAGGACGAGGGGCAAGGTGATGTCTGAA----- 4444
Qy ArgLeuArgArgLeuGluLysLysArgArgLysAla-----GlnCysLys 1573
Db -----TGCAGCCTGGAGAAGAACGAGAGGCTTGCATTCGCTTCCGATATAAGACGTGGACATTT 4498
Qy ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisHisLeu 1589
Db CCCTCAGCAGCGTACATGCCCAAAACCGGACGTTCGTTCCAGTATAAGACGTGGACATTT 4558
Qy CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609
Db GTGGTCTCCCGCCCTTTGNAATACATTCATCATGGCCATGATAGCCCTCAACACTGGTGTG 4618
Qy MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629
Db CTGATGATGAAGTCTATGATGCACCTATGATGACGAGTGTGATGCTGAAATGCTCAAC 4678
Qy TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe 1649
Db ATCGTGTTCATCCATGCTTCTCCATGGAATGCTGCTGAAGATCATCGCTTGGGGTG 4738
Qy ArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIle 1669
Db CTGAACATTTTACAGAGATGCTTGAATGCTTGTGACTTTGCTACTGTGTGGGAAGTATT 4798
Qy MetGlyIleThrLeuGluGluIle---GluValAsnAlaSerLeuProIleAsnProThr 1688
Db ACTGATATTATTAGTAACAGAGATTCGGAAACGAAC-----AATTTTCATC 4843
Qy IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708
Db AACCTCAGTTCCTCCGCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCCAGGCG 4903
Qy ValGlyMetArgAlaAlaPheLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
Db TACACCATCGGCATCTGTGTGGACCTTTGTTCAGTCTTCTCAAGGCCCTGCTCCCTACGCTG 4963
Qy GlyLeuLeuPheMetLeuPhePheIlePheAlaLeuGlyValGluLeuPheGly 1748
Db TGTCTGCTCATTCGCCATGCTGTTCTTCTATCTACGCCATCATCGCATGCGAGGTGTTGGG 5023
Qy AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg 1768
Db AATATTGGCCTGGATGATGAC-----ACCAGCATCAACCGCCACCAACAATCTCCCG 5074
Qy AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGly 1788
Db ACCTTTTTCAGACCTTCATGCTGTGTTTCAGAGCGCCACCGGGGAGGCTCGCCACGAG 5134
Qy IleMetLysAspThrLeuArgAsp-----CysAspGlnGlu-----SerThrCysTyr 1804
Db ATCATGCTCTGCTGCTGAGCAACAGGCTGTGATGAGCAGGCAATGCCACCGAGTGT 5194
Qy AsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeu 1824
Db ----- 5195
Qy GGAAGTGAATTTGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGATG 5254

```
QY 1825 ValAsnValValIleAlaValLeuMet----- 1833
Db 5255 TTGAACCTCTTGTGCTGTGATCATGGACAATTTTGAGTACCTCAGCGGGACTCTTCC 5314
QY 1834 -----LysHisLeuGluGlu-SerAsnLysGluAlaLysGluGluAlaGluLe 1849
Db 5315 ATCTAGGTCTCTCACCACCTGGATGATTCATCCGGGTCTGGGCTGAATACGACCGGCT 5374
QY 1849 uGluAlaGluLeuGluMetLysThrLeu-SerProGlnProHisSerProLeuG 1869
Db 5375 GCCTGTGGCGCATCAGTTACATGACATGTTGAGATGCTGAAACACATGTCCTCCGCT 5434
QY 1869 LysSerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProG 1889
Db 5435 CTGGG-----GCTGGGAAGAAATGCCCTCGAGTGTGTTACAAGCGCTG 5482
QY 1889 lYalAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProT 1909
Db 5483 GTTCG---CATGAACATGCCCATCTCCACGAGGACATGACTGTTCACTTTCACGTCCACG 5539
QY 1909 hrMetGlnProHisProThr-----GluLeuProGlyPro----- 1920
Db 5540 CTGATGCCCTCATCCGAGCGGCAGCTGGAGATCAAGCTGCCCCAGCTGGGACAAAGCAG 5599
QY 1921 -----AspLeuLeuThrValArgLysSerGly----- 1929
Db 5600 CATCAGTGTGACGGGAGTTGAGGAAGGAGATTTCCGTTGTGTGGGCAATCTGCCCCAG 5659
QY 1929 ----- 1929
Db 5660 AAGACTTTGGACTTGCTGTGTACCACCCCTGATGAGATGACAGTGGGGAAGGTT 5719
QY 1930 -----ValSerArgThrHisSerLeuProAsnA 1939
Db 5720 TATSCAGCTCTGATGATTTTGACTTCTACAGCAGAAACAAACCCACGAGACCATGATG 5779
QY 1939 spSerTyMetCysArg-----HisGlySerThrAlaGluGlyPro-----LeuG 1954
Db 5780 CAGCAGGCTCTCGAGGCGCTCTCCAGATGGTCTGTGTCCTGTTCCACCCCTCTGAAG 5839
QY 1954 lYHis-----ArgGlyTrpGlyLeuPro-LysAla 1963
Db 5840 GCCACCTTGGAGCAGACACACCGCGTGTGCTCCGAGGAGCGCGGTTTCTCTTCGACAG 5899
QY 1964 GlnSerGlySerValLeuSer-----ValHisSerGlnProAla----- 1976
Db 5900 AAGAGTTCCACTCTCCTCAGCAATGGCGGGCCATACAAACCAAGAGAGTGGCATCAA 5959
QY 1977 ---AspThrSerTyIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro--- 1994
Db 5960 GAGTCTGTCTCTGGGCACTCAAGGACCAGGATGACCCCATGAGCCGAGCCGACCC 6019
QY 1995 -----HisSerAlaProThrTrpGlyThrIleProLysLeuProProGly 2010
Db 6020 CTGGAGCGTGGCCACTCCACAGAGATC-----CCTGTGGGG 6055
QY 2011 ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArg----- 2026
Db 6056 CGGTGAGGAGCAGTGGCTGTGGACGTTGATGTCAGAGCATAAACCCGAGGGGCGCTGAT 6115
QY 2027 -----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAla 2043
Db 6116 GGGGAGCCCGCTGGGTGGAGAGCCAGGTCGAGCGGCTCCATGCCCGCTTGGC 6175
QY 2044 GluValSerGlyPro-----SerProProLeuAlaArgAlaTySerPheTrpGly 2060
Db 6176 GCCGAGACTCAGCCGCTCAGATGCCAGCCCATGACGAGCGTCCATC----- 6223
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080
Db 6224 -----TCCACCGCTGGCCAGCGG---CCCCGTGGAC-TCATCTTTGACGACCAACCC 6273
QY 2081 ThrProProAlaProCysProGly-----ProGluProAsnTrpGlyLysGlyPro 2097
```

```
Db 6274 GGACGCGCCACCCCTAGCAGGCGTGTGCGCACCAACCA-----CCA 6318
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 6319 CCG-----CTG 6324
QY 2118 LeuProProGlyGlyGlnGlu---GluProProSerProArgAspLeuLysLysCysTy 2136
Db 6325 CCACCGCCGAGGAGCAGGAAGCAGAGTCCCTGGAGAAAGGGGCCAGCGTGTCTGC--- 6381
QY 2137 SerValGluAlaGlnSerCysGlnArgProThrSerTrpLeuAspGluGlnArgArg 2156
Db 6382 -----CGATATGATGGCGCCACCAAGCAG----- 6405
QY 2157 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPro 2176
Db 6406 -----TGCTGTGGGCGCGGCTGCCCGGAGAGGGGCTA-CAG 6446
QY 2177 SerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSer 2196
Db 6447 GCTGCCGCGGGAACAGAGAGCGCGGAGCGCGGCGGTCCAGAGCGGAGCGGAGC 6506
QY 2197 ProProSerIleThrIleAspProProGluSerGln----- 2208
Db 6507 CCT-----CATCTCTCTCGGAGAGCAGCGCTTCTACTCTGCGACC 6551
QY 2209 -----GlyProArgThrProProSerProGlyIleCysLeuArgArgArg 2223
Db 6552 GCTTTGGGGCGGTGAGCCCCCGAAGCCCAAGCCCTCCCTCAGCAGCCCAACGTCGC 6611
QY 2224 AlaProSerSerAspSerLysAspPro----- 2232
Db 6612 CAACAGCTGCCAGGAGCGCGGACCCCAACAGGGCAGTGTTCGTGAATGGGAGCC 6671
QY 2233 -----LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerPro 2247
Db 6672 CTTTGTGTCACATCTGTGTAGTACCCCGCGCGGTGGCGGAGCGAGCTCCCC 6731
QY 2248 LysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6732 AGACGCGCTTGACTC-----CCCGCCCGCAGCATCACCT 6764

RESULT 4
US-11-350-336-5
; Sequence 5, Application US/11350336
; Publication No. US20060135751A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/11/350,336
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7162
US-11-350-336-5

Alignment Scores: 7.41e-71 Length: 7364
Pred. No.:
```


1544	-----AAGGAGAAGATGTTCCGGTTT	1564	Qy	1027	Glu-----HisProGluLeuArgLys	1033
697	ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu	716	Db	2519	GACCCCGAGGAGCGGCTGCGCTTCCCACTACGGCCACCTGCGGCGCCGACATGAAGACG	2578
1564	-----	1564	Qy	1034	SerLeuLeuProProLeuIleIleHisThr-AlaAlaThrProMetSerLeuPro-----	1051
717	GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe	736	Db	2579	CACCTGGACCGCGCGCTGTTGGTGGAGCTGGCGCGCGCGCGCGCGCGCGTGGGA	2638
1565	-----TTTATC	1570	Qy	1052	-----LysSerThrSe	1055
737	ArgLysIleValAspSerLysTyPheGlyArgGlyIleMetIleAlaIleLeuValAsn	756	Db	2639	GGCAAAAGCCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTCGACCTCCGCGCAGGCAC	2698
1571	CGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGCTGTGGTGGCCCTGAAC	1630	Qy	1055	rThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSer-----	1071
757	ThrLeuSerMetGlyIleGluTyHisGluGlnProGluGluLeuThrAsnAlaLeuGlu	776	Db	2699	CACCGGCACCGCGACAAGACCAAGACCCCGCGCGGGGGACCAAGACCAGGAGCAGAGAGGCC	2758
1631	ACACTGTGTGGCCATGGTGCATTACACACCGCGCGGGCGCTTACACGACCTGTAT	1690	Qy	1072	-----SerGlySerAlaGluProGlyIleAlaHisGluMetLysSerProPr	1087
777	IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuVal	796	Db	2759	CCGAAGCGGAGAGCGGGAGCCCGGTGCCGCGGAGGAGCGCGCGCGCCAGCCGACG	2818
1691	TTTGCAGAGTTGTTTCTCGGTCTCTCTCTCACAGAGATGTCCTGAAGATGTATGCG	1750	Qy	1087	oSerAlaArg-----SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe	1105
797	TyrGlyProPheGlyTyIleLysAsnProTyAsnIlePheAspGlyValIleVal	816	Db	2819	CACAGCAAGGAGCGCGCGGGCCCCCGAGGCGCGGAGCGCGCGCGAGCCCGAGGC	2878
1751	CTGGGGCCCAAGACTACTTCGGTCTCTTCAACTGCTTCGACTTTGGGGTCACTGTG	1810	Qy	1105	rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe	1125
817	IleSerValTrpGluIleValGlyGln-----GlnGlyGlyGlyLeuSer	831	Db	2879	CCGAGGGCGCGCGCGGCACCAACCGCGCGGCTCCC-----CGAGGAGCGCGCCGAG	2932
1811	GGGAGCGCTTTTGAAGTGGTCTGGCGGCCCATCAAGCGGGAAGCTCCTTTGGGATCAGT	1870	Qy	1125	rGlyGlu-----	1127
832	ValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeu	851	Db	2933	CGGAGCGCCCGACCGCGCGCACCGGCACCGATCCGAGCAAGGAGTGCGCCGCGC	2992
1871	GTGCTGGCGGCCCTCCGCTGCTGAGGATCTTCAAAGTCCAGAACTACTGGAGCTCCCTG	1930	Qy	1127	-----	1127
852	GlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu	871	Db	2993	GCCAAAGGCGAGCGCGCGCGCACCGCGCGGCCCGCGAGCGGGGCCCCCGGAGGCGC	3052
1931	CGGAACCTGGTGGTCCCTGCTGAATCCATGAAGTCCATCATCAGCCTGCTCTTCTTG	1990	Qy	1128	-----ArgArgSerLeuLeuSe	1133
872	LeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPhe	891	Db	3053	GAGAGCGGGAGAGCGCGCGCGGCACCGGGCCCGGCACAAGCGCGAGCTGCTCAC	3112
1991	CTCTTCTGTTTCAATGTGCTTTCGCCCTGCTGGGGATGCAGCTGTTTGGGGACAGTTC	2050	Qy	1133	r-GlyGluGlyGln-GluSerGlnAspGluGluSerSerGluGluGluArgAlaSer	1152
892	AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp	911	Db	3113	GAGCTGTGGAAGGAGACACGAGGAGGAGGCGCCACGGAAGAGGAGGCTGAGATAGT	3172
2051	AACTTCCAGGATGAGATCCCA-----ACCAACTTCGACACCTTCCCTGCC	2098	Qy	1153	ProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPhe	1172
912	AlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyxAsn	931	Db	3173	GAAGCCGACAAGGAAAAGAGAGTCCGGAACCCAGCCCGGGAGCCACACTGTGACCTG	3232
2099	GCCATCCTCACTGTCTTCCAGATCCTGACGGGAGGAGCTGGAATGCGATGTATCAC	2158	Qy	1173	AspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySer	1192
932	GlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyxPheIleAla	946	Db	3233	GAGACCTGGGACTGTGACTGTGGTCCCATGCACACTGCCAGCACCTGTCTCCAG	3292
2159	GGGATCGAATCGCAAGCGCGCTCAGCAAGGCGATGTTCTCGTCTCTTTTACTTCA	2218	Qy	1193	AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeu	1212
947	LeuMetThrPheGlyAsnTyxValLeuPheAsnLeuLeuValAlaIleLeuValGluGly	966	Db	3293	AAGGTGGAGGAACAGCCAGAGGATGCAGACAATCAGCGGAACGTCCTCGCATGGCAGT	3352
2219	CTGACACTGTTCCGAAACTACACTCTGCTGAATGCTTTCTGGCCATCGCTGTGACAAC	2278	Qy	1213	ArgProAspAspPro-----ProLeuAsp	1220
967	Phe---GlnAlaGluLuleSerLys-----ArgGluAspAlaSerGlyGln	981	Db	3353	CAGCCCGCAGACCCGAAACACTATTGTACATATCCAGTGTGTGACGGGCCCTCTTGGG	3412
2279	CTGGCCAAACGCGCAAGACTGACCAAGGATGAAGAGGAGTGAAGAAAGACGCCAATCAG	2338	Qy	1221	GlyAspAspAlaAspAspGluGlyAsnLeu-----SerLysGlyGluArg	1235
982	-----LeuSerCysIleGln	986	Db	3413	GAAGCCACGGTCTGTTCCCGCTGTTAACTGTGACCTGGAAAGCCCAAGCAGAGGGAAGAAG	3472
2339	AAGCTTGCTCTCAAAAGGCCAAAGAGTGGCTGAAGTCAGGCCCATGCTGTCGCCGAAC	2398	Qy	1236	-----ValArgAlaTrpIleArgAlaArgLeuProAlaCysTyx	1248
987	LeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhePhe	1006	Db	3473	GAGGTGGAAGCGGATGACGTGTATGAGGAGCGGCCCGCCCTATCGTCCCATACAGC---	3529
2399	ATCTCCATCGCGCCAGGAGCAGAACTCGGCCAAAGCGCGCTCGGTGGGAGCAGCGG	2458	Qy	1249	LeuGluArgAspSerTrpSerAlaTyxIlePheProGlnSerArgPheArgLeuLeu	1268
1007	SerProSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGly	1026	Db	3530	-----TCCATGTTCTGTTTAAAGCCCCCAACCACTGCTGCTCGCGCTTC	3571
2459	GCCAGCCAGCTACGGCTGCAGAACCTGCGCGGCCAGCTGCAGCGGCTGTACAGCGAGATG	2518	Db			

Qy 1269 CysHisArgIleIleThrHisLeuMetPheAspHisValValLeuValIleIlePheLeu 1288
Db 3572 TGCACATACATCGTACCATGAGTACTTCGAGTGTGTCATTTCTCGTGTATCGCCTTG 3631
Qy 1289 AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1308
Db 3632 AGCAGCATCGCCTGGTGTGAGGACCA---GTGGCAGACTCGCCAGGAACAAC 3688
Qy 1309 PheLeuThrLeuSerAsnFyrIlePheThrAlaValPheLeuAlaGluMetThrValLys 1328
Db 3689 GCTCTGAAATACCTGGATTACATTTTTCACCTGGTGTCTTACCTTTGAGATGGTATAAG 3748
Qy 1329 ValValAlaLeuGlyTyrPheCysPheGlyGluAlaTyrLeuArgSerSerTrpAsnVal 1348
Db 3749 ATGATGACCTGGGACCTGCTCTTCAACCCTGGAGCCTATTTCGGGACCTTGTGGAAACAT 3808
Qy 1349 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetVal---Ser 1367
Db 3809 CTGGAC-----TTCATTGTGTGAGTGGCCCTTGGTGGCTTTGCTTTCTCA 3856
Qy 1368 AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1387
Db 3857 GGATCCAAAGGAAGACATCAATCAAGTCTCTGAGAGTCCTTCTGTGCTCGG 3916
Qy 1388 ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1407
Db 3917 CCCTCAAGACCATCAACCGCTGCCCAAGCTCAAGGCTGTGTTGACTGTGTGTGAAC 3976
Qy 1408 SerLeuLysProIleGlyAsnIleValIleValIleCysCysAlaPheIleIlePheGly 1427
Db 3977 TCCTGAAGAATGTCCTCAACATCTTGATTGTCTACATGTCTTTCATGTTTCATATTGCC 4036
Qy 1428 IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlu----- 1444
Db 4037 GTCATTCGGTGCAGCTCTTCAAGGGAAGTTTTTCTACTGCACAGATGAATCCAAGGAG 4096
Qy 1445 -----AspThrArgAsn-----IleThrAsnLysSerAspCysAlaGluAlaSer 1459
Db 4097 CTGGAGAGGACTGCGAGGGTCAATATTGGATTATGAGAAGGAGGAAGTGAAGCTCAG 4156
Qy 1460 TyrArg---TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4157 CCAGGAGTGGAGAATAACGACTTTTCACTACGACAAATGTCTCTGGGCTCTGCTGACG 4216
Qy 1479 LeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAla 1498
Db 4217 CTGTTACAGTCTCCACGGGAGAGGCTGCCCATGTGTGTGAACACTCCGTGGATGCC 4276
Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db 4277 ACCTATGAGGAGCAGGGTCCAAAGCCCTGGGTACCGCATGGAGCTGTCCATCTTCTACGTG 4336
Qy 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
Db 4337 GTCTACTTGTGTCTTCCCTTCTTCTCGTCAACATCTTTGTGGCTTTGATCATCATC 4396
Qy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys 1558
Db 4397 ACCTTC-----CAGGACAGGGGGAAGAGGTGATGTCGAA----- 4432
Qy 1559 ArgLeuArgArgLeuGluLysLysArgLysAla-----GlnCysLys 1573
Db 4433 -----TGCAGCCTGGAGAAGACGAGAGGGCTTGCAATTGACTTCGCCATCAGCGCCAAA 4486
Qy 1574 ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisLeu 1589
Db 4487 CCCTTGACCGGTACATGCCCAAAACCGGACGTCTTCCAGTATAGAGCTGGACATTT 4546
Qy 1590 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValThr 1609
Db 4547 GTGCTCTCCCGCCCTTTGATACTTTCATCATGCGCATGATAGCCCTCAACACTGTGGTG 4606
Qy 1610 MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629

Db 4607 CTGATGATGAAGTTCTATGATGCACCCCTATGAGTACGAGCTGATGCTCAAAATGCTCGAAC 4666
Qy 1630 TyrIlePheThrValIlePheValLeuLysSerValPheLysLeuValAlaPheGlyPhe 1649
Db 4667 ATCGTGTTCACATCCATGTTCTTCCATGGAATCGCTGCTGAAGATCATCGCTTTGGGGTG 4726
Qy 1650 ArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIle 1669
Db 4727 CTGAACATATTTCAGAGATGCTGGAATGTCTTTGACTTTGTCACTGTGTGGGAAGTATT 4786
Qy 1670 MetGlyIleThrLeuGluGluIle---GluValAsnAlaSerLeuProIleAsnProThr 1688
Db 4787 ACTGATATTTAGTAACAGAGATGCGGAACAAC-----AATTTCATC 4831
Qy 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708
Db 4832 AACCTCAGCTTCCTCGCCTCTTTTCGAGCTGCGCGCTGATCAAGCTGCTCCCGCAGGGC 4891
Qy 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
Db 4892 TACACCATCCGCATCCTGCTGTGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTACGTG 4951
Qy 1729 GlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGly 1748
Db 4952 TGTCTGCTCATTCGCCATGCTGTTCTTCATCTAGCCCATCATCGGCATGCAAGTGTGGG 5011
Qy 1749 AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg 1768
Db 5012 AATATTGCCCTGATGATGAC-----ACCAGCATCAACCGCCCAACAACATCTCCGG 5062
Qy 1769 AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGly 1788
Db 5063 ACCTTTTTCGCAACCCCTGATGCTGTTTCAGAGCGCCACGGGGAGGCTTGGCACGAG 5122
Qy 1789 IleMetLysAspThrLeuArgAsp-----CysAspGlnGlu-----SerThrCysTyr 1804
Db 5123 ATCATGCTGCTGCTGCGTGAACAACAGGCTGTGTGATGAGCAGGCAATGCCACCGAGTGT 5182
Qy 1805 AsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeu 1824
Db 5183 GGAAGTACATTTGCCCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5242
Qy 1825 ValAsnValValIleAlaValLeuMet----- 1833
Db 5243 TTGAACCTCTTTGTGGCTGTGATCGATCGAATTTTTCAGTACCTCACCGCGGACTCTTCC 5302
Qy 1834 -----LysHisLeuGluGlu-SerAsnLysGluAlaLysGluAlaGluLe 1849
Db 5303 ATCCTAGGTCTCTCACCACTTGGATGATTCATCCGGGTCTGGGTGAATAACGACCGGCT 5362
Qy 1849 uGluAlaGluLeuGluLeuMetLysThrLeu-SerProGlnProHisSerProLeuG 1869
Db 5363 GCGTGTGGCGCATCATCAATGACATGTTTGAAGATGCTGAACACATGTCCCCGCCCT 5422
Qy 1869 LysSerProPheLeuTrpProGlyValGlyProAspSerProAspSerProLysProG 1889
Db 5423 CTGGG-----GCTGGGGAAGAAATGCCCTGCTCGAGTGTCTTACAGCGGCTG 5470
Qy 1889 LysAlaLeuHisProAlaAlaHisAlaSerAlaSerHisPheSerLeuGluHisPro 1909
Db 5471 GTTCG---CATGAACATGCCCATCTCAACGAGGACATGACTGTTCACCTTCAGTCCACG 5527
Qy 1909 hrMetGlnProHisProThr-----GluLeuProGlyPro----- 1920
Db 5528 CTGATGGCCCTCATCCGCGGCGCATCTGGAGATCAAGCTGGCCCCCGCTGGGACAAACGAG 5587
Qy 1921 -----AspLeuLeuThrValA:rgLysSerGly----- 1929
Db 5588 CATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCGTTGTGTGGCCCAATCTGCCCCAG 5647
Qy 1929 ----- 1929

Db 506 GGGGACAAAACGCCCATGTCGGAGCGCTGGACGACACACGAGCGCCTATTTCATCGGGATC 565
Qy 128 PheAlaValGluMetValValLysMetValAlaLeuGly---llePheGlyLysLysCys 146
Db 566 TTTTGTCTTCAGGACGAGGATCAAAATCATCGCTCTGGCTTTTCTCCACAAGGCTCT 625
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValleAlaGlyMetLeuGlu 166
Db 626 TACTCTGGGAACGGCTGGAAACGTCATGGACTTCGTGCTGCTCTCACAGGGATCTTGCC 685
Qy 167 TyrSer-----LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArg 183
Db 686 ACGCTGGAACTGACTTCGACCTGCCA-----ACACTGAGGGCTGTGCGT 730
Qy 184 ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 203
Db 731 GTCTGAGGCCCTGAAGCTGGTGTCTGGGATTCCAAATTTGACGTGGTGTCTCAAGTCC 790
Qy 204 LeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhePhe 223
Db 791 ATCATGAAGGCCATGTTCCACTCTCGAGATTGGGCTGCTCTCTTTTGCCATCCTC 850
Qy 224 IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu 243
Db 851 ATGTTTGCATCATTTGGCTGGAGTTCTACATGGCAAGTTCCACAGGCTGTTTC--- 907
Qy 244 ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsn 263
Db 908 -----CCCAACAGCACAGATGCGGAG----- 928
Qy 264 GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg 283
Db 928 ----- 928
Qy 284 SerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeuAspTyrGlu 303
Db 929 -----CCCGTG-----GGTGACTTCCCTGTGGCAAGGAGGCCCA 964
Qy 304 AlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys 323
Db 965 GCCCGGCTGCGAGGGCGACACTGAGTGC-----CGGGAGTACTGGCA----- 1009
Qy 324 SerAlaGlyClnHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAla 343
Db 1010 -----GGACCCAACTTTGGCATCACCAACTTGACAATATCTCTGTTTGC 1054
Qy 344 TrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVal 363
Db 1055 ATCTTGACCGTGTTCAGTGCATCACCATGGAGGCTGGACTGACATCTCTATAATACA 1114
Qy 364 MetAsp---AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGly 382
Db 1115 AACGATCGCGCGCAACACCTGGAACCTGGCTACTTCTATCCCTCATCATCATCGG 1174
Qy 383 SerPhePheMetIleAsnLeuCysLeuValIleAlaIleAlaThrGlnPheSerGluThrLys 402
Db 1175 TCCTTCTTATGCTCAACCTGCTGGCGTCTCTCGGGGAGTTTGCAGGAGCGA 1234
Qy 403 ArgArgGluSer-----GlnLeuMetArgGluGlnArgValArgPhe 416
Db 1235 GAGAGGGTGAGAACCGCGCGCTTCCTGAAGCTGCGCGGAGGAGGAGATCGAG--- 1291
Qy 417 LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 436
Db 1292 -----CGAGAGCTC 1300
Qy 437 LeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArg 456
Db 1301 AACGGGTACCTGAGTGGATCTTCAAGCGGAGGAAGTCATGTGCGCGAGGAGGACAG 1360
Qy 457 AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThr 476
Db 1361 AATGCA-----GAGGAGAAG 1375

Qy 477 GlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHis 496
Db 1376 TCCCTTTGGAGCTGCTGAAGAGAGCGGCCACCAAGAAGAGACAAATACCTGATCCAC 1435
Qy 497 HisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArg 516
Db 1435 ----- 1435
Qy 517 AlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPro 536
Db 1436 ---GCAGAGAGGAGGAGGACCGCTTTGCAGAT----- 1465
Qy 537 ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe 556
Db 1465 ----- 1465
Qy 557 TyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerPro 576
Db 1465 ----- 1465
Qy 577 SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer 596
Db 1465 ----- 1465
Qy 597 ProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyPro 616
Db 1465 ----- 1465
Qy 617 ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeu 636
Db 1465 ----- 1465
Qy 637 GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLys 656
Db 1466 -----CTCTGTGCTGTGGATCCCTTCATCTTCCGGAGG----- 1495
Qy 657 AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly 676
Db 1496 GCCAGCTCTCAAGAGCGGGAAGACAGAGAGCTCGTCATCTTCCGGAGG----- 1543
Qy 677 GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe 696
Db 1544 -----AAGGAGAAGATGTTCCGGCTTT 1564
Qy 697 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu 716
Db 1564 ----- 1564
Qy 717 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736
Db 1565 -----TTTATC 1570
Qy 737 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 756
Db 1571 CGCGCGCATGTAAGCTCAGAGCTTCTACTGCGTGTGCTGTGCGTGTGCGCTCGAAC 1630
Qy 757 ThrLeuSerMetGlyIleGluTyrHisGlnGlnProGluGluLeuThrAsnAlaLeuGlu 776
Db 1631 ACATGTGTGTGCCCATGTGTACCAACAGCGCGCGGCTTACCAGCACCTGTAT 1690
Qy 777 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuVal 796
Db 1691 TTTTGCAGAGTTTGTCTTCTGCTCTCTTCTCACAGAGATGTCCTGAAGATGTATGGC 1750
Qy 797 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 816
Db 1751 CTGGGCGCCAGAGCTACTTCCGCTCTCTCAACTGCTTGGACTTGGGGTCACTCGTG 1810
Qy 817 IleSerValTrpGluIleValGlyGln-----GlnGlyGlyGlyLeuSer 831
Db 1811 GGGAGCGCTTTTGAAGTGTGTGGGGCGGCATCAACCGGGAGAGCTCTTTTGGGATCAGT 1870

3977	Db	TCCCTGAAGAAATGCTCTCAACATCTTGATGTGCTACATGCTCTTCATGTTTCATATTTGCC	4034
1428	Qy	IleLeuGlyValGlnLeuPheLysGlyLePheValCysGlnGlyGlu-----	1444
4037	Db	GTCAATTGGGTGCAGCTCTTCAAAGGGAAGTTTTTCTTACTGCACAGATGAATCCAAGGAG	4096
1445	Qy	-----AspThrArgAsn-----IleThrAsnLysSerAspCysAlaGluAlaSer	1459
4097	Db	CTGAGAGGAGCTACAGGGGTTCAGTATTTGGATTATGAGAAGGAGGAAGTGGAAAGCTCAG	4156
1460	Qy	TyrArg--TrrValArgHisLeuTyAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
4157	Db	CCCAGGCAGTGAAGAATACGACTTTCATACGACCAATGTCTCTGGGCTCTGCTGACG	4216
1479	Qy	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498
4217	Db	CTGTTTCACAGTCTCCACGGGAGAAGGCTGGCCCATGTGTGAAACACTCCGTGGATGCC	4276
1499	Qy	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
4277	Db	ACCTATGAGGACGAGGGTCCAAAGCCCTGGGTACCGCATGGAGGTGTCCATCTTCTACGTG	4336
1519	Qy	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
4337	Db	GTCTACTTTGGTGTCTTCCCTCTTCTCGTCAACATCTTTTGGCTTTGATCATCATC	4396
1539	Qy	AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLys	1558
4397	Db	ACCTTC-----CAGACGACGGGGACAAGGTGATGTCGAA-----	4432
1559	Qy	ArgLeuArgArgLeuGluLysLysArgArgLysAla-----GlnCysLys	1573
4433	Db	-----TGCAGCCTGGAGAACAACGAGAGGCTTGCACTTCGCGCATCAGCGCCAAA	4486
1574	Qy	ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisHisLeu	1589
4487	Db	CCCCAGACGGTACATGCCCCAAACCGGCGTGTCTCCAGTATAAGACGTGGACATTT	4546
1590	Qy	CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValThr	1609
4547	Db	GTGCTCTCCCGCCCTTGAATACTTCATATGCGCCATGATAGCCCTCAACACTGTGGTG	4606
1610	Qy	MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn	1629
4607	Db	CTGATGATGAAGTTCTATGATGCACCCTATGAGTACGAGCTGATGCTGAAATGCCTGAAC	4666
1630	Qy	TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe	1649
4667	Db	ATCGTGTTCATCCATGTTCTCCATGGAAATGCGTGTGGAAGATCATCGCCTTTGGGGTG	4726
1650	Qy	ArgArgPhePheGlnAspArgTrrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIle	1669
4727	Db	CTGAACATATTCAGAGATGCTGGAATGTCTTTGACTTTGTCTGTTTGGGAAGTATT	4786
1670	Qy	MetGlyIleThrLeuGluGluIle--GluValAsnAlaSerLeuProIleAsnProThr	1688
4787	Db	ACTGATATTTAGTAACAGAGATTGCCGAAACGAAC-----AATTTCATC	4831
1689	Qy	IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuMetAla	1708
4832	Db	AACCTCAGCTTCTCCCGCCTCTTTTCGAGCTCGCGGCTGATCAAGCTGTCTCCGCCAGGCG	4891
1709	Qy	ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu	1728
4892	Db	TACACCATCCGCATCTCTGTGTGACCTTTGTTCAGTCTTCAAGGCCCTTGCCTCAGTG	4951
1729	Qy	GlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGly	1748
4952	Db	TGTCGTCTCATGCGCTGTCTTCTTCTATCAGCCATCATCGGCATGCGAGGTGTTGGG	5011
1749	Qy	AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg	1768
5012	Db	AATATGCTCCCTGGATGATGAC-----ACCAGCATCAACGCCCAACAACATCTCCGG	5062

Qy	1769	AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAenTrpAsnGly	1789
Db	5063	ACGTTTTTGAAGGCCCTGTACTGCTGTTTCAGAGAGCCACGGGGAGGCCTCGCACGAG	5122
Qy	1789	IleMetLysAspThrLeuArgAsp-:::-CysAspGlnGlu-:::-SerThrCysTyr	1804
Db	5123	ATCATGTGTCCTGCCTGAGCAACCAGGCCCTGTGATGAGCAGGCCAAATGCCACCGAGTG	5182
Qy	1805	AsnThrValIleSerProIleTyrrPheValSerPheValLeuThrAlaGlnPheValLeu	1824
Db	5183	GGAAGTGACATTGCTACTTCTACTCTCGTCTCCTTCATCTCTGTGCTCTCTTCTGATG	5242
Qy	1825	ValAsnValValIleAlaValLeuMet-:::-:::-:::-:::-:::-:::-:::-:::-::-	1833
Db	5243	TTGAACTCTTTGGTGTGATCATGGACAATTTGATGACTCTACGGGGGACTCTTCC	5302
Qy	1834	-:::-LysHisLeuGluGlu-SerAsnLysGluAlaLysGluAlaGluLe	1849
Db	5303	ATCCTAGGTCTCTACCACTTTGGTAGTTTCATCGGTCTGGGCTGAATACGACCCGGCT	5362
Qy	1849	uGluAlaGluLeuGluLeuMetLysThrLeu-SerProGlnProHisSerProLeuG	1869
Db	5363	CGGTGTGGCGCATCAGTTCAATAGCATGTTTGAGATGCTGAAACACATGTCCCCGCCT	5422
Qy	1869	lysProPheLeuTriProGlyValGluGlyProAspSerProAspSerProLysProG	1889
Db	5423	CTGGG-:::-GCTGGGGAGAATAATGCCTCGCTGAGTTCCTTACAAGCGCCTG	5470
Qy	1889	lYAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHiProT	1909
Db	5471	GTTCCG--CATGAACATGCCCATCTCCAACGAGGACATGACTGTTCACTTCAGCTCCACG	5527
Qy	1909	hrMetGlnProHisProThr-:::-GluLeuProGlyPro-:::-:::-:::-:::-:::-	1920
Db	5528	CTGATGCCCTCATCCGAGCGGACTGGAGATCAAGCTGCCCCCAGCTGGGACAAAGCAG	5587
Qy	1921	-:::-AspLeuLeuThrValArgLysSerGly-:::-:::-:::-:::-:::-	1929
Db	5588	CATCAGTGTACGCGGAGTTTGAGGAAGGAGATTTCCTGTTGGGCCAATCTGCCCCAG	5647
Qy	1929	-:::-:::-:::-:::-:::-:::-:::-:::-:::-:::-:::-:::-:::-:::-	1929
Db	5648	AAGACTTTGGACTTGTTGTACCAACCCCATAAGCCTGATGAGATGACGTGGGGAAGGTT	5707
Qy	1930	-:::-ValSerArgThrHisSerLeuProAsnA	1939
Db	5708	TATCGACTCTGATGATATTTGACTTCTAACAGCAGACAAAACACCAGAGACCAGATG	5767
Qy	1939	spSerTyMetCysArg-:::-HisGlySerThrAlaGluGlyPro-:::-LeuG	1954
Db	5768	CAGCAGGCTCTGTGAGGCTCTCCAGATGGTCTGTCTGCTGTTTCCACCTCTGAAG	5827
Qy	1954	lyHis-:::-:::-:::-:::-:::-ArgGlyTPrglyLeuPro-LysAla	1963
Db	5828	GCCACCTGGAGAGACACAGCGGCTGTCTCCGAGGAGCCCGGTTTTCTTCGCAG	5887
Qy	1964	GlnSerGlySerValLeuSer-:::-ValHisSerGlnProAla-:::-:::-:::-	1976
Db	5888	AAGATTCCACTCCCTCAGCAATGGCGGGCCATACAAAAACCAAGAGATGGCATCAA	5947
Qy	1977	--AspThrSerTyrlleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro---	1994
Db	5948	GAGTCTGCTCTGTGGGCATCTAAAGAGCCAGGATGCACCCCATGAGCGCAGGCCACCC	6007
Qy	1995	-:::-HisSerAlaProThrTpGlyThrIleproLysLeuProProProGly	2010
Db	6008	CTGAGCGTGGCCACTCCAGAGATC-:::-:::-:::-:::-:::-CCTGTGGGG	6043
Qy	2011	ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArg-:::-:::-:::-	2026
Db	6044	CGGTCAAGGACCTGGCTGTGGACGTTTCAGATCGAGAGCATAAACCGGAGGGGCCCTGAT	6103

QY	2027	-----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAla	2043
Db	6104	GGGGAGCCCGCTGGGCTGGAGACCGAGGCTCGAGCGGCTCCATGCCCCGCTTGGC	6163
QY	2044	GluValSerGlyPro-----SerProLeuAlaArgAlaTyrSerPheTrpGly	2060
Db	6164	GCCGAGACTCAGCCGCTCAGATGCGAGCCCATGAAGCGCTCCATC-----	6211
QY	2061	GlnSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMet	2080
Db	6212	-----TCCACGCTGGCCAGCGG---CCCGTGGGAC-TCATCTTTGCAGCACCC	6261
QY	2081	ThrProProAlaProCysProGly-----ProGluProAsnTrpGlyLysGlyPro	2097
Db	6262	GGACCGCCACCCCTAGCCAGCGCTGCTCGCACCCACCA-----CCA	6306
QY	2098	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117
Db	6307	CCG-----CTG	6312
QY	2118	LeuProProGlyGlnGlu---GluProProSerProArgAspLeuLysLysCysTyr	2136
Db	6313	CCACCGCGCGAGGACGAGGAGCAGAGTCTCTGGAGAGGGGCCAGCTGTGTC---	6369
QY	2137	SerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArg	2156
Db	6370	-----CGATATGGATGGCGCACCAAGCAG-----	6393
QY	2157	HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPro	2176
Db	6394	-----TGCTGGGGCGGGCTGCCCGCGGAGGGGCCCTA-CAG	6434
QY	2177	SerAsnLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSer	2196
Db	6435	GCTCCCGCGGGAACGAGAGCGCGGAGGAGCGGGCGGTCCAGGAGCGGAGGCAGC	6494
QY	2197	ProProSerIleThrIleAspProProGluSerGln-----	2208
Db	6495	CCT-----CATCTCTCTCGGAGAGCAGCGCTTCTACTCTCGCAGCC	6539
QY	2209	-----GlyProArgThrProProSerProGlyIleCysLeuArgArgArg	2223
Db	6540	GCTTTGGGGCGCTGAGCCCCCGAGCCCAAGCCCAAGCCCTCCCTCAGCAGCCACCAACGTCGC	6599
QY	2224	AlaProSerSerAspSerLysAspPro	2232
Db	6600	CAACAGCTGGCAGGAGCGCGGACCCC	6626
RESULT 6			
US-11-350-336-9			
; Sequence 9, Application US/11350336			
; Publication No. US20060135751A1			
; GENERAL INFORMATION:			
; APPLICANT: Lipscombe, Diane			
; APPLICANT: Schorge, Stephanie			
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF			
; FILE REFERENCE: B1055/7000			
; CURRENT APPLICATION NUMBER: US/11/350,336			
; CURRENT FILING DATE: 2006-02-07			
; PRIOR APPLICATION NUMBER: US/10/033,026			
; PRIOR FILING DATE: 2001-12-28			
; PRIOR APPLICATION NUMBER: US 09/268,163			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: US 60/077,901			
; PRIOR FILING DATE: 1998-03-13			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 9			
; LENGTH: 7011			
; TYPE: DNA			
; ORGANISM: Rattus norvegicus			
; FEATURE:			
; NAME/KEY: CDS			

LOCATION: 1..7008

US-11-350-336-9

Alignment Scores:

Pred. No.: 1,81e-68

Score: 1728.50

Percent Similarity: 38.9%

Best Local Similarity: 25.5%

Query Match: 14.5%

DB: 8

Length: 7011

Matches: 669

Conservative: 353

Mismatches: 855

Indels: 752

Gaps: 89

US-09-611-257A-37 (1-2266) x US-11-350-336-9 (1-7011)

QY	27	GlyAlaGlyGlyArgProGlySerAlaGluLysAspProGlySerAlaAspSer	46
Db	73	GGGGCGGGGGGGCGGTGGCCGGGGGGTCTGCCCGCGGCGCAGCGGGTCTTG	132
QY	47	GluAlaGluGlyLeuProTyrProAlaLeuAlaProValPhe	61
Db	133	TACAAGCAGTCCATTGGGCAACGGCACCGACCATGGCCCTGTACAACCCATCC	192
QY	62	-----PheTyrLeuSerGlnAspSerArgPro	70
Db	193	AAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCTTTCAGCGAGGACAA	252
QY	71	ArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIleSerMet	90
Db	253	CGAAATATGCTAAGCGCATACCGAATGGCCGCCCTTTCGAATATATATATAT	312
QY	91	IleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAla	110
Db	313	ATCATGCCCACTGATATGTCTTGGCCCTG-----GAGCAGCACCTCCCTG	360
QY	111	SerGlnArgCysArgIleLeuGlnAlaPheAspAsp-----PheIlePheAla	127
Db	361	GGGGACAAGACTCCCATGTCTGAACGACTGGATGACACACGGAACCTTACT	420
QY	128	PheAlaValGluMetValValLysMetValAlaLeuGly---IlePheGlyLys	146
Db	421	TTTTTGTTCGAGCGGCGCATCAAGATCATAGCTCTGGGCTTGGTGTCTTCC	480
QY	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMet	166
Db	481	TACTCTCGGAATGGCTGGAACGCTCATGACTTTCGTGGTGGTCTCTCACAG	540
QY	167	TyrSer-----LeuAspLeuGlnAsnValSerPheSerAlaValArgThr	183
Db	541	ACAGCTGGAACTGACTTTTGATCTCGGC-----ACCCTGAGGGGTGTGGCT	585
QY	184	ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVal	203
Db	586	GTGCTTAGGCCCTTGAAGTGTGTGTGGAATTCAGACTTGCAGGTGGTCTCA	645
QY	204	LeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	223
Db	646	ATCATGAAGGCATGGTCCCGCTGCTGCAGATCGGGCTGTCTTCTTCCGCA	705
QY	224	IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	243
Db	706	ATGTTCTGCTATCATCGGCTCGAGTCTTATATATGGGCAAAATTCATAG	762
QY	244	ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	263
Db	763	-----CCCAACAGCACAGATGACAG-----	783
QY	264	GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	283
Db	783	-----	783
QY	284	SerValProThrLeuArgGlyAspGlyGlyGlyProCysGlyLeuAspTyr	303
Db	784	-----CCTGTG-----GGTGACTTCTTGTGGCAAGGAGGCCCTCT	819

Qy	304	AlaTyr	AsnSerSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys	322
Db	820	GCTCGTCTGTGTGACAGTCACACCAATGC	-----CGGAGTACTGGCCA-----	864
Qy	324	SerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAla	343	
Db	865	-----GGACCCAACTTTGGCATCCAAATTTTGACAAACATCCTGTTGGC	909	
Qy	344	TrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVal	363	
Db	910	ATCTTACCGGTGTTCCAGTGATCACCATGGAGGGCTGGACTGACATCTCTACAAATACA	969	
Qy	364	MetAsp-----AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGly	382	
Db	970	AATATGCGCGCGGCAACACGTGGAATCTGGTTGTTACTTCATCCCCCTCATCATATTGGC	1029	
Qy	393	SerPheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLys	402	
Db	1030	TCCTTCTTCATGCTCAACTCGTGTCTTCAGGAGAGTTGGCCAAAGACGG	1089	
Qy	403	GlnArgGluSer-----GlnLeuMetArgGluGlnArgValArgPhe	416	
Db	1090	GAGCGAGTCGAGAACCGCGTCCTTCTCTGAAGCTCCCGACGACGACGAGATTGAG---	1146	
Qy	417	LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu	436	
Db	1147	-----CGAGAACTG	1155	
Qy	437	LeuLysTyrLeuValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArg	456	
Db	1156	AATGGGTACTTGGAGTGATCTTCAAGCGGAGGAAGTCATGTTGGCAGAGGAGACAAG	1215	
Qy	457	AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThr	476	
Db	1216	AACGCA-----GAAGACAAG	1230	
Qy	477	GlnPro-----SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuVal	495	
Db	1231	TCCCTTTGGATGCAGTGTTCAGAGAGCTGCTACCAAGAAGAGCCGAAATGACCTCATC	1290	
Qy	496	HisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaPro	515	
Db	1291	CAT-----	1293	
Qy	516	ArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPro	535	
Db	1294	-----GCAGAAGAGGGGAGCACCG--	1314	
Qy	536	ProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSer	555	
Db	1314	-----	1314	
Qy	556	PheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSer	575	
Db	1314	-----	1314	
Qy	576	ProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThr	595	
Db	1314	-----	1314	
Qy	596	SerProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGly	615	
Db	1315	-----TTTGTAGACCTCTGCTGCTGGGTCT	1341	
Qy	616	ProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeu	635	
Db	1342	CCCTTGTCTGTCAGCCTC-----	1362	
Qy	636	LeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeu	655	
Db	1363	-----AAGAGTGGGAACAGACGACTCA-----	1386	
Qy	656	LysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAla	675	

1387	Db	----	TCGTACTCTCCGGAGG-----	1401
676	Qy	GlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGlu	695	
1402	Db	----	-----AAGAGAAGATGTTCCCGG	1419
696	Qy	PheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSer	715	
1420	Db	TTCC-----	-----	1422
716	Qy	LeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuLeuLeuLeuLeu	735	
1423	Db	-----	-----CTT	1425
736	Qy	PheArgLysIleValAlaAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuVal	755	
1426	Db	ATCCGTCGTATGTTGAAGCAGACAGACTTCTACTGGTGGTACTGTGCGTGGTGGCCCTG	1485	
756	Qy	AsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeu	775	
1486	Db	AACACGTTGTGTGGCCATGTTGACACTAATAATCAGCCTCAGCGGCTTACCACGTGCACTG	1545	
776	Qy	GluIleSerAsnIleValPheThrSerLeuPheAlaLeuMetLeuLeuLeuLeuLeuLeu	795	
1546	Db	TACTTTCCAGAGTTGTTTTCCTGGGTCTCTTCCCTCACAGAGATGTCCTCGAAGATGTAC	1605	
796	Qy	ValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal	815	
1606	Db	GGTCTAGGGCCCAAGACTACTTCCGGTCTTCCCTCAACTGCTTTGACCTTGGGGTGATT	1665	
816	Qy	ValIleSerValTrpGluIleValGlyGln-----GlnGlyGlyGlyLeu	830	
1666	Db	GTGGGAGTATCTTGAAGTAGTCTGGGTGCCATCAAGCCAGGAACCTCTTCGGAATC	1725	
831	Qy	SerValLeuGlnThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAla	850	
1726	Db	AGTGCTGTCGGGCTCTCCGACTGCTGAGAGATTTCAAAGTCACCAAGTATTGGAACTCC	1785	
851	Qy	LeuGlnArgGlnLeuValLeuMetLysThrMetAspAsnValAlaThrPheCysMet	870	
1786	Db	CTGAGGAACCTGTTGTTTCCCTCCTCAACTCCATGAAGTCCATCATCAGCCTTCTCTTC	1845	
871	Qy	LeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLys	890	
1846	Db	CTGCTTTTCCTTTCAATGTTGTTCTCGCTGTTGGGATGCAGCTGTTTGGGGACAG	1905	
891	Qy	PheAlaSerGlnArgAspGlyAspThrLeuProAspArgLysAsnValAlaThrPheCysMet	910	
1906	Db	TTCAACTTTCAAGATCAGACTCCAAC-----ACCAATTTTGATACCTTCCCA	1953	
911	Qy	TrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyr	930	
1954	Db	GCTGCCATCCTCACTGTGTTTTCAGATCTTGACAGGAGAGGACTGGAAATCAGTCATGAT	2013	
931	Qy	AsnGlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyrPheIle	945	
2014	Db	CATGGGATTCAGTCAACAAGGAGGTGTCAGCAAGGCATGTTTTCATCTTTTACTTTCATC	2073	
946	Qy	AlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGlu	965	
2074	Db	GTCCCTCAGACTGTTTGGAAACTACACCTGTTCAACGTTTTCTTGGCCATTCGTGTGGAC	2133	
966	Qy	GlyPhe---GlnAlaGluGluIleSerLys-----ArgGluAspAlaSerGly	980	
2134	Db	AACCTTTGCCAATGCCAGGAGTTTGACCAAGGATGAAGAGAGATGAAGAGCAGCAAT	2193	
981	Qy	Gln-----LeuSerCysIle	985	
2194	Db	CAGAAGCTTGCTCTTCAGAAAGGCCAAAGAAGTAGCTGAAGTCAGCCCCCATGTCTGCTGCC	2253	
986	Qy	GlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhe	1005	


```
Db 2254 AACATCTCCATTGCTGCCAGGCAGCAGAACTCGGCCAAAGCGCGCTCAGTATGGGAGCAG 2313
Qy 1006 PheSerProSerLeuAspGlyAspGlyAspArgLysCysLeuAlaLeuValSerLeu 1025
Db 2314 CGGGCCAGTCAGCTAAGAGCTCCAGAACCTCGGTGCCAGCTGTGAGGACACTGTACAGTGAG 2373
Qy 1026 GlyGlu-----HisProGluLeuArg 1032
Db 2374 ATGGACCCGAGGAGCGCGCTGCGTTATGCCAGCAGCGCCACGTGAGGCCAGACATGAAG 2433
Qy 1033 LysSerLeuLeuProProLeuIleIleHis----- 1042
Db 2434 ACACATGAGCAGCAGCCCTAGTGTGGAACCTGTGCGGATGCCCTGCGGGAGCCCGGCC 2493
Qy 1042 ----- 1042
Db 2494 GGGAAACAGTCAAAAGCTGAGGGCAGCGAGGCCACCGAAGGTGGGATCCACACGCCGA 2553
Qy 1043 -----ThrAlaAlaThrPro----- 1047
Db 2554 CACCACCGGCATCGTGATAGGACAGACACCTCAGCCTCAACCCCTGTGGAGGCGAACAG 2613
Qy 1048 -----MetSerLeuProLysSerThrThrGlyLeuGlyGluAlaLeuGlyProAla 1065
Db 2614 GACAGGACAGACTGCCCAAAGGCCAAAGCAGCAGACCGGGGCCCGGGAGGAACGTGCG 2673
Qy 1066 SerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSer 1085
Db 2674 CGCCCTCGTGAAGTCACAGCAGGAGGCT---CCAGGGCTGACACACAGTGCCTGTGT 2730
Qy 1086 ProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSer 1105
Db 2731 GAGCGCAGTAGACCTCACCACCGCGCGGATCCCGGAGGAGGCCACTGAACCGGAACT 2790
Qy 1106 ArgArg-----SerSerArgAsnSerLeuGlyArg 1115
Db 2791 CGGGCCACCGTGCACCGGCACGCACAGGACTCAAGCAAGGAAGCAAGGAGGCACT 2850
Qy 1116 AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu 1135
Db 2851 GCACCGTGCCTT-----GTACCCAGGGCGAGCGTCCGCAAGACATCGAGGCCCG 2901
Qy 1136 -----GlyGlnGluSerGlnAspGluGluSerSerGluGluArgAla-Se 1152
Db 2902 CGTACGGGCCCGGTGACAGACAGAACAGTGAGAGCCACACGCGAGCCACCGTGCAAG 2961
Qy 1152 rProAlaGlySerAspHis-----ArgHisArgGlySerLeuGluArgGlu----- 1167
Db 2962 CATAAGGTGCCAACCAACTTTCAGCCCCCAGAGAGGGAGGTTCAGAGAAAGGAGCAAC 3021
Qy 1168 -----AlaLysSerSerPheAspLeuProAspThrLeuGlnVal-ProG 1182
Db 3022 GTGGTGAAGGGATAAGAACTCAATCAACAGCCCAAGAACCTCGTGTGACCTG 3081
Qy 1182 lyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsnGlyL 1202
Db 3082 GAGGCCAT-----TGCGTTACAGCGTGGGCTCTCTGCACATGCTGCCACGACCTGT 3135
Qy 1202 ysSerAlaSerGlyArgLeuAlaArg----- 1210
Db 3136 CTCAGAAAGTGGACCAACAGCAGAGGATGCAGAACACCGCTAATGTCAACCGGATG 3195
Qy 1211 -----AlaLeuArgProAspAspPro-----ProLeuAspGlyAspAlaA 1225
Db 3196 GGCAGTCAGCCCTCAGACCCAGCACCACCTGTGCATGTCCAGTGCACATGACAGGCCCT 3255
Qy 1225 sPAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrp----- 1239
Db 3256 CCGGGGAGGCCACTGTAGTCCCA-GTGTAAACCGGACCTTGAAGGCCAAGCGGAGGG 3314
Qy 1240 -----IleArgAlaArgLeuProAlaCysTyThrLeuGluArg-----Asps 1253
Db 3315 CAAGAAGGAGGAGGAGGCTGACGATGTCTGAGAAAGAGGAGGCCCGCCAGGCCCATCGTTC 3374
```

```
Qy 1253 erTrpSerAlaTyrllePheProGlnSerArgPheArgLeuLeuCysHisArgIleI 1273
Db 3375 CAGT--TCCATGTTCTCGCTCAGCCCAACCACTACTCGTTCGCTTCTGCCATTACATTG 3433
Qy 1273 leThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrI 1293
Db 3434 TGACCATGGGTACTTTGAGATGGTGTCTTCTGTGTCTATCGCTTGAGCAGCATTCGCC 3493
Qy 1293 leAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuS 1313
Db 3494 TGCTCTCTGAGGATCCC---GTGCGGACCGACTCACTTCGGAACAATGCTCTCAAGTACA 3550
Qy 1313 erAsnTyrllePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeu 1333
Db 3551 TGGACTACATCTTTACAGGAGTCTTCACCTTTGAGATGGTCAATAAGATGATAGACTTGG 3610
Qy 1333 lyTrpCysPheGlyGluGlnAlaTyrlleArgSerSerTrpAsnValLeuAspGlyLeuL 1353
Db 3611 GCCTGTGTGTCACCTCGGGCCCTACTTCGGGACCTGTGGAAACATCTTGACTTCATTG 3670
Qy 1353 euValLeuIleSerValIleAspIle---LeuValSerMetValSerAspSerGlyThrL 1372
Db 3671 TTGTCACTGAGCCCTGGTGGCATTTGCATTTCTCGAGCTTCATGGGAGGATCCAAAGGA 3730
Qy 1372 ysIleLeuGlyMetLeuArgValLeuArgLeuArgThrLeuArgProLeuArgValI 1392
Db 3731 AAGACATCAATACCATCAAGTCTCTGAGAGTCTCGGAGCTCTGCGGCCCTCAAGACCA 3790
Qy 1392 leSerArgAlaGlnGlyLeuLysLeuValValGlnThrLeuMetSerSerLeuLysProI 1412
Db 3791 TCAAGCGGTGCTTAACCTCAAGCTGTGTTGACTGTGTGGTGAACCTCTCTGAAGAATG 3850
Qy 1412 leGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValG 1432
Db 3851 TCTTGAACATCTCGTACATGCTCTCATGTTTATATTATTTGCGCTCATCGCCGCTCC 3910
Qy 1432 lnLeuPheLysGlyLysPhePheValCysGlnGlyGlu-----AspT 1446
Db 3911 AACTCTTCAAAGGAAGTTCTTTTACTGCACCTGATGAGTCCAGGAGCTGGAGGGGACT 3970
Qy 1446 hrArgAsn-----IleThrAsnLysSerAspCysAlaGluAlaSerTyArg---TrpV 1463
Db 3971 GCAGGGTTCAGTATTGATTATGAGAGGAAGAGGTAGAAGCCAGCCAGGAGCTGGA 4030
Qy 1463 alArgHisLysTyArgAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuA 1483
Db 4031 AGAAATATGACTTCCACTATGACAATGTCTCTGGCCCTTGCTGACTCTGTTTACGGTGT 4090
Qy 1483 laSerLysAspGlyTrpValAspIleMetTyArgPheGlyLeuAspAlaValGlyValAspG 1503
Db 4091 CCACAGAGAGGGGTGGCCCATGGTGTGAAACACTCTGTGTGAGCCCACTATGAGGAGC 4150
Qy 1503 lnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyArgPheIleSerPheLeuLeuI 1523
Db 4151 AGGGCCCAAGCCCCGGGTTTCGGATGGAGCTTTCATCTCTATGTGTCTACTTTGTGG 4210
Qy 1523 leValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPheHisLysC 1543
Db 4211 TCTTCCCTTTTCTTGTCAACATCTTTGTGGCCTTGATCATCATCATCCTTC----- 4263
Qy 1543 ysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLeuArgL 1563
Db 4264 -----CAGGAGCAGGGGACAAGGTGATGCTCTGAG-----TGCAGTCTC 4300
Qy 1563 euGluLysLysArgArgLysAla-----GlnCysLysProTy-----T 1576
Db 4301 TGAATAAAGAAATCAGAGGGCTTGCATTTGTCATCAGCGCCCAAAACCCCTGACACGGT 4360
Qy 1576 yrSerAspTyArg-----PheArgLeuLeuValHisLysLeuCysThrSerHisT 1594
Db 4361 ACATGCCCTCAGAAACAGCAGTGTTCAGTATATAGACATGAGCATTTGTGGTCTCTCCAC 4420
```



```

Db      180 CTCACAAAAGCTCCGAGATCTCTATGGCAATCCACCACCAAGAGTCATCGGAGAGCCCCT   239
          ::::::::::||| ||| ||| :::: ||| |||
Qy      53 rProAlaLeuAlaIProValValPhePheTyrLeuSerGlnAspSer-----68
          ||| ||| ||| ||| :::: ||| |||
Db      240 GGAGGACTTGACCC-----TTCTATAGCACCCCAAAGAAGACTTTCATCGTACTGA    290
          ::::::::::||| ||| ||| :::: ||| |||
Qy      68 -----28
Db      291 TAAAGGCAAGACCATCTCCGGTTTCAGTGCACCACAACGCCTTGTATGTCTCAGTCCCTT   350
          ::::::::::||| ||| ||| :::: ||| |||
Qy      69 -ArgPro----ArgSerTrpCysLeuAArgThrValCysAsnProTrpPheGluArlleSe   87
          ||| ||| ||| ||| :::: ||| |||
Db      351 CCACCCCATCCGAGAGCGCTGTGAAGATTCTGGTTTCACCTGCCTCTTCAACATGCTCAT    410
          ::::::::::||| ||| ||| :::: ||| |||
Qy      87 rMetLeuValIIeLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIl   107
          ||| ||| ||| ||| :::: ||| |||
Db      411 CATGTGCACCATCTCTCACCAACTGCGTGTATGGCCCCAGCAGCACCTTCACCCC-----465
          ::::::::::||| ||| ||| :::: ||| |||
Qy      107 eAlaCysAspSerGlnArycArgileLeuGlnAlaPheAspAspPheIIePhe---Al   126
          ::::::::::||| ||| ||| :::: ||| |||
Db      466 -----TGGACCAAGTATGTCGAGTACACCTTCACGCC   497
          ::::::::::||| ||| ||| :::: ||| |||
Qy      126 apHePheAlaValGlumetValValllysMetValAlaLeuGlyIIePheGlyLysLysCy   146
          :::: ||| ||| ||| ||| :::: ||| |||
Db      498 CATTTACACCTTTGAGTCTTGCTCAAGATTCTGGCTCAGAGCTTC-----TG   545
          ::::::::::||| ||| ||| :::: ||| |||
Qy      146 s-----TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIl   161
          ::::::::::||| ||| ||| :::: ||| |||

```

Qy		161	eAlaGlyMetLeuGlnYrSerLeuAspLeuGlnAenValSerPheSerAlaValArgTh	181
Dd		606	CATGGCATACACAACGAATTTCGGACCTGGGCATGTC-----TCAGCCTTACGCCAC	659
Qy		181	rValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuVa	201
Dd		660	CTTCGGAGTCTCCGGGCCCTGAAACTATATACGTCAATTTCAGGCGTGAGACCATCGT	719
Qy		201	lThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheVa	221
Dd		720	GGGGGCCCTGATCCAGTCTCTGAAGAAGCTGGCTGATGTGATGGTCTCACAGTCTTC	779
Qy		221	lPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCy	241
Dd		780	CCTCAGCGCTTTTCCTCATCGCCCTGCAGCTCTTCATGGGGCAACCTTAAGGCACAAGTG	839
Qy		241	sPheLeuProGluAsnPhe-----	247
Dd		840	CGTG-----CGCAACTTTCACAGCGCTCAACGCGCACACGGCTCCGTGGAGGCCACGG	893
Qy		248	-----SerLeuProLeuSerValAspLeuGluArgTy-TyrGlnThrGluAs	263
Dd		894	CTTGGTCTGGGAATCCCTGGACCTTTTACCTCAGTGATCCAGAAAATACCTGTCTCAAGAA	953
Qy		263	nGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysAr	283
Dd		954	CGGCACCTCTGATGTGTACTGTGTGG-----	981
Qy		283	gSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeuAspTyrGl	303
Dd		981	-----	981
Qy		303	uAlaTyrAnSerSerSerAnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnC	323
Dd		982	-----AACAGCTCTGACGTGGGACATGT-----CCGAGGGCTACCGGTCCCT	1025
Qy		323	sSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAl	343
Dd		1026	AAAGCGAGCGGAG--AAACCCGACACCGGCTACACCAAGCTTCGATTCTCTTTCCTGGCGG	1082
Qy		343	aTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVa	363

Db 1083 CTTTCTTGCACTCTTCCGCGCTGATGACGCGAGGACTGCTGGGAGCGCCTCTATCAGCAGAC 1142
Qy 363 lmetAspAlaHisSerPheTyrAenPheIleTyrPheIleLeuLeuIleValGlyse 383
Db 1143 CCTCAGGTCCGCGAGGAAGACTCTACATGATCTTCTTCATGCTTGTCTATCTTCTGGGGTC 1202
Qy 383 rPhePheMetIleAsnLeuCysLeuValValIleAlaThrClnPheSerGluThrLysG1 403
Db 1203 CTTTCTACTGTTGAACCTGATCTTGGCGGTGGTGGCAATGCCATGAGGAG----- 1254
Qy 403 nArgGluSerClnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLe 423
Db 1255 -----CAAACCAAGCCACCAT 1271
Qy 423 uAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrI1 443
Db 1272 CGCTGAGACGAGGAGAAGAAAGCGCTTCCAGAGGCCATGGAA-----AT 1319
Qy 443 eLeuArgLys-----AlaAlaArgArgLeuAlaGlnValSerArgAlaAl 458
Db 1320 GCTCAAGAAAGAACACAGAGGCCCTCACCATCAGGGGTGTGGATACCGTGTCCGCTAGCTC 1379
Qy 458 aGlyValArgValGlyLeuLeuSerPro---AlaProLeuGlyGlyGlnGluThrG1 477
Db 1380 C-----TTGGAGATGCTCCCTTTGGCCCCAGTAAACAGCCATGAGAGAAG 1424
Qy 477 nProSerSerCysSerArgSerHisArgLeuSerValHisLeuValHisH1 497
Db 1425 A-----AGCAAGAGGAGAAACGATGCT------ 1449
Qy 497 sHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeu----- 512
Db 1450 -----TCAGGAACCTCAGGAGTGTGGGGAGGA 1475
Qy 513 -ArgAlaProArgAlaSerProGluIleGlnAspArgAspAlaAsnGly----- 528
Db 1476 CAGGCTCCCAAGTCTGACTCAGAAGATGTCGCCAGAGCAATGAATCATCTCAGCCTCAC 1535
Qy 529 -----SerArgArgLeuMetLeuProProSerThrProAlaLeu----- 542
Db 1536 CCGTGGCCTCAGCAGGACTTCTATGAGCCACGTTCCAGCGCGGGAGCATTTTCACCTT 1595
Qy 543 -----SerGlyAlaProProG1 548
Db 1596 TCGCAGCGCAGACCTGGGTTCTGAAGCAGATTTTGCAGATGATGAAACACAGCAGCGGG 1655
Qy 548 yGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCy 568
Db 1656 GGAGCGGAGCCACCACACA-----TCACCT 1682
Qy 568 sGlnAlaProProArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLy 588
Db 1683 GCTGGTGCCCTGCGCCCTGCGCGGACCATGTCACAGGACAG----- 1725
Qy 588 sValTyrProThrValHisThrSerProProGluThrLeu-----LysGluLysAl 606
Db 1726 -----CCAGTCCCGGAACCTCGGCTCGTGCCACGCGCTCATGGCAAAAGAACAG 1778
Qy 606 aLeuValGluVal-----AlaAlaSerSerGlyProProThrLeuThrSe 621
Db 1779 CACTGGGAGTGAATGGGGTGTCTCATTTACCTGGGGGAGCGGCCAGCCAGGCCACATC 1838
Qy 621 rLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSerTh 641
Db 1839 CCC-AGGAACCACTCCTCG----- 1859
Qy 641 rGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyAl 661
Db 1860 -----CCCTGTGATGCTAGACACCCGCG-----AGACACGACCAACGCCAT 1900
Qy 661 aCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeuAl 681
Db 1901 CGGAGGAGCGCGCGGCCCA----- 1922

Qy 681 aAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG1 701
Db 1923 -GATGCTGACCTCCAGGCTCC-----GTGTGTAGATGGCTTCGAGGAGCCAG 1969
Qy 701 nHisSerAspLeu-----ArgAspProHisSerArg-----ArgGlnAr 714
Db 1970 GAGCAGCGGAGCGGGCCCTCAGCGCATGTCAGCGCTCTCACCAGCGCACTGGAAGAGTTAG 2029
Qy 714 gSerLeuGlyProAspAla-----GluProSer----- 723
Db 2030 AGAGTCTCCCAAGTGTCCACCATGCTGGAAACCGTCTCGCCACGCGTACCTGATCT 2089
Qy 724 -SerValLeu-AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerL 743
Db 2090 GGGAGTGTCCCGCTGTGGATGTCATCAAGCAGGAGTGAAGTTGGTGGTCACTGAGCC 2149
Qy 743 ystYrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleG 763
Db 2150 CGTTTACTGACCTCACCATCACTATGTGCATCGTACTCAACACACTTTCATGCGCTGG 2209
Qy 763 lutyHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheT 783
Db 2210 AGCACTACAACATGACAAGTGAATTTCAGAGAGATGCTGCAGGTGCGAAACCTGGTCTTCA 2269
Qy 783 hrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrI 803
Db 2270 CAGGGATTTTCAGCAGCAGAGATGACCTTCAAGATCATTTGCCCTCGACCCCTACTACT 2329
Qy 803 lelysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleV 823
Db 2330 TCCAACAGGGCTGGAAACATCTTCGACAGCATCATCGTCTATCTTAGCCTCATGAGCTGG 2389
Qy 823 alGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuL 843
Db 2390 GCCTGTCCGCGATGACCAACTTGTGGTGTGGCTCTTCCGCTGTCTGGGTCTTCTCA 2449
Qy 843 ysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetA 863
Db 2450 AGCTGCCCAATCATCGCCCAACCTGAACACATCATCAAGATCATCGGAACTCAGTGG 2509
Qy 863 spAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuG 883
Db 2510 GGSCACTGGGGAACCTGACACATGCTGTGACCATCATCGTGTTCATCTTTGTGTGTGGTGG 2569
Qy 883 lyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr---LeuProA 902
Db 2570 GCATGAGCTCTTTGGCAAGAACTACTCGAGCTGAGGAGACGCGACTCAGGCTGTCTGC 2629
Qy 902 spArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrG 922
Db 2630 CTGCTGGCACATGATGGACTTCTTTCATGCGCTTCTCTCATCATCTTCGATCTCTGTG 2689
Qy 922 lngluAspTrpAsnLysValLeuTyrAsnGlyMet---AlaSerThrSerSerTrpAlaA 941
Db 2690 GAGAG---TCGATCGAGCACTGTGGACTGTGAGAGTGTGCGGCGACTATTATGCC 2746
Qy 941 laLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValA 961
Db 2747 TGTGTGTCTTCTTGT 2806
Qy 961 laIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyG 981
Db 2807 CCTTGTGTCTAGCTCCTTTCAGTGCAGACAACCTCACA---GCCCTGTATGAGGACAGAG 2863
Qy 981 lngluSerCysIleGlnLeu-ProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 2864 AGATGAACAACCTCCAGCTGGCGCTCGCCCGCATCCAGAGGGGCGCTTGTGTCAAGC 2923
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGly----- 1014
Db 2924 GGAACCACTGGGATTTCTGTGTGTCTCTGTGGCAGCGGCTCTAGAACCCGCGAGCCC 2983

QY	1015	-----AspArgLysLysCysLeuAlaLeuVal-----SerLeuGlyGluHisProGlu	1030
Db	2984	TTGCCGCCAGGCCAGCTGCCAGCTGCATTGCCACCCCTACTCCCGCCACCCCCAG	3043
QY	1031	LeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeu	1050
Db	3044	AGACGAGAAAGTGCTCCACCACCGCAAGGAACAC-----	3079
QY	1051	ProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgThrSer	1070
Db	3080	-----GGTTTG-----AGGAAGCGGAGC	3097
QY	1071	SerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArg	1090
Db	3098	AACAGCCAGGCGACCCCGGGGATC-----	3124
QY	1091	SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArg---ArgSerSer	1109
Db	3125	-----CAGAGCCCGTGTGTGCCCATCGCTGGCCGAGTCAGACAGATGACC	3175
QY	1110	ArgAsnSerLeuGlyArgAlaProSerLeuLysArgSerProSerGlyGluArgArg	1129
Db	3176	AAGAAGATGAGAGACAGCTGGCGACGAGGAGGAGTCCAGCAAGCAGCAGGAAT	3235
QY	1130	SerLeuLeuSerGlyGluGlyGlnGlu-----SerGlnAsp	1141
Db	3236	CCGACGCTGTG-TCCGGTGGCCAGAGGCCCTCCGGATTCCAGGACCTGGAGCCAGGTG	3294
QY	1142	GluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHisArg	1161
Db	3295	TCAGCGACTGCTCCTCTGAGGCCGAGGCCAGTGCATCTCAGGCCGACTGGCGGCACAG	3354
QY	1162	GlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValPro	1181
Db	3355	TGGAAGCGGNAACCCAG-----	3372
QY	1182	GlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsnGly	1201
Db	3373	-----GCCCGAGGTCGGTGAGACCCCGAGGACAGTGTGCTCCGAGGGC	3417
QY	1202	LysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAppProProLeuAspGly	1221
Db	3418	AGCACAGCAGCATGACCAACACCGCTGAGTCTCTGGAGCAGATCCCTGACCTCGGCCAG	3477
QY	1222	AspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIleArg	1241
Db	3478	GATGTCAAGGCCAGAGACTGCTTCACTGAAGC-----TGTTCCGG	3522
QY	1242	AlaArgLeuProAlaCysTyrlieuGluArgAspSerTrpSerAlaTyrlilePheProPro	1261
Db	3523	---CGCTCTCCTGCTGTCGGTGGACACACAGGCCCCAGGGAAGTCTGG-----	3573
QY	1262	GlnSerArgPheArgLeuLeuCysHisargIleIleThrHisLysMetPheAspHisVal	1281
Db	3574	---TGGCGGTTCGCAAGACCTGTACCACATCGGGAGCAGCTGGTTCCAGACATC	3630
QY	1282	ValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAsp	1301
Db	3631	ATCATCTTCATGATCTACTAGCAGTGGAGCGCTGGCTTCGAGGACATCTACCTAGAG	3690
QY	1302	ProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrlilePheThrAlaValPhe	1321
Db	3691	GAGCGGAAGACCATCAAGGTTCTGTGTAGTATGCCGACAGATGTTACATATGCTCTC	3750
QY	1322	LeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrl	1341
Db	3751	GTGCTGGAGATCTGCTCAAGTGGGTGGC-----TACGGCTTCAAGAGTAC	3798
QY	1342	LeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIle	1361
Db	3799	TTCAACAAATGCTGGTGGTTCGACTTCCTCATCGTAGACGTCTCT-----	3846
QY	1362	LeuValSerMetValSerAspSer---GlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	3847	CTGGTCAGCTGGTGGCCCAACACCTGGCTTTCGAGATGGGCCCATCAAGTCACTG	3906
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	3907	CGACGCTCGTGCATCCGTCCTCTGAGAGCTCTGTACGATTTGAGGCATGAGGGTG	3966
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys	1420
Db	3967	GTGGTCAATGCCCTGGTGGCGCCATCCCGTCCATCATGAACGTCCTCTCGTCTGCCTC	4026
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal	1440
Db	4027	ATCTTCGGCTCATCTTCAGCATCATGGCGTGAACCTCTTTCGGGGAAGTTGGGAGG	4086
QY	1441	Cys-----GlnGlyGluAspThrArgAsnIleThr-----AsnLysSer	1453
Db	4087	TGCATCAACAGACAGAGGAGACTTGGCTTTGAACCTACACCATCGTGAACAACAAGAGC	4146
QY	1454	AspCysAlaGluAlaSerTyArg-----TrpValArgHisLysTyArgAsnPhe	1469
Db	4147	CAGTGTGAGTCCTTGAACTTGACCGGAGAAATTGTACTGGCAAGGTGAAGTCAACTTT	4206
QY	1470	AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVal	1489
Db	4207	GACAACTGGGGCCGGTACCTGGCCCTTCTGCAGGTGGCAACATTTAAAGGCTGGATG	4266
QY	1490	AspIleMetTyrlAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHis	1509
Db	4267	GACATTATGATGAGCTGTGGACTCCAGGGGGGTATGAAGAGCCTCAGTGGGAATAC	4326
QY	1510	AsnProTrpMetLeuLeuTyrlPheIleSerPheLeuLeuIleValAlaPhePheValLeu	1529
Db	4327	AACTCTACATGTACATCTATTTTGTCTATTTTTCATCATCTTGGGTCTTCTTCCACCTG	4386
QY	1530	AsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGlu	1549
Db	4387	AACCTCTTTATGGTGTTCATCTTCAACCTTCAACCAACAGAGAAGAAAGTTAGGGGGC	4446
QY	1550	GluGluAlaArgArgArgGluGlu-----LysArgLeuArgArgLeuGluLysLysArg	1567
Db	4447	CAGGACATCTTCATGACAGAGGAGCAGAGAAGTACTACAATGCCATGAAGAAGCTGGGC	4506
QY	1568	ArgLysAlaGlnCysLysProTyrlTyrlSerAspTyrlSerArgPheArgLeuValHis	1587
Db	4507	TCCAAGAAGCCCAAGAGCCCATCCCGGCCCTTGAAACAGTACCAGGCTTCATATTC	4566
QY	1588	HisLysCysThrSerHisTyrlLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVal	1607
Db	4567	GACATTGTGACCAAGCAGGCCCTTTGACGTCACCATCATGTTTCTGATCTGCTTGAATATG	4626
QY	1608	ValThrMetAlaMetGlu---HisTyrlGlnGlnProGlnIleLeuAspGluAlaLeuLys	1626
Db	4627	GTGACCATGATGGTGGAGACAGATGACCAAAAGTCTGTAGAAAATCAACATCTTGCCCAAG	4686
QY	1627	IleCysAsnTyrlIlePheThrValIlePheValLeuGluSerValPheLysLeuValAla	1646
Db	4687	ATC---AACCTGCTCTTTGTGGCCATCTTCAGCGGAGTGTATGTCAAGCTGGCTGCC	4743
QY	1647	PheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeu	1666
Db	4744	CTGCGC---CACTACTACTTCACCAACAGCTGGAATATCTTCGACTTCTGCTGTTGTCATC	4800
QY	1667	LeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsn	1686
Db	4801	CTCTCATCGTGGGACATGCTGCTCTCGGACATC-----ATCCAGAAGTACTTCTTCTCC	4854
QY	1687	ProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLys	1706
Db	4855	CCGACGCTCTTCGAGTATCGCGCTGGCCCGAATAGCCCGCATCTCTAGACTGATCCGA	4914
QY	1707	MetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGly	1726

```
Db 4915 GGGCCCAAGGGGATCCGACCTGCTCTTCCCTCCTCATGATGTCCTGCGCTGCTTTC 4974
Qy 1727 AsnLeuGlyLeuLeuPheMetLeuLeuPhePheAlaLeuGlyValGluLeu 1746
Db 4975 AACATCGGGCTGCTCTTCTCGTCATGTTTCTACTTCTTCCATCTTGGCATGCCAAC 5034
Qy 1747 PheGlyAspLeuGlyCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThr 1766
Db 5035 TTCCCTTATGTCAAGTGGAG-----GCTGGCATCGACGACATGTTCAAC 5079
Qy 1767 PheArgAsnPheGlyMetAlaPheLeuThrLeuPheValSerThrGlyAspAsnTrp 1786
Db 5080 TTCAGACCTTCGCAACAGCATGCTGTGCTCTTCCAGATCACCACGTCGCGCGGTGG 5139
Qy 1787 AsnGlyIleMetLysAspThrLeuArgAsp-----CysAsp----- 1798
Db 5140 GATGGCTCTCTCAGCCCCATCTCAACACTGGGCGGCTACTGCGACCCCACTCTGCC 5199
Qy 1799 -----GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheVal 1814
Db 5200 AACAGCAATGGCTCTCGGGGGAGTGGCGGAGCCCGTGGGCATCTCTTCTTCAAC 5259
Qy 1815 SerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLys 1834
Db 5260 ACCTACATCATCATCTCTTCTCTCTCATCTGTGTCAACATGTACATGTCATCGCATCCTGGAG 5319
Qy 1835 HisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGlu 1854
Db 5320 AACTTACGCTGGCCAGGAGGAGACCGAGCCCTG-----AGTAGGAGCAC 5370
Qy 1855 LeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrp 1874
Db 5371 TTCGATATGTTATGATAGATCTGGAGAAATTTGACCCAGAGGCCACTCAGTTTATTGAG 5430
Qy 1875 ProGlyVal-----GluGlyProAspSerProAspSerPro-----LysPro 1888
Db 5431 TATCGGTCTGCTGTCTGATTTGGCGATGTCCTCTGTGAGCCACTCGGTATCGCAAGCCC 5490
Qy 1889 GlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisPro 1908
Db 5491 AACAGATAG-CCTCATCAACATGGACCTGCC-----CATGGT 5528
Qy 1909 ThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSer 1928
Db 5529 GAGTGGGGACCGCATCA-----TTCATGGA----- 5555
Qy 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
Db 5556 -----CATTTCTTT-----TGCCCTCAC----- 5573
Qy 1949 AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerVal 1968
Db 5574 CAAAGGGTCTGGGGAGTCTGGGAGATGGAGCGCCCTGAAGATCCAGATGGAGA--- 5630
Qy 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988
Db 5631 ---GAAGTTTCATGG-CAGCCCAACCCAT-----CCAAGATCTCCT 5665
Qy 1989 ProHisLeuLeuGlnProHisSerAla----- 1997
Db 5666 ACAGAGCCCATCACCACACACTCCGCGCAGCAAGAGGTGTGCGGCATGTTATTC 5725
Qy 1998 -----ProThrTrpGlyThr-----IleProLysLeuProPro----- 2008
Db 5726 AGAGAGCTTCCGAGGACCTGCTGCAACGCTCTTTGAAGCATGCTCTCTTCTTCTTC 5785
Qy 2009 -----ProGlyArgSerProLeuAlaGlnArgProLeuArg 2020
Db 5786 GTCAGCAGCGCGGCGGCTCTCCGAGAGGATGCCCCCTGAGCAGAGGGCTCATCG 5845
Qy 2021 ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040
Db 5846 CCTACGTGATGATGAGAACT-----TCTCCGACCCC 5878
```

```
Qy 2041 LeuLeuAlaGluValSerGlyProSerProLeuAlaArgAlaTyrSerPheTrpGly 2060
Db 5879 TTGGCCCACTCCAGCTCTCCATCTCTCCCTCCATCTCT----- 5917
Qy 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080
Db 5918 -----TCCCACTCTCTATGACAGTGTCACTA 5944
Qy 2081 ThrProProAla 2084
Db 5945 GAGCCACCAAGCG 5956

RESULT 8
US-11-313-450-13
; Sequence 13, Application US/11313450
; Publication No. US20060110778A1
; GENERAL INFORMATION:
; APPLICANT: Adorante, Joseph S.
; TITLE OF INVENTION: High-Throughput Screens For Identifying
; TITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers
; FILE REFERENCE: 17407 CIP (AP)
; CURRENT APPLICATION NUMBER: US/11/313,450
; PRIOR FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/989797
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252771
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5934
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-313-450-13

Alignment Scores:
Pred. No.: 1 31e-62 Length: 5934
Score: 1595.50 Matches: 540
Percent Similarity: 43.2% Conservative: 378
Best Local Similarity: 25.4% Mismatches: 786
Query Match: 13.4% Indels: 421
DB: 8 Gaps: 72

US-09-611-257A-37 (1-2266) x US-11-313-450-13 (1-5934)
Qy 2 AspGluGluGluAspGlyAlaGlyAlaGlu---GluSerGlyGlnProArgSerPheMet 20
Db 127 GATGAAGAAGCCCCAAAGCAAGCAGTGTGGAAGTGGCAAGCTGCAACACTGCTTCATC 186
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySer----- 36
Db 187 ---TATGGGACAT-TCTTCCCGCATGGTGTGTGAGAGCCCTGGAGGACTTGGACCCCTA 242
Qy 37 -----AlaGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrPro 54
Db 243 CTATGCAAGCAAAAGACATTTTCATAGTATTGTAACAAAGGAAACAAATCTTCGTTTCAA 302
Qy 55 AlaLeuAlaProValValPhePheTyr-LeuSerGlnAspSerArgProArgSerTrpCy 74
Db 303 -----TGCCACACCTGCTTTATATATGCTTTCTCTTCCTTCAGTCTCTTAAGAAGAATATC 356
Qy 74 sleuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAs 94
Db 357 TATTAAGATTATTAGTACACTCTTATTACATGCTCATCATGTGTCACATTTCTGACAAA 416
Qy 94 nCysValThrLeuGlyMetPheArgPro-----CysGluAspIleAlaCysaspSe 111
Db 417 CTGCATATTTTATGACCATGAATAACCCCGGAGTGGACCAAAATGTC----- 465
Qy 111 rGlnArgCysArgIleLeuGlnAlaPheAspPheIlePhe---AlaPhePheAlaVa 130
```

Db	466	-----GAGTACACTTTTACGTGAATATATACTTT	494
Qy	130	lGluMetValValysMetValAlaLeuGlylle---PheGlyLysCysTyrLeuGl	149
Db	495	TGAATCATTGTGTAATAATCTTCCAAAGAGCTTCTGTGTAGGAGAAATTCACITTTCTTCG	554
Qy	149	yAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerIle	169
Db	555	TGACCCGTGGAACTGGCTGATTTTGTGCGTCATTGTTTTCGCGTATTTAACAGAAATTTGT	614
Qy	169	uAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuAr	189
Db	615	AAACCTAGGCAATGTT-----TCAGCTCTTCAACTTTTCAGAGTATTGAGAGCTTTGAA	668
Qy	189	gAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuPr	209
Db	669	AACTATTCTTGTATCCAGCCCTGAAGACAAATGTAGGGGCTTTGATCCAGTCAGTGAA	728
Qy	209	oMetLeuGlyAsnValLeuLeuCysPhePheValPhePheIlePheGlyIleValGl	229
Db	729	GAAGCTTTCTGATGTCATGCTCCTGACTGTGTTCTGTCTGAGTGTGTTGCACATAATTGG	788
Qy	229	yValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe-----LeuProGluAs	246
Db	789	ACTACAGCTGTTCATGGGAAACCTGAAGACATAAATGTTTCGAATAATTCACCTTGAATAATA	848
Qy	246	nPheSerLeuProLeuSerVal-----AspLeuGluArgTyrTyr	259
Db	849	TGAACACTATAGAAAGCATATAGTAATCCCTAGAGAGTGAAGAGACTTTAGAAAATATTT	908
Qy	259	rGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMe	279
Db	909	TTATTACTTGGAGGATCCAAAGATGCTCTCTCTGTTGTTTCAGCACAGATTCAGGTCA	968
Qy	279	tArgSerCysArgSerValProThrLeuArgGlyAspGlyCysGlyProProCysGl	299
Db	969	G-----TGTC	974
Qy	299	yLeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTy	319
Db	975	AGAGGGGTAC-----ACCTGTGTGAATAATGGCAGA--	1005
Qy	319	rTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAs	339
Db	1006	-----AACCTGATTATGGCTACACAGAGCTTTGACAC	1037
Qy	339	nIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIl	359
Db	1038	TTTCAGCTGGGCTTCTTAGCCTTGTGTAGGCTAATGACCAAGATTAATCTGGGAAACCT	1097
Qy	359	eMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIl	379
Db	1098	TTACCAACAGAGCGCTGCGTGTGTCGGCAAAACCTACATGATCTTCTTGTTCGTAGTGAT	1157
Qy	379	eIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSe	399
Db	1158	TTTCTGGGCTCTTTTATCTAATAAACTTGATCTCTGCTGTGTTGTCATGGCATATCA	1217
Qy	399	rGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAs	419
Db	1218	AGAACAGAACCCAGGCAACATTTGAAGAAGCTTAACAGAAAGAAATTAGAATTTCAACAGAT	1277
Qy	419	nAlaSerThrLeuAlaSerPheSerGluProGlySerCys-----	432
Db	1278	GTTAGACCTCTTAAAAAGACAGCAAGAACTGAGGCAATTCAGCGGCGCGGTGA	1337
Qy	433	-TyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaIaArgArgLeuAl	452
Db	1338	ATATACAAGTATTAGGAGAAGCAGAATTATGGCCCTCTCAGAGAGTTCTTCTGAAACATC	1397
Qy	452	aGlnValSer-----ArgAlaAlaGlyValArgValGl	463
Db	1398	CAAACTGAGCTCTTAAAGTGCTAAAGAAAGAAAGAAACAGAGAAAGAAAGAAATCAAAA	1457
Qy	463	yLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProProSerSerSerCysSe	483
Db	1458	GAAGCTCTCCAGCTGGAGAGAGAAAGGAGATGCTGAGAAATTTGTCGAAATTCAGAAATCAGA	1517
Qy	483	rArgSerHisArgLeuSerValHisLeuValHisHisLeuValHisHisHisHisHisH	503
Db	1518	GGACAGCATCAGAGAAAGAAAGTTTCCACCTTGTGTCGAAGGCGCATAGGCGAGCATGA	1577
Qy	503	shistyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAs	523
Db	1578	AAAG-----AGGTGTCTACCCCAATCAGTACCA-----	1608
Qy	523	pArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProAlaLeuSe	543
Db	1609	CTCAGCATTCGTGGCTCC-----TTGTT	1631
Qy	543	rGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLe	563
Db	1632	TTCTGCAAGCGGAGAGCAGACAGCAAGACTCTTTTGTAGTTTC-----	1671
Qy	563	uGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSerGlyArgTh	583
Db	1672	-----AAAGCAGAGAGAGAGA	1688
Qy	583	rValGlySerGlyIlyValTyr-ProThrValHisThrSerProProProGluThrLeuL	603
Db	1689	TATAGGATCTGAGACTGAAATTTGCCGATGATGAGCACA-----	1726
Qy	603	ysGluLysAlaLeuValGluValAlaAlaSerSerGlyPro-----ProThr-	618
Db	1727	-----GCATTTTGGAGACAATGAGACGAGAGGGGCTCACTGTTTGTGCCCCACAG	1778
Qy	619	-----LeuThrSerLeuAsnIleProProGlyProTyrSerSerM	632
Db	1779	ACCCAGAGCGCAGCAGCAGTAACATCAGCCCAAG--CCAGTAGGTCCCCACCAATGC-	1834
Qy	632	etHisLysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSer-----SerCysLysI	650
Db	1835	-----TGCGGTGAACGGGAAATGCACAGTCTGTGGACTGCAACGG	1877
Qy	650	leSerSerProCysLeuLysAlaAspSerGlyAlaCysGlyPro--AspSerCysProT	669
Db	1878	TGTGCTCTCCCTGTTGATGACCTCAGCCCTCATGCTCCCAATGACAGC-----T	1931
Qy	669	yrCysAlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerA	689
Db	1932	TCTGCCAGAGGGCAGC-ACCAATCAAATACACAGAAAGGCGT-----	1974
Qy	689	spSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH	709
Db	1975	-----TGTAGTTCCTATCTCTCTTCAGAGGATATG-----CTGAATGATCCC-	2016
Qy	709	isSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla----	727
Db	2017	-----AACCTCAGACAGAGCAATG-----AGTAGAGCAAGCATATTAAACAAACA	2062
Qy	727	-----	727
Db	2063	CTGTGGAAGAACTTGAAGAGTCCAGACAAAAATGTCACCTTGTGGTGACAGATTGAC	2122
Qy	728	-----PheTrpArgLeuIleCysAsp-----ThrPheArgLys----	738
Db	2123	ACAAATCTTGTATCTGGAAT-----TGCTTCCATATTGGATAAAATTCAAAAAGTGTA	2176
Qy	739	-----IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValA	756
Db	2177	TCTATTTTATTGTAATGATCCCTTTTGTAGATCTTGTGCAATACCATTTGCATAGTTTAA	2236
Qy	756	snThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuG	776
Db	2237	ACACATTATTTATGGCTATGGAAACCCACCCCAATGACTGAGGAAATTCAAAAATGTACTTG	2296

QY 776 lulleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuV 796
Db 2297 CTATAGGAATTTGGCTTTTACTGGAATCTTTCAGCTGAAATGGTATTAAACCTGATTG 2356
QY 796 alTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValV 816
Db 2357 CCATGGATCCATATGAGTATTCCAGTAGGCTGGAAATATTTTTCAGAGCTTATTGTGA 2416
QY 816 alIleSerValTrpGluIleValGlnGlnGlyGlyLeuSerValLeuArgThrP 836
Db 2417 CTTTAAAGTTAGTGGAGCTCTTCTAGCAGATGTGGAAGGATTGTCAGTTCTGCGATCAT 2476
QY 836 heArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuV 856
Db 2477 TCAGACTGCTCCGAGTCTCAAGTTGGCAAAATCCTGGCCCAACATTTGAACATGCTGATTA 2536
QY 856 alValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheI 876
Db 2537 AGATCATTTGGTAACTAGTAGGGCTCTAGGTAACTCCTTAGTTAGTTGGCCATCATCG 2596
QY 876 lePheIlePheSerIleLeuGlyMetHisLeuPheGly- 889
Db 2597 TCTTCAATTTGCTGTGCTCGCATGCGATCTCTTTGGTAAAGAGCTACAAAGAATGTGCT 2656
QY 889 ylsysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 909
Db 2657 GCAAGATC-----AATGGTACACTGTATCGCTCCCA---CGGTGCACATGAACGACT 2704
QY 909 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 929
Db 2705 TCTTCCACTCTCTCCTGATTGTTCCGCTGCTGTGTGGAGAG---TGGATGAGACCA 2761
QY 929 euTyrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuM 948
Db 2762 TGTGGGACTGTATGGAGTGCCTGGTCAAGCTATGTGCCCTTATTGTTTACATGATGTC 2821
QY 948 etThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheG 968
Db 2822 TGTGTCATTGGAAACCTGTGTGCTTAACCTATTCTGCGCTTATTATTGAGCTCATTTA 2881
QY 968 lnaAlaGluIleLeuSerLysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuP 988
Db 2882 GTTCAGACAATCTTACAGCAATTGAA----- 2907
QY 988 roValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPheSerP 1008
Db 2908 -----GAAGACCTGTATGCAAAACCTCCAGATTGCGAGTCAGCTAGAAATATAA 2956
QY 1008 roSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluH 1028
Db 2957 AGGGAATAATATTATGTGAAACAAACCTTACGTGAATTTATTCTAAAGAGCATTTTCCAAA 3016
QY 1028 isProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProm 1048
Db 3017 AGCCAAGATTCCAGGAGATGAGCAACGAGAGATCTGAAATACTTAAGAGGAAAACT 3076
QY 1048 etSerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArg 1068
Db 3077 AT---ATTCTTCAACCATACATTGCTGAATGAGCAAGGTCACAATTTCTCTCAAGGAAA 3133
QY 1068 rgThrSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProSer 1088
Db 3134 AAGATAAAATCACTGGTGGTGGGAGCGAGCGTGGACAAACACTTCATGGAAGAC----- 3186
QY 1088 erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1108
Db 3187 -----A 3187
QY 1108 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 1128
Db 3188 GTGATGGTCAATCATTTATTACAAATCCAGCTCTACAGTGACAGTGCCA----- 3237
QY 1128 rgArgSerLeuLeuSerGlyGluGlnGlnSerGlnAspGluGluSerSerGluG 1148

Db 3238 -----ATTGCACCTGGGAA-----TCCGATTTGGAAAAATATGAATGCTG 3277
QY 1148 luGluArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 1168
Db 3278 AGGAACCTTAGCAGTGATTTCGATAGTAGAATAC----- 3309
QY 1168 laLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlas 1188
Db 3310 -----AGCAAAAGTGGAGT 3322
QY 1188 erGlyArgGlySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 1208
Db 3323 TAAACCGGTCAAGCTCTCTCAGAG-----TGCAGC----- 3351
QY 1208 euAlaArgAlaLeuArgProAspAspProLeuLeuAspGlyAspAspAlaAspAspGluG 1228
Db 3352 -----ACAGTTGATNAACCTTTTCTCGGAGAGGAGAGACAGCAGG 3394
QY 1228 lyAsnLeuSerLysGlyGluArgValArgAlaTrpIleArg-----AlaArgL 1244
Db 3395 CTGAACCTATGAATTCGATGAGCCAGAGGCTGTTTCACAGATGGTTGTGTACGGAGGT 3454
QY 1244 euProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerA 1264
Db 3455 TCTCATGCTGCCAAGTTAATCATAGAGTCAGGGAAGGAAAAAATCTGG-----TCGA 3505
QY 1264 rgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeu 1284
Db 3506 ACATCAGGAAAACTGCTACAGATTGTTGAAACACAGTGGTTTGAAAGCTTCATTGTCC 3565
QY 1284 alIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHis 1304
Db 3566 TCATGATCTCTGCTCAGCAGTGGTCCCTTTTGAAGATATTATTATTTGAAAGGAAAA 3625
QY 1304 erAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaG 1324
Db 3626 AGACCATTAAAGATTATCTCGAGTATGCGACACAAGATCTTCACTTACATCTTCACTTGG 3685
QY 1324 luMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaThrLeuArgS 1344
Db 3686 AATGTCTCTAAATGGATAGCA-----TATGGTTATATAAACATATTTTCACCA 3733
QY 1344 erSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValS 1364
Db 3734 ATGCTGTGCTTGGCTGGATTTCTTAATTGTTGATGTTCTTCTTGGTTACTTTTAGTGCAA 3793
QY 1364 erMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuA 1384
Db 3794 ACACCTCT-----GGCTACTCAGATCTTGGCCCCCATTAATCCCTTCGACACACTGA 3844
QY 1384 rgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluT 1404
Db 3845 GAGCTTTAAGACCTCTAAGAGCCTTATCTAGATTTGAAGGAATGAGGTCGTTGTGTAATG 3904
QY 1404 hrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheI 1424
Db 3905 CACTCATAGGAGCAATTCCTTCCATCATGAATGTGCTACTTGTGTCTTATTATTCTGGC 3964
QY 1424 leIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCys----- 1441
Db 3965 TGATATTTCAGCATCATGGGAGTAAATTTGTTCTGCGCAAGTTCTATGAGTATTAAACA 4024
QY 1442 -----GlnGlu-----AspThrArgAsnIleThrAsnLysSerAspCys----- 1455
Db 4025 CCACAGATGGTCACCGTTTCTGCAAGTCAAGTCCAAATCGTTCCGAATGTTTTCGCC 4084
QY 1456 -----AlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuG 1473
Db 4085 TTATGAATCTTAGTCAAAATGTCGATGGAAAAACCTGAAACGTAACCTTTGATTAATCTCG 4144
QY 1473 lyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMet 1493

Db 4145 GACTTGGTTACCTATCTCTGCTTCAAGTTGCAACTTTTAAAGGATGGACGATTATTATGT 4204
Qy 1493 YrAspGlyLeuAspAlaValGlyValAspGlnProIleMetAsnHisAsnProTrpM 1513
Db 4205 ATGCACAGTGGATTCTGTAAATGTATAGCAAGCAGCCCAAAATATGATATAGCTCTACA 4264
Qy 1513 etLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheV 1533
Db 4265 TGTATATTATTGTCGCTTTATCATCTTTGGGTCATTCTTCACTTTGAACCTTGTTCA 4324
Qy 1533 alGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAla 1553
Db 4325 TTGGTGTGCATAGATAATTTCAACCAACAGAAAGAGCTTGGAGGTCAAGACATCT 4384
Qy 1553 rgArgArgGluGlu-----LysArgLeuArgArgLeuGluLysLysArgArgLysAlaG 1571
Db 4385 TTATGACAGAGAAGACAGAAATATATATGCAATGAATGAATAAGCTGGGTCCAGAACG 4444
Qy 1571 lncysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCyst 1591
Db 4445 CACAAAAGCCAAATTCCTCGACCGGGAACAAATCCAAGGATGTATATTGACCTAGTGA 4504
Qy 1591 hrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetA 1611
Db 4505 CAATCAAGCCTTTGATATTAGTATCATGTTCTTATCTGTCTCAACATGTTAACCATGA 4564
Qy 1611 laMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrI 1631
Db 4565 TGGTAGAAAGGAGGGTCAAGTCAACATATGACTGAAGTTTTATATTGGATAAATGTGG 4624
Qy 1631 lePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgA 1651
Db 4625 TTTTATATATCTTTTCTACTCGAGAACTGTGCTAAACTGATCTCCCTCAGA---CACT 4681
Qy 1651 rgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG 1671
Db 4682 ACTACTTCACTGAGTAGGAATATTTTGTATTTTGTGTTGTGATTATCTCCATTGTAG 4741
Qy 1671 lyleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleA 1691
Db 4742 GTATGTTTCTAGCTGAATTG-----ATTGAACGTATTTGTGTCCCTTACCTGTTCC 4795
Qy 1691 rgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyM 1711
Db 4796 GAGTATCGGCTTCCAGGATTGCGCAATCCTACGCTAGTCAAGAGGCAAGGGGA 4855
Qy 1711 etArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuL 1731
Db 4856 TCCGCACGCTGCTCTTGTGTTGATGATGCTCCCTTCTGCGTGTGTTAAACATCGCGCTCC 4915
Qy 1731 euPheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuG 1751
Db 4916 TGCTCTTCTGCTGATGTTCACTACGCCATCTTTGGAAATGTCACACTTGGCTATGTA 4975
Qy 1751 lncysAspGluThrHisProCysGlyGlyLeuGlyArgHisAlaThrPheArgAsnPheG 1771
Db 4976 AAAAGAA-----GATGGAATTAATGACATGTTCAATTTTGAGACCTTGTG 5020
Qy 1771 lyleMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetL 1791
Db 5021 GCAACAGATGATGTTGCTGTTTCCAAATTTACAACTCTGCTGCTGGGATGATGCTAG 5080
Qy 1791 ysAspThrLeuArg-----AspCysAspGln----- 1799
Db 5081 CACTTATCTTAACAGTAAGCACCAGCTGTGACCCCAAAAGTTTCATCTCGGAAGTT 5140
Qy 1800 -----GluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheVal 1818
Db 5141 CAGTTGAAGGAGACTGTTGGTAACCCATCTGTTGGAATATTCTACTTTGTTAGTTATATCA 5200
Qy 1818 eutThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluG 1838
Db 5201 TCATATCTCTCTGTTGTTGGTGAACATGTACATTCAGTCATCTGAGAAATTTTAGTG 5260

Qy 1838 luSerAsnLysGluAlaLysGluGlu---AlaGluLeuGluAlaGluLeuGluLeuGluM 1857
Db 5261 TTGCCACTGAAGAAAGTACTGAACTCTGAGTGAGGAGTACTTTGAGATGTTCTTATGAG- 5319
Qy 1857 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyV 1877
Db 5320 -----GTTTGGGAGAAGT 5332
Qy 1877 alGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisA 1897
Db 5333 TTGAT---CCCGATGCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCTG 5389
Qy 1897 laArgSerAlaSerHisPheSerLeuGluHisProThrMet-----GlnProHisProT 1915
Db 5390 CC-----CTGGATCTCTCTCTCATAGCAAAACCCCAACAAAG 5428
Qy 1915 hrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHis 1935
Db 5429 TCCAGCTCATGTCATGAGTCTGCCATGTT-----AGTGGT---GACCGGATCCATT 5479
Qy 1935 erLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyH 1955
Db 5480 GTCTT-----GACATCTTATTT-----GCTTTTACAAAGCGTGTTTTGGGT- 5520
Qy 1955 isArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnP 1975
Db 5521 -----GAGAGTGGGAGATGGATCTCTTCGTTCCACAGA 5554
Qy 1975 roAlaAspThr-SerTyrIleLeuGlnLeuLeuProLysAspAlaProHisLeuLeuGlnPro 1994
Db 5555 TGGAAAGAAAGTTCTGTCGCAAACTCTTCCAAAGTGTCTATGAACCCCATCAACCA 5614
Qy 1995 His 1995
Db 5615 CAC 5617
RESULT 9
US-11-251-465-8
; Sequence 8, Application US/11251465
; Publication No. US20060094061A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter
; APPLICANT: Klaassen, Hubertus
; TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
; TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
; TITLE OF INVENTION: Inflammatory Diseases
; FILE REFERENCE: P30,172-A USA
; CURRENT APPLICATION NUMBER: US/11/251,465
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,384
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 6371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-251-465-8
Alignment Scores:
Pred. No.: 1,41e-62 Length: 6371
Score: 1595.50 Matches: 540
Percent Similarity: 43.2% Conservative: 378
Best Local Similarity: 25.4% Mismatches: 786
Query Match: 13.4% Indels: 421
DB: 72
US-09-611-257A-37 (1-2266) x US-11-251-465-8 (1-6371)
Qy 2 AspGluGluAspGlyAlaGlyAlaGlu---GluSerGlyGlnProArgSerPheMet 20

QY	689	spSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH	709	roSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluH	1028	
Db	2023	-----TGTAGTTCTCTATCTCTTCAGAGGATATG-----CTGAATGATCCC-	2064	3005	ACGGATAAATATATGTGAACAAACCTTAGTGGAATTTATTCTAAAGCAATTTCCAAA	3064
QY	709	isSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla	727	1028	isProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProM	1048
Db	2065	--AACCTCAGACAGAGCAATG-----AGTAGAGCAAGCATATTAAACAACA	2110	3065	AGCCAAGATTTCCAGGAGATAGAACAAGCAAGATCTGAATACTTAAGAGGAAAACT	3124
QY	727	-----	727	1048	etSerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArg	1068
Db	2111	CTGTGGAAGAACTTGAAGAGTCACAGACAAAAATGTCACCTTGGTGTACAGATTTCAC	2170	3125	AT---ATTTCTAACCATACACTTCTGCTGAATGAGCAAAAGGTCAAAATTTCTCAAGGAAA	3181
QY	728	-----PheTrpArgLeuIleCysAsp-----ThrPheArgLys-----	738	1068	rgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProS	1088
Db	2171	ACAAATCTTCATCTGGAAT-----TGCTCTCCATATTGGATAAAATTCAAAAGTGTA	2224	3182	AAGATAAATCAGTGGTTTTGGAGAGCAGCTGACAAACACTTTCATGGAAGAC	3234
QY	739	-----IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuVal	756	1088	erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS	1108
Db	2225	TCTATTTTATGTAATGAGTCCCTTTGTAGATCTTGCATTTACCATTTGCATAGTTTAA	2284	3235	-----	3235
QY	756	snThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuG	776	1108	erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA	1128
Db	2285	ACATATTATTATGGCTATGGAACACCAACCAATGACTGAGGAATTCAAAATGCTACTTG	2344	3236	GTGATGTCAATCATTTATTTCACAAATCCAGCCTCACAGTCACAGTCCCA	3285
QY	776	luIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuV	796	1128	rgArgSerLeuLeuSerGlyGlyGlnGlnSerGlnAspGluGluGluSerSerGluG	1148
Db	2345	CTATAGGAATTTGGTCTTACTGGAATCTTTGCAGCTGAAATGGTATTAAACCTGATTG	2404	3286	-----ATTGCACCTGGGAA-----TCCGATTTGGAAAAATATGAATCGTG	3325
QY	796	alTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal	816	1148	luGluArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA	1168
Db	2405	CCATGGATCCATATGATATTTCCAAGTAGGCTGGAATATTTTGACAGCCTTATTGTGA	2464	3326	AGGAACCTAGCAGTATTCGGATAGTCAATAC-----	3357
QY	816	alIleSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrP	836	1168	laLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaA	1188
Db	2465	CTTTAAGTTTATGAGAGCTCTTTCTAGCAGATGTGGAAGGATTTGACGTTCTGCATCAT	2524	3358	-----	3370
QY	836	heArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuV	856	1188	erGlyArgGlySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL	1208
Db	2525	TCAGACTGCTCGAGTCTTCAAGTTGGCAAAATCTGGCCCAACATTTGAACATGCTGATTA	2584	3371	TAAACCGGTCAAGCTCTCTCAGAG-----TCAGC-----	3399
QY	856	alValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheI	876	1208	euAlaArgAlaLeuArgProAspAspProProLeuAspGlyAspAlaAspAspGluG	1228
Db	2585	AGATCATTTGGTAACCTAGTAGGGGCTCTAGGTAACTCACCTTAGTGTGGCCCATCATCG	2644	3400	-----ACAGTTGATAACCTTTTGCCTGGAGAGAGAGAGACAGAGG	3442
QY	876	lePheIlePheSerIleLeuGlyMetHisLeuPheGly-----	889	1228	lyAsnLeuSerLysGlyGluArgValArgAlaTrpIleArg-----AlaArgL	1244
Db	2645	TCTTCATTTTGTCTGTGTGGCATGCGAGCTCTTTGGTAAGAGCTACAAAGAAATGTGTCT	2704	1244	euProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProGlnSerA	1264
QY	889	ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	909	1264	rgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuV	1284
Db	2705	GCAAGATC-----AATGATGACTGTAGCTCCCA---CGGTGGCAGCATGAACGACT	2752	3554	ACATCAGGAAAAACCTGCTACAAGATTTGTTGAACACAGATTGGTTTGAAGACTTTCATTGTCC	3613
QY	909	euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL	929	1284	alIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisS	1304
Db	2753	TCTTCCACTCCTCCTGATTTGTGTTCCGCGTCTGTGTGGAGAG---TGGATAGAGACCA	2809	3614	TCATGATCCTGCTCAGCAGTGTGTGCCCTGGCTTTTGAAGATATTTATTTGAAGAGAAA	3673
QY	929	euTyrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuM	948	1304	erAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaG	1324
Db	2810	TGTGGAGCTGTATGAGGTCGTGCTCAAGCTATGTGGCTTATGTTTACATGATGTCGA	2869	3674	AGACCATTAAGATTAATCTCTGGAGTATGACAGACAGATCTTCACTTACATCTTTCATCTCG	3733
QY	948	erThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheG	968	1324	luMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgS	1344
Db	2870	TGTCATTGGAAACCTGGTGGTCTTAAACCTATTCTGGCCCTTATTATTAGCTCATTTTA	2929	3734	AAATGCTCTTAAATGGATAGCA-----TATGTTTATAAAACATATTTCAACCA	3781
QY	968	lnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuP	988	1344	erSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValS	1364
Db	2930	GTTTCAGACAATCTTACAGCAATTTGA-----	2955	3782	ATGCGCTGGTGTGGCTGGATTTCCCTAAATGTGTGATTTCTTTTGGTTACTTAGTGCGAA	3841
QY	988	roValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhePheSerP	1008	1364	erMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuA	1384
Db	2956	-----GAAGACCCCTGATGCAACAAACCTCCAGATTGCAGTACTAGATTAATAAA	3004			

Db 3842 ACACCTCTT-----GGCTACTCAGATCTTGGCCCATTAATCCCTTCGGACACTGA 3892
Qy 1384 rgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValGluT 1404
Db 3893 GAGCTTTAAGACCTCTAAGACCTTAICTAGATTGAAGNATGAGGGTCGTGTGAATG 3952
Qy 1404 hrLeuMetSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPheI 1424
Db 3953 CACTCATAGGACCAATTCCTTCCATCATGAATGTGCTACTTGTGTCTTATATTCTGGC 4012
Qy 1424 leIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCys----- 1441
Db 4013 TGATATTACCATCATGGAGTAATTTGTTTGTCTGCAAGTCTTATGAGGTGTTAACA 4072
Qy 1442 -----GlnGlyGlu-----AspThrArgAsnIleThrAsnLysSerAspCys----- 1455
Db 4073 CCACAGATGGTGCACGGTTTCCTGCAAGTCAAGTTCCAATCGTTCGAATGTTTCCCC 4132
Qy 1456 -----AlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuG 1473
Db 4133 TTATGAATGTAGTCAAAATGTGCGATGGAAGAACCTGAAAGTGAACCTTTGATAATGCG 4192
Qy 1473 lyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMet 1493
Db 4193 GACTTGGTTACCTATCTCTGCTTCAAGTTCGACTTTTAAGGGATGGACGATTATTATGT 4252
Qy 1493 yrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpM 1513
Db 4253 ATGCAGCAGTGGATTCTGTTAATGTAGCAAGCAGCCCAATATGAATATAGCTCTACA 4312
Qy 1513 etLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPheValLeuAsnMetPheV 1533
Db 4313 TGTATATTTATTTGTCGCTTTATCATCTTTGGGTCACTTTCACCTTGAACCTTGTTC 4372
Qy 1533 alGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluAla 1553
Db 4373 TTGGTGTCATCATAGATAATTTCAACCAAGAAAGAGAGCTTGGAGGTCAAGACATCT 4432
Qy 1553 xArgArgGluGlu-----LysArgLeuArgArgLeuGluLysLysArgArgLysAlaG 1571
Db 4433 TTATGACAGAAAGAACAGAAATACTATAATGCAATGAAAGAAAGCTGGGTCCAAGAGC 4492
Qy 1571 lnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisIleLeuCys 1591
Db 4493 CACAAAAGCCAATTCCTCGACCAAGGGAACAAATCCAAGGATGTATATTGACCTAGTGA 4552
Qy 1591 hrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValThrMetA 1611
Db 4553 CAATCAAGCCTTTGATATATTAGTATCATGCTTCTTATCTCTCAACATGCTGAACCATGA 4612
Qy 1611 laMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrI 1631
Db 4613 TGTAGAAAAGGAGGTCAAGTCAACATATGACTGAAGTTTATATTGATGAATATGTTGG 4672
Qy 1631 lePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArg 1651
Db 4673 TTTTATATCCTTTTCACTGGAGATGTGTGCTAAAACCTGATCTCCCTCAGA--CACT 4729
Qy 1651 rgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG 1671
Db 4730 ACTACTTCACTAGTAGTGAATATTTTGTGTTTGTGGTGTGATTTATCTCCATTTGTAG 4789
Qy 1671 lyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleA 1691
Db 4790 GTATGTTCTAGCTGATTG-----ATTGAAACGATATTTTGTGTCCTCCCTTACCCTGTCC 4843
Qy 1691 rgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyM 1711
Db 4844 GAGTGATCCGCTTTCGACGAGATTGGCCGATCTACGCTAGTCAAGAGGAGCAAGGGGA 4903
Qy 1711 etArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuL 1731

Db 4904 TCCGCACGCTGCTCTTTTGTCTTGTATGATGTCCTCTCTCGGTGTGTTTAAACATCGCCCTCC 4963
Qy 1731 euPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG 1751
Db 4964 TGCTCTTCCCTGGTCATGCTTTCATACGCCATCTTTTGAATGTCCAACCTTTCCCTATGTTA 5023
Qy 1751 luCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG 1771
Db 5024 AAAAGGAA-----GATGGAATTAATGACATGTTCAATTTTTCGAGACCTTTG 5068
Qy 1771 lyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetL 1791
Db 5069 GCAACAGTATGATTGCTTCCAAATTAACACCTCTGCTGGCTGGATGATTTGCTAG 5128
Qy 1791 ysAspThrLeuArg-----AspCysAspGln----- 1799
Db 5129 CACTATTCTTAACAGTAAGCCACCCGACTGTGACCCAAAAAAGTTTCATCTCGAAGATT 5188
Qy 1800 -----GluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValL 1818
Db 5189 CAGTTGAAGGAGACTGTGGTAACCCATCTGTGGAAATATTCTACTTTTGTAGTTATATCA 5248
Qy 1818 euThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluG 1838
Db 5249 TCATATCTCTCTCTGCTGTGGTGAACATGTACATTGCAGTCATACCTCGAGAAATTTTAGT 5308
Qy 1838 luSerAsnLysGluAlaLysGluGlu---AlaGluLeuGluAlaGluLeuGluLeuGluM 1857
Db 5309 TTCCCACTGAAGAAAGTACTGAACCTCTGAGTGAGGATGACTTTTGAGATGTTCTATGAG- 5367
Qy 1857 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1877
Db 5368 -----GTTTGGGAGAAGT 5380
Qy 1877 alGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisA 1897
Db 5381 TTGAT---CCCGATGCGACCCAGCTTTATAGAGTTCTCTAAACCTCTCTGATTTTGCACGTG 5437
Qy 1897 laArgSerAlaSerHisPheSerLeuGluHisProThrMet-----GlnProHisProT 1915
Db 5438 CC-----CTGGATCTCTCTCTCTCATAGCAAAACCCAAACAAG 5476
Qy 1915 hrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThrHis 1935
Db 5477 TCCAGCTCATGTCATGATCTGCCATGCTT-----AGTGGT---GACCGGATCCATT 5527
Qy 1935 erLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyH 1955
Db 5528 GTCTT-----GACATCTTATTT-----GCTTTTACAAGCGTGTTTTGGGT- 5568
Qy 1955 isArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnP 1975
Db 5569 -----GAGATGGGAGATGGATTCTCTCTGTTCCACAGA 5602
Qy 1975 roAlaAspThr-SerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro 1994
Db 5603 TGGAAAGAAAGTTTCATGCTCTGCAAACTCTTCCAAAGTGTCTTGAACCCATCACAACCA 5662
Qy 1995 His 1995
Db 5663 CAC 5665

RESULT 10
US-11-266-748A-56579
; Sequence 56579, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A			CURRENT FILING DATE: 2005-11-03		
PRIOR APPLICATION NUMBER: EP 04105479.2			PRIOR FILING DATE: 2004-11-03		
PRIOR APPLICATION NUMBER: EP 04105482.6			PRIOR FILING DATE: 2004-11-03		
PRIOR APPLICATION NUMBER: EP 04105483.4			PRIOR FILING DATE: 2004-11-03		
PRIOR APPLICATION NUMBER: EP 04105507.0			PRIOR FILING DATE: 2004-11-03		
PRIOR APPLICATION NUMBER: EP 04105485.9			PRIOR FILING DATE: 2004-11-03		
PRIOR APPLICATION NUMBER: EP 04105484.2			PRIOR FILING DATE: 2004-11-03		
PRIOR APPLICATION NUMBER: US 60/662,276			PRIOR FILING DATE: 2005-03-14		
PRIOR APPLICATION NUMBER: US 60/700,293			PRIOR FILING DATE: 2005-07-18		
NUMBER OF SEQ ID NOS: 48396			SOFTWARE: PatentIn version 3.3		
SEQ ID NO 56579			LENGTH: 6371		
TYPE: DNA			ORGANISM: Homo Sapiens		
US-11-266-748A-56579					
Alignment Scores:					
Pred. No.:	1,41e-62	Length: 6371			
Score:	1595.50	Matches: 540			
Percent Similarity:	43.2%	Conservative: 378			
Best Local Similarity:	25.4%	Mismatches: 786			
Query Match:	13.4%	Indels: 421			
DB:	8	Gaps: 72			
US-09-611-257A-37 (1-2266) x US-11-266-748A-56579 (1-6371)					
Qy	2	AspGluGluGluAspGlyAlaGlyAlaGlu---	GluSerGlyGlnProArgSerPheMet	20	
Db	175	GATGAAGAAGCCCAAGCAGTGTGGAGGTGGCAACCAACTGCCCTTCATC	234		
Qy	21	ArgLeuAenAspLeuSerGlyAlaGlyArgProGlyProGlySer-----	36		
Db	235	---TATGGGACAT--TCCTCCGGCATGTGTCTAGAGCCCTGGAGGACTTGGACCCCTA	290		
Qy	37	-----AlaGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrPro	54		
Db	291	CTATGCAGACAAAGACTTTCATAGTATTGAACAAAGGAAACAATCTTCGGTTCAA	350		
Qy	55	AlaLeuAlaProValPhePheTyr--LeuSerGlnAspSerArgProArgSerTrpCy	74		
Db	351	-----TGCCACACCTGCTTATATATATGCTTCTCTCTCAGTCTCTAAGAAGAATATC	404		
Qy	74	sLeuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAs	94		
Db	405	TATTAAAGATTTTAGACATCTCTTATTCAGCATGCTCATCTGTCGATTTCTGACAAA	464		
Qy	94	nCysValThrLeuGlyMetPheArgPro-----CysGluAspIleAlaCysAspSe	111		
Db	465	CTGCATATTTAGACCATGAATAACCGCGGACGTGGACCAAAATGTC-----	513		
Qy	111	rGlnArgCysArgIleLeuGlnAlaPheAspPheIlePhe-----AlaPheAlaVa	130		
Db	514	-----GAGTACACTTTTACTGGAATATATATCTT	542		
Qy	130	lGluMetValValLysMetValAlaLeuGlyIle---PheGlyLysLysCysTyrLeuGl	149		
Db	543	TGAATCAGTGTGAATAATCCTTGCAAGAGGCTTCTGTGTAGGAGAAATTCACCTTCTTCG	602		
Qy	149	yAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLe	169		
Db	603	TGACCCGTGGAACCTGGCTGGATTTTGTGTCATTTGTTTGGCTATTTAACAGAAATTTGT	662		
Qy	169	uAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuAr	189		
Db	663	AAACCTAGGCAATGTT-----TCAGCTCTCGAACTTTTCAGAGTATTGAGAGCTTGAA	716		
Qy	189	gaIalleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuPr	209		
Db	717	AACTATTTCTGTAATCCAGGCTGAAGACAATTTGATGGGCTTTGATCCAGTCAGTGAA	776		
Qy	209	oMetLeuGlyAsnValLeuLeuLeuCysPheValPheIlePheGlyIleValGl	229		
Db	777	GAAGCTTTCTGATGTCATGATCTGACTGTGTTCTCTCTGAGTGTGTTTCCACTAATGG	836		
Qy	229	yValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe-----LeuProGluAs	246		
Db	837	ACTACAGCTGTTTCATCGGAAACCTGAAGCATAAATGTTTCGAAATTCACCTGAAATAA	896		
Qy	246	nPheSerLeuProLeuSerVal-----AspLeuGluArgTyrTy	259		
Db	897	TGAACATTAGAAAGCATAAATGAATACCCCTAGAGAGTGAAGAAGACTTTTAGAAAAATTT	956		
Qy	259	rGlnThrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMe	279		
Db	957	TTATTACTTGGAAAGGATCCAAAGATGCTCTCCCTTTGTGGTTTCAGACACATTCAGTCA	1016		
Qy	279	tArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProCysGl	299		
Db	1017	G-----	1022		
Qy	299	yLeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTy	319		
Db	1023	AGAGGGGTAC-----ACCTGTGTGAAATTTGGCAGA--	1053		
Qy	319	rTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAs	339		
Db	1054	-----ALCCCTGATTATGGCTTACAGGACTTTTGACAC	1085		
Qy	339	nIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIl	359		
Db	1086	TTTCAGCTGGGCTTCTTAGCTTATAGCTAATACCCCAAGATTTACTGGGAAACCT	1145		
Qy	359	eMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIl	379		
Db	1146	TTACCAACAGACGCTGCTGCTGTCGCAAAACCTACATGATCTTCTTTGTCGTAGTAT	1205		
Qy	379	eIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSe	399		
Db	1206	TTTCTGGGCTCTTTTATCTAATAAATTTGATCTGCTGTGTTGCCATGGCATATGA	1265		
Qy	399	rGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAs	419		
Db	1266	AGACAGAACCCAGGCACAAACATTGAAGAGCTAAACAGAAAGAATTTAGAATTTCAACAGAT	1325		
Qy	419	nAlaSerThrLeuAlaSerPheSerGluProGlySerCys-----	432		
Db	1326	GTTAGACCTCTTAAAAAAGAGACAGAAAGAGCTGAGGCAATTCGAGCGGACGGCTGA	1385		
Qy	433	-TyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaIaArgLeuAl	452		
Db	1386	ATATACAAGTATTAGGAGAAGCAGAAATTTATGGGCTCTTCAGAGAGTTCTTCTGAAACATC	1445		
Qy	452	agLlnValSer-----ArgAlaAlaGlyValArgValGl	463		
Db	1446	CMAACTGAGCTCTAAAGTCTTAAGAAAGAAAGAAAGAAAGAAAGAAATCAAAA	1505		
Qy	463	yLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnThrGlnProSerSerSerCysSe	483		
Db	1506	GAAGCTCTCCAGTGGAGGAGAAAGGGAGATCTCGAGAAATTTGCGAAATCAGAAATCAGA	1565		
Qy	483	rArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisH	503		
Db	1566	GGACAGCATCAGAAAGAAAGTTTCCACCTTGGTGTGAGGCGCATAGCGGAGCACATGA	1625		
Qy	503	shisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAs	523		

Db 1626 AAG-----AGTTGTCTACCCCAATCAGTCACCA-----1656
Qy 523 pArgAspAlaasnGlySerArgArgLeuMetLeuProProSerThrProAlaLeuSe 543
Db 1657 -CTCAGCATTCGTGGCTCC-----TTGTT 1679
Qy 543 rGlyAlaProGlyGlyAlaGluSerValHisSerPheTyHisAlaaspCysHisLe 563
Db 1680 TTCTGCAAGCGAAGCAGCAGACAAGCTCTTTTAGTTTC-----1719
Qy 563 uGluProValArgCysGlnAlaProProArgSerProSerGluAlaSerGlyArgTh 583
Db 1720 -----AAAGCAGAGGAAGAGA 1736
Qy 583 rValGlySerGlyLysValTyr-ProThrValHisThrSerProProGluThrLeuL 603
Db 1737 TATAGGATCTGAGACTGAATTTGCGGATGATGACACA-----1774
Qy 603 yGluLysAlaLeuValGluValAlaAlaSerSerGlyPro-----ProThr- 618
Db 1775 -----GCATTTTGGAGACAATGAGCAGAGAAGGGGCTCACTGTTTGTGCCCCACAG 1826
Qy 619 -----LeuThrSerLeuAsnIleProProGlyProTyr-SerSerm 632
Db 1827 ACCCAGGAGCAGCAGCAGTACATCAGCCCAAG-----CCAGTAGGTCCCCCAATGC- 1882
Qy 632 eThiLysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSer-----SerCysLysI 650
Db 1883 -----TGCCGGTGAACGGGAAATGCACAGTCTGTGACTGCAACGG 1925
Qy 650 leSerSerProCysLeuLysAlaAspSerGlyAlaCysGlyPro-----AspSerCysPro 669
Db 1926 TGTGGTCTCCCTGGTTGATGGAGCCTCAGCCCTCATGCTCCCAATGGACAGC-----T 1979
Qy 669 yrcysAlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSera 689
Db 1980 TGTCCNAGGGCAGC-ACCAATCAATAACACAGAAAGCGT-----2022
Qy 689 spSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH 709
Db 2023 -----TGTAGTCTCTATCTCTTTCAGAGGATATG-----CTGAATGATCCC- 2064
Qy 709 isSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla- 727
Db 2065 --AACCTTCAGACAGAGCAATG-----AGTAGAGCAAGCATATTAAACAACA 2110
Qy 727 -----2177
Db 2111 CTGTGGAGAACTTGAAGAGTCCAGACAAATAATGTCCACCTTGTGGTACAGATTTGGCAC 2170
Qy 728 -----PheTyrArgLeuIleCysAsp-----ThrPheArgLys- 738
Db 2171 ACAAAATCTTGATCTGGAAT-----TGCTCTCCATATTGGATAAAATTCAAAAGTGTA 2224
Qy 739 -----IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuVala 756
Db 2225 TCTATTATTATGTAATGATCCTTTGTAGATCTTGCATTTGCAATTACCATTTGCATAGTTTAA 2284
Qy 756 snThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuG 776
Db 2285 ACACATTTATTATGGCTATGGAACACACCCCAATGACTGAGGAATTCAAAATTTGATCTTG 2344
Qy 776 luileSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuV 796
Db 2345 CTATAGGAATTTGGCTTTTACTGGAAATCTTTGAGCTGGAATTTGGTATTAAATCTGATTG 2404
Qy 796 alTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal 816
Db 2405 CCATGGATCCATATAGTATTTCACAGTAGGCTGGAATATTTTTCAGAGCTTTATTGTGA 2464
Qy 816 alIleSerValTyrGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrP 836
Db 2465 CTTTAAAGTTTAGTGGAGCTCTTTCTAGCAGATGTGGAAGGATTTGTCAGTTTCTCGCATCAT 2524

Qy 836 heArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgInLeuV 856
Db 2525 TCAGACTGCTCCGAGTCTTCAAGTTGGCAAAATCCTGGCCCAACATTGAACATGCTGATTA 2584
Qy 856 alValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheI 876
Db 2585 AGATCATTTGTGTAACCTAGTAGGGGCTCTAGGTAACTCCTCAGCTTGTGTCCTCATCG 2644
Qy 876 lePheIlePheSerIleLeuGlyMetHisLeuPheGly-----C 889
Db 2645 TCTTCATTTTGTGTGGTCTGGCATGCAGCTCTTTGGTAAGACGCTACAAAGAATGTGCT 2704
Qy 889 yLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 909
Db 2705 GCAAGATC-----AATGATGACTGTACGCTCCCA---CGGTGGCAGACATGAACGACT 2752
Qy 909 euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL 929
Db 2753 TCTTCCACTCTCTCTGATTTGTTCGCGTGTGTGTGGAGAG---TGGATAGAGACCA 2809
Qy 929 euTyrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeu 948
Db 2810 TGTGGACTGTATGGAGTCTGCTCAAGCTATGTCCCTTATTGTTTACATGATGGTCA 2869
Qy 948 etThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheG 968
Db 2870 TGTTCATTTGAAACCTGCTGCTTAAACCTATTCTGGCCTTATTATTAGCTCATTTA 2929
Qy 968 lnAlaGluIleLysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuP 988
Db 2930 GTTCAGACATCTTACAGCAATTGAA-----2955
Qy 988 roValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhePheSerP 1008
Db 2956 -----GAAGACCTGTATGCAAAACCTTACGTCGATTTATTCTAAAAGCATTTTCCAAAA 3004
Qy 1008 roSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyLuh 1028
Db 3005 AGGGAATAAATATGTAACAAACCTTACGTCGATTTATTCTAAAAGCATTTTCCAAAA 3064
Qy 1028 isProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProM 1048
Db 3065 AGCCAAAGATTTTCCAGGGAGATAAGACAAGCAGAGAATCTGTAATCTAAGAAGGAAAACT 3124
Qy 1048 etSerLeuProLysSerThrSerThrGlyLeuGluAlaLeuGlyProAlaSerArgA 1068
Db 3125 AT---ATTTCTAACCATACCTTGTGAAATGACAAAGGTCACAATTTCTCAAGGAAA 3181
Qy 1068 rgThrSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProS 1088
Db 3182 AAGATAAATCAGTGGTTTTGGAAGCAGCGTGGCAAAACACTTCATGGAAGAC-----3234
Qy 1088 erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1108
Db 3235 -----A 3235
Qy 1108 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 1128
Db 3236 GTGATGGTCAATCATTTATTCACAATCCCACTCCAGCTCAGGTGACAGTGGCCA-----3285
Qy 1128 rgArgSerLeuSerGlyGlyGlnGlnSerGlnAspGluGluGluSerSerGluG 1148
Db 3286 -----ATTGACCTGGGAA-----TCCGATTTGGAAAAATATGATGCTG 3325
Qy 1148 luGluArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 1168
Db 3326 AGGAACCTTAGCAGTATTCGGATAGTGAATAC-----3357
Qy 1168 lalysSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlas 1188
Db 3358 -----AGCAAAAGTGAGAT 3370


```
QY 1188 erGlyArgGlySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 1208
Db 3371 TAAACCGGTCAAGCTCTCAGAG-----TGCAGC----- 3399
QY 1208 euAlaArgAlaLeuArgProAspAspProLeuLeuAspGlyAspAlaAspGluG 1228
Db 3400 -----ACAGTTGATAACCCCTTTGCTCGAGAGGAGGAAGACGAGG 3442
QY 1228 lyAsnLeuSerLysGlyGluArgValArgAlaTrpIleArg-----AlaArgL 1244
Db 3443 CTGAACCTATGAATTCGATGAGCCAGAGCGCTGTTTCACAGATGGTTGTGTACGGAGGT 3502
QY 1244 euProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProGlnSerA 1264
Db 3503 TCTCATGCTGCCAAGTTAAACATAGATGATCGAGGAAAGGAAAAATCTGG-----TGG 3553
QY 1264 rgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuV 1284
Db 3554 ACATCAGGAAAACTGCTACAAGATTGTTGAACACAGTTGGTTTGAAGACTTCATTGTGCC 3613
QY 1284 alIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHis 1304
Db 3614 TCATGATCCCTGCTCAGCAGTGGTCCCTGGCTTTTGAAGATATTATATTGAAGGAAAA 3673
QY 1304 erAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaG 1324
Db 3674 AGACCAATTAAGATTATCTCGAGTATGCAGACAAGATCTTCACATTACATCTTCATTCTGG 3733
QY 1324 luMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgS 1344
Db 3734 AAATGCTTCTAAAATGATGAC-----TATGGTTATAAAACATATTTTCACCA 3781
QY 1344 erSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuVals 1364
Db 3782 ATGCTGTGTGGCTGATTCCTAATGTTGATGTTCTTGTGTTACTTTAGTGGCAA 3841
QY 1364 erMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuLeuA 1384
Db 3842 ACACCTCTT-----GGCTACTCAGATCTTGGCCCAATTAATCCCTTCGGACACTGA 3892
QY 1384 rgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysValValGluT 1404
Db 3893 GAGCTTTAAGACCTCTAAGACCTTATCTAGATTTGAAGGAATGAGGGTCGTTGTGAATG 3952
QY 1404 hrLeuMetSerSextLeuLysProIleGlyAsnIleValIleCysCysAlaPheI 1424
Db 3953 CACTCATGAGGCAATTCCTCCATCATGAATGCTACTTGTGTCTTATATTCTTGGC 4012
QY 1424 leIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCys----- 1441
Db 4013 TGATATTCAGCATCATGGAGTAATAATTTGTTTGGTGGCAAGTTCTATGAGTGTATTAACA 4072
QY 1442 -----GlnGlyGlu-----AspThrArgAsnIleThrAsnLysSerAspCys----- 1455
Db 4073 CCACAGATGGGFCACGGTTTCTCGCAAGTCAAGTTCCAAATCGTTCCGAAGTTTGGCC 4132
QY 1456 -----AlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuG 1473
Db 4133 TTATGAATGTAGTCAAAATGTCGATGCGAATGGAACCTGAAAGTGAACITTGATAATGCG 4192
QY 1473 lyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetT 1493
Db 4193 GACTTGGTTACCTATCTCTGCTCAAGTTGCAACTTTTAAAGGGATGGACGATTATTATGT 4252
QY 1493 yrAspGlyLeuAspAlaValGlyValAspGlnProIleMetAsnHisAsnProTrpM 1513
Db 4253 ATGCGACGATGATTCTGTTAATGTAGACAAGACGACCCAAATATGAATATAGCCTTACA 4312
QY 1513 etLeuLeuTyrPheIleSerPheLeuIleValAlaPhePheValLeuAsnMetPhev 1533
Db 4313 TGTATATTATTTTGTGCTTTATCATCTTTGGGTCACTTCCTTTGAACTTGTTC 4372
QY 1533 aiGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaA 1553
Db 4372
QY 4373 TTGCTGTCATAGATAATTTCAACCAACAGAAAAAGAGCTTTGGAGGTCAAGACATCT 4432
QY 1553 rgArgArgGluGlu-----LysArgLeuArgArgLeuGluLysLysArgArgLysAlaG 1571
Db 4433 TTATGACAGAAGAACAGAAAAATACTATAATCAATGAAAAAGCTGGGTCCAAGAAC 4492
QY 1571 lnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysT 1591
Db 4493 CACAAAAGCCAAATTCCTCGACAGGGAACAAATCCAAGATGTATATTGGACTTAGTGA 4552
QY 1591 hrSerHisTyrLeuAspLeuPheIleThrGlyLeuIleGlyLeuAsnValValThrMetA 1611
Db 4553 CAATCAAGCCTTTGATATTAGTATCATGTTCTTATCTCTCAACATCGTAACCATGA 4612
QY 1611 laMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrI 1631
Db 4613 TGTGAAAAAGGAGGGTCAAAAGTCAACATATGACTGAAGTTTATATTGATATAATGTGG 4672
QY 1631 lePheThrValIlePheValLeuGluSerValPheLysLeuValAlaIlePheGlyPheArgA 1651
Db 4673 TTTTATAATTCCTTTTTCACGAGAAATGTTGCTTAAAACTGATCTCCTCAGA---CACT 4729
QY 1651 rgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG 1671
Db 4730 ACTACTTCAGTAGGATGGAATATTTTGTGTTGTGTTGTTGATATCTCCATTGTAG 4789
QY 1671 lyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleA 1691
Db 4790 GTATGTTTCTAGCTGATTG-----ATTGAAACGTATTTTGTGTCCTCCCTACCTGTTC 4843
QY 1691 rgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyM 1711
Db 4844 GAGTGATCCGTCCTGCCAGGATTCGCGAATCTTACGTTCTAGTCAAAGGACCAAGGGA 4903
QY 1711 etArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValIleGlyAsnLeuGlyLeuL 1731
Db 4904 TCCGACGCTGCTCTTTGCTTTGATGATGTCCTCTCTGCGTTGTTTAACTCGCGCTCC 4963
QY 1731 euPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG 1751
Db 4964 TGCTCTCTCGTTCATGTTCTATCGCCATCTTTGGAAATGTCCTCAACTTTGCTATGTTA 5023
QY 1751 luCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG 1771
Db 5024 AAAAGGAA-----GATGGAATTAATGACATGTTCAATTTTGAGACCTTTG 5068
QY 1771 lyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetL 1791
Db 5069 GCAACAGTATGATTTGCTGCTGTTCCAAATTCACACCTCTGCTGGCTGGATGGATGCTAG 5128
QY 1791 ysAspThrLeuArg-----AspCysAspGln----- 1799
Db 5129 CACCTATTCTTAACAGTAAGCCACCCGACTGACCCCAAAAAAGTTTCATCTCGGAAGTT 5188
QY 1800 -----GluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValL 1818
Db 5189 CAGTTGAAGGACACTGGTGAACCCATCTGTTGGAAATATTCTACTTTGTTAGTTATATCA 5248
QY 1818 euThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluG 1838
Db 5249 TCATATCTCTCTGTTGTTGGTGAACATGTACATTCAGTCATCATCGGAGAATTTTAGTG 5308
QY 1838 luSerAsnLysGluAlaLysGluGlu---AlaGluLeuGluAlaGluLeuGluGluM 1857
Db 5309 TTGCCACTGAAGAAAGTACTGAACCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAG- 5367
QY 1857 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1877
Db 5368 ----- 5380
QY 1877 aiGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHiA 1897
Db 1897
```

Db 5381 TTGAT---CCGATGCCAGCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTCACAGCTG 5437
 Qy 1897 laArgSerAlaSerHisPheSerLeuGluHisProThrMet-----GlnProHisProt 1915
 Db 5438 CC-----CTGGATCTCTCTCTCTCATAGCAAAACCCCAAAAG 5476
 Qy 1915 hrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArgThrHis 1935
 Db 5477 TCCAGCTCATTTGCCATGGATCTGCCATGGTT-----AGTGGT---GACCGGATCCATT 5527
 Qy 1935 erLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyH 1955
 Db 5528 GTCTT-----GACATCTTATT-----GCTTTTACAAAGCGGTGTTTGGT- 5568
 Qy 1955 isArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValHisSerGlnP 1975
 Db 5569 -----GAGAGTGGGAGATGGATTCTCTTCGTTTCACAGA 5602
 Qy 1975 roAlaAspThr-SerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro 1994
 Db 5603 TGAAGAAAGGTTTCATCTGTGCAAACTCTTCCAAAGTGCTCTATGAACCCCATCACACCA 5662
 Qy 1995 His 1995
 Db 5663 CAC 5665

RESULT 11

US-11-266-748A-29006
 ; Sequence 29006, Application US/11266748A
 ; Publication No. US2006013463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; FILE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266, 748A
 ; PRIOR FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 29006
 ; LENGTH: 7193
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-29006

Alignment Scores:

Pred. No.:	1,86e-62	Length:	7193
Score:	1594.00	Matches:	615
Percent Similarity:	37.4%	Conservative:	351
Best Local Similarity:	23.8%	Mismatches:	781
Query Match:	13.4%	Indels:	836
DB:	8	Gaps:	85

US-09-611-257A-37 (1-2266) x US-11-266-748A-29006 (1-7193)

Qy 2 AspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMetArg 21
 Db 133 GATGATGAAAAAATGCGAGCATCAACGGCAGCAGCAAGCGGACCCACCGAAGGCGAA 192
 Qy 22 Leu-----AsnAsp-LeuSerGlyAlaGlyGlyArgProGlyProGlyse 36
 Db 193 CTATGCAAGAGGACCACAGACTTCTCTCTTCTGGTGAAGGACCAACTTCTCAGCCGAATAG 252
 Qy 36 rAlaGluLys-----AspProGlySerAlaAspSerG1 47
 Db 253 CTCACGAAACTGTCCTGCTTGGGCAAGCTGCAATCGATGCTGCTAGACAGGCGCAAGGC 312
 Qy 47 uAlaGluGlyLeuProTyrProAlaLeuAlaProVal----- 59
 Db 313 TGCCCAAACTATGAGCACCTCTGCACCCACCTGTAGGATCTCTCTCCCAAGAAACG 372
 Qy 60 -----Va 60
 Db 373 TCAGCAATACGCCAAGAGCAAAAAACAGGGTAACCTCGTCCACAGCGCGCTGCCCGCGC 432
 Qy 60 lPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAs 80
 Db 433 CCTTTTCTGTTTATCACTCAATAACCCCATCCAGAGAGCTGCAATTAGTATAGTATAGT- 487
 Qy 80 nProTrp-----PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLe 98
 Db 488 -GAATGGAAACCATTTGACATATTTATATTATTTGGCTATTTTGGCCAAATTTGTGGGCTT 546
 Qy 98 uGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuG1 118
 Db 547 AGCTATTTCATCCCATTTCCCTGAAGATGATTTCTAATTCAACAAAT---CATAACTTGA 603
 Qy 118 nAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAl 138
 Db 604 AAAAGTAGAATATGCTTCTCTGATTTATTTTACAGTCGAGACATTTTGTGAAGATTATAGC 663
 Qy 138 aLeuGly---IlePheGlyLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPh 157
 Db 664 GTATGGATTATTGCTACATCCCAATCTTATGTTAGGAATGGATGGATTTACTGGATTT 723
 Qy 157 ePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSer----- 175
 Db 724 TGTATAGTAATAGTAGGATTG-----TTTAGTGAATTTTGGAAACAATAACCAAGA 777
 Qy 176 -----PheSerAlaValAr 180
 Db 778 AACAGAAAGCGGAAACCACTCAAGCGCAAACTCGAGGCTTTGATGTCAAAGCCCTCCG 837
 Qy 180 gThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLe 200
 Db 838 TGCCCTTTTCGAGTGTTCGGACCACTTCGACTAGTGTGAGGGGTGCCAGTTTACAAGTTGT 897
 Qy 200 uValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePh 220
 Db 898 CCTGAACCTCCATTATAAAAGCCATGGTTCCTCTCTTCATAGTACGCTTTTGTGATTATT 957
 Qy 220 eValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgGlnAr 240
 Db 958 TGTAAATCATAATCTATGCTATTATAGGATGGAACTTTTATTTGGAATAATGCACAAAAC 1017
 Qy 240 gCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrG1 260
 Db 1018 ATGTTTTTTTGTGACTCA-----GATATC----- 1042
 Qy 260 nThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetAr 280
 Db 1043 -GTAGCTGAAGAGGAGCCAGCTCCATGCGGTCTCA----- 1078
 Qy 280 gSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLe 300
 Db 1079 -----GGGAATGGAGCCGAGTGT----- 1096
 Qy 300 uAspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTy 320

1097	-----	ACTGCCAATGGC-----	1108	Db	1660	AGCCATCTCAAAATCCAAATCAGCCGACGCTGGCGTCGCTGGAACCGATTCAATCGCAG	1719
320	rThrAsnCySerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340	Qy	669	yrCysAlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerA	689	
1109	-ACGGAATGTAGGAGTGGCTGGGTGGCCGACGAGGAGCATCACCACCTTTGATAACTT	1167	Db	1720	AAGA-TGTAGGCGCCGCCCTG-	1738	
340	eGlyTyAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMe	360	Qy	689	spSerGluAlaValTyArgPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH	709	
1168	TGCCTTTGCCATCTTACTGTGTTTCAGTCATCACCATGGAGGGCTGGACAGCGTGCT	1227	Db	1738	-----	1738	
360	tTyPheValMetAspAlaHisSerPhe---TyAsnPheIleTyPheIleLeuLeuIle	379	Qy	709	ieSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	729	
1228	CTACTGGTAAATGATGCGATAGGGAATGCCATGGGTGTATTTTGTAGTCTGAT	1287	Db	1739	-----	1757	
379	eIleValGlySerPhePheMetIleAsnLeuCySerLeuValValIleAlaThrGlnPheSe	399	Qy	729	rpArgLeuIleCyAspThrPheArgLysIleValAspSerLysTyPheGlyArgGlyI	749	
1288	CATCCTTGGCTCATTTTCTGCTTAACCTGGTTCTTGGTGTCTTAGTGGAGAAATCTC	1347	Db	1758	GGCTGGTTATC-----	1768	
399	rGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAs	419	Qy	749	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyHisGluGlnProG	769	
1348	AAAGGAAGAGAGAGCAAGACACGGGAGATTTCCAGAAGCTCCGG-----	1396	Db	1769	-----	1823	
419	nAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyArgGluLeuLeuLysTy	439	Qy	769	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	789	
1397	-----	1431	Db	1824	ATTGGTTGACACAGATTCAAGATATGCCAACAAAGTCCTCTTGGCTCTGTTCACCTGC	1883	
439	rLeuValTyIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaG1	459	Qy	789	luMetLeuLeuLysLeuLeuValTyGlyProPheGlyTyIleLysAsnProTyArgAsnI	809	
1432	CTTGATGGATC-----	1444	Db	1884	AGATGCTGGTAAATAATGTACAGCTTGGGCTCCAAAGCATATTTCTCTCTTTTCAACC	1943	
459	yValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSe	479	Qy	809	lePheAspGlyValIleVal-----ValIleSerValTrpGluI	822	
1445	-----	1455	Db	1944	GGTTTGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	2003	
479	r-SerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisH	499	Qy	822	leValGlyGlnGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly	842	
1456	GGACATCGATCCGAGAGATGAGGAGAGAG-----	1484	Db	2004	TCATGTCCTCCCTG-----GGGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2057	
499	isHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis	519	Qy	842	eLysLeuValAlaArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrM	862	
1484	-----	1484	Db	2058	TCAAAGTGACAGGCATCTCCCTGAGCAACTTAGTGGCATCTTATTAACCTCCA	2117	
519	roGluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeuProProSerT	539	Qy	862	etAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleL	882	
1485	-----	1502	Db	2118	TGAAGTCCATCGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2177	
539	hrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyHisA	559	Qy	882	euGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProA	902	
1502	-----	1502	Db	2178	TTGGGATGCAGCTGTTGGCGCAAGTTTAAATTTTGAT-----GAAACGCAACCA	2228	
559	laAspCyHisLeuGluProValArgCysGlnAlaProProArg-----	574	Qy	902	spArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrG	922	
1503	-----	1542	Db	2229	AGCGGAGACCTTTTGACAATTTCCCTCAAGCATTCTCAGTGTTCAGATCTCTGACAG	2288	
575	-----	1574	Qy	922	lnGluAspTrpAsnLysValLeuTyArgAsnGlyMet-----AlaSerT	936	
1543	CACAGAGAAGCTCAGCGGTGAAGCGGAGAAC-----	1574	Db	2289	CGGAGACTGGAATCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	2348	
593	alHisThrSerProProGluThrThrLeuLysGluLysAlaLeuValAlaAlaAs	613	Qy	936	hrSerSerTrpAlaAlaLeuTyPheIleAlaLeuMetThrPheGlyAsnTyValLeuP	956	
1575	-----	1599	Db	2349	CAGGAATGATCGCTGTCATCTACTTTCATCATCTCTTTCATCTCTTTCATCTCTTTCAT	2408	
613	erSerGlyPro-----	629	Qy	956	heAsnLeuLeuValAlaIleLeuValGluGlyPhe---GlnAlaGluIleLeuSerLysA	975	
1600	CTGGTGGACGAGAGCGCGCCGAGCGGGGGCCCTCTGGGTGTCGCGCGTGGG----	1655	Db	2409	TGAATGTCTTGTGGCCATCGCTGTAGCAATTTGGCTGATGCTGAAAGCTCTGAAC----	2464	
629	yrSerSerMethHisLysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysL	649	Qy	975	tgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAla	995	
1656	-----	1659	Db	2465	-----	2465	
649	ysIleSerSerProCySerLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysPro	669	Qy	995	spAlaAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyA	1015	
			Db	2466	CTGCTCAGAAAGAGAGCGGAA-----	2495	

Db	4155	TTGTTGAAGCTTCTCAGCAGGGGGGAAAGGCATCCGGACATTCGTGTGGACTTTTATTAAAGT	4214	Db	5208	ATGTGTTCAAAAGAAATGGTGCCTCTTGGAAACCATGTCATCAT	5254
Qy	1720	-----GlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheI	1738	Qy	1960	euProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSert	1980
Db	4215	CTTTTCAGGCGCTCCCGTATGTG-----GCCCTTCCTCATAGCCATCTGTTCTTCA	4265	Db	5255	-----GTTAATAGTGTAGAGAGATTCCTCCTC	5282
Qy	1738	lePheAlaLaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProC	1758	Qy	1980	yrIleLeuGlnLeuProLysAspAlaProHisLeuGlnProHisSerAlaProThr	2000
Db	4266	TCTATCGGCTCATGGCATGCAGATGTTTGGAAAGTTGCCATGAGAGATAACACCCAG-	4324	Db	5283	AGCAGACCAATACACCCCGCTCCCTCGTCATGTCCTCAAGGCCCTTCAATCCACCTGCAA	5342
Qy	1758	ysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuP	1778	Qy	2000	rpGlyThr-----lleProLysLeuProProGlyArgSerProLeu-----	2014
Db	4325	-----ATCAATAGGAACAATAACTTCAGACGTTTCCCGCGCGTCTGCTGCTCT	4376	Db	5343	GTGATACTGAGAACCGCTGTTTCTCCAGCAGGAAATTCGGTGTGTATATAACCATCAT	5402
Qy	1778	heArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeu-----ArgA	1796	Qy	2015	-----AlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsps	2029
Db	4377	TCAGGTGTCAACAGGTGAGCGCTGGCAGGAGATCATGTGGCTGTCTCCAGGGNAGC	4436	Db	5403	ACCATAATTCATAGGAAAGCAAGTTCCACCTCAACAAATGCCAATCTCAATATGCCA	5462
Qy	1796	spCysAspGlnGluSer-----ThrCysTyzAsnThrValI	1808	Qy	2029	erLeuAspValGlnGlyLeuGlySerArgGluAspLeu-----LeuAlaGluValSer-	2046
Db	4437	TCTGTGACCTGAGTCAGATTACAAACCCCGGGAGGAGTATACATGT--GGGAGCAACT	4493	Db	5463	ATATGTCCAAAGCTGCCATGGAAAGCGCCAGCATTTGGAAACCTTGACGATGTGTCTG	5522
Qy	1808	leSerProIleTyzPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVal	1828	Qy	2047	-----GlyProSerProp	2051
Db	4494	TTGCCATTGTCTATTTTCATCAGTATTTTACATGCTCTGTGATTTTCTGATCATCAATCTGT	4553	Db	5523	AAATGGGCATCTTCTCCACAAAGCATGACCGGGAGCCTCAGAGAAGGTCCAGTGTGA	5582
Qy	1828	allIleAlaValLeuMet-----	1833	Qy	2051	roleuAlaArgAlaTyzSerPheTyzGlyGlnSerSerThrGlnAlaGlnGln-	2068
Db	4554	TTGGGTGTGCATCATCATGATAATTTGCATCTATCGACCGGGAGCTGTCTATTTTGGGGC	4613	Db	5583	AAAGAACCCGCTATTATGAAACTTACATTAGGTCCGACTCAGGAGATGAACAGCTGCCAA	5642
Qy	1834	--LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGlu-	1852	Qy	2069	--HisSerArgSerHisSerLysIleSerLysHisMetThrProAlaProCysProG	2088
Db	4614	CTCACCATTAGATGAATTC--AAAGAAATGTCAGATAATGACCCCTGAGCAAAAG	4670	Db	5643	CTATTTCCCGGGAAAGCCAGAGATACATGGCTATTTTCAGGGACCCC--CACTGCTTGG	5699
Qy	1853	-----LeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlyS	1870	Qy	2088	lyProGlu-----	2094
Db	4671	GAAGGATAAAACACCTTGATGTGTCTCTGCTTCGACGCATCCAGCCTCCCTCGGGGT	4730	Db	5700	GGGAGCAGGAGTATTTTCAGTAGTCAGGAATGCTACGAGGATGACAGCTCGCCCTGGA	5759
Qy	1870	erProPheLeuTrpPro-----GlyValGluGlyProA	1881	Qy	2094	lyLys-----GlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeus	2111
Db	4731	TTGGGAAGTTATGTCACACAGGTAGCGTGCAGAGATTAGTTGCCATGAACATGCCTC	4790	Db	5760	GCAGGCAAAACTATGGCTACTACAGCAGATACCCAGGCAGAAACATCGACTCTGAGAGGC	5819
Qy	1881	spSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlas	1901	Qy	2111	erTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgA	2131
Db	4791	TCAACAGTGACGGGACATCATGTTTAAATGCAACCCCTGTTTGGTTCGAACGGCTC	4850	Db	5820	CC-----CGAGGCTACCATCATCCCCAGAGATTTCTGGAGGACGATCAGCTCGCCC	5869
Qy	1901	erHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeu-----	1917	Qy	2131	spLeuLysLysCysTyzSerValGluAlaGlnSerCysGlnArgArg-----ProT	2148
Db	4851	TTAAGATCAAGACCGAAGGAAACCTGGAGCAAGCTAAT--GAAGAACTTCGGGTGTGA	4907	Db	5870	-----GTTTGTCTATGAT--TCACGGAGATCTCCAAGGAGACGCTACTACCTCCCA	5918
Qy	1918	-----	1919	Qy	2148	hrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlyS	2168
Db	4908	TAAAGAAATTTGGAAAGAAACCAACCATGAAATTAATTACTTGACCAAGTTGTCCCTCCAGCTG	4967	Db	5919	CCCCA-----GCATCCACCGGAGATCCTCTTCAACTTTGAGTGCCTGCG-CCGGCAG	5971
Qy	1919	lyProAspLeuLeuThrValArgLys-----	1927	Qy	2168	erGlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProG	2188
Db	4968	GTGATGATCAGGTAAACCGTGGGGAAGTTCTATGCCACTTTCTCCTGATACAGGACTACTTTA	5027	Db	5972	AGCAGCCAGGAAGAGGTCCCGTCTGCTCCCATCTT-----CCCCATCGCAGCGCCCTG	6025
Qy	1927	-----	1927	Qy	2188	lySer-----ArgProLysLysLysLeuSerP	2197
Db	5028	GGAAATTCAGAAACCGAAAGAACCAAGGACTGGTGGGAAAGTACCCTCGGAAGAACACA	5087	Db	6026	CCTCTGCATCTAATGCAGCAACAGATCATGGCAGTTGCGCGCTAGATTCAAGTAAAGCC	6085
Qy	1928	-----SerGlyValSerArgThrHisSerLeu-----	1936	Qy	2197	roProSerIleThr-----lleAspProProGluSerGlnGlyProArgThrProProS	2215
Db	5088	CAATTGCCCTACAGCGCGGATTAAAGCACTGACACTGCATGCATGCGGCCAGAAATCCCGCGTG	5147	Db	6086	CAGAAATGACTACCCAGGTCACTCGACCCCGGTCTGGGCCACCCCTCCAGCAACCCCTCCC	6145
Qy	1937	-----	1940	Qy	2215	erProGlyIle-----CysLeuArgArgAlaProSerSerSerSerSerSerSerProL	2233
Db	5148	CTATATCGTGTATTGCAAGATGACGACCTGAGGAAACAAAAACGAGAAGAAGAAGATG	5207	Db	6146	TAACCGGACTGGACACCGGTGTACACCCCTGTATCCAAAGTGGAGGAGTGGAGGCGCT-	6204
Qy	1940	erTyzMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyL	1960	Qy	2233	euAlaSerGlyProProAspSerMetAlaAlaSerProSerPro-----L	2248
				Db	6205	-----GGACCAAGTGAACGGCAGCTGCGCTCCCTGCACCGCAGCTCTCTGGTACACA	6256

[illegible]

QY	769	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	789
DB	1824	ATTGGTTGACAGATTCAAGATTTCGCCAACAAAGTCTCTTTGGCTCTGTTTCACTGCG	1883
QY	789	luMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	809
DB	1884	AGATGCTGGTAAATAATGTACAGCTTGGGCTTCCAGCATATTTCGTCTCTCTTTCAACC	1943
QY	809	lePheAspGlyValIleVal-----ValIleSerValTrpGluI	822
DB	1944	GGTTTCATTGCTTCGTGGTGTGGTGGAAATCACTGAGACGATCCTGGTGGAACTGGAAA	2003
QY	822	leValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgIleLeuMetArgVal	842
DB	2004	TCATGTCCTCCCTCG-----GGATCTCTGTGTTTCGGTGTGTGGCCCTCTTAAGAATCT	2057
QY	842	eulysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrM	862
DB	2058	TCAAAGTGACCGACTGGACTTCCTTCGAGCAACTTAGTGGCATCTTATTAAATCCCA	2117
QY	862	etAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleI	882
DB	2118	TGAAGTCCATCGCTTCGCTTCGCTTCGCTTCCTTCCTTCATATTATCATCTTTTCCTGTC	2177
QY	882	eulGlyMetHisLeuPheGlyCysLysPheAlaSerGlyArgAspGlyAspThrLeuProA	902
DB	2178	TTGGATGTCAGCTGTTTGGCGCGCAAGTTTAATTTTCAT-----GAAACGCAAAACCA	2228
QY	902	spArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrG	922
DB	2229	AGCGGACGACCTTTGACAATTTCCCTCAAGCACTTCTCAAGTGTTCAGATCCTGCACAG	2288
QY	922	lnGluAspTrpAsnLysValLeuTyrAsnGlyMet-----AlaSerT	936
DB	2289	GCGAAGACTGGAAATGCTGTGATGACATGGCATCATGGCTTACGGGGGCCCATCCTCTT	2348
QY	936	hrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuP	956
DB	2349	CAGGAATGATCGCTCGCATCTACTTCATCATCTCTTCATTGTTGGTAACTATATTCTAC	2408
QY	956	heAsnLeuLeuValAlaIleLeuValGluGlyPhe--GlnAlaGluGluIleSerLysA	975
DB	2409	TGAATGTCCTCTTGGCCATCGCTGTAGACAATTTGGCTGATGCTGAAAGTCTGAAC---	2464
QY	975	rgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyA	995
DB	2465	-----A	2465
QY	995	spAlaAsnLysSerGluSerGluProAspPheSerProSerLeuAspGlyAspGlyA	1015
DB	2466	CTGCTCAGAAAGAAAGACGGAA-----GAAAGG	2495
QY	1015	spArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerL	1035
DB	2496	AGAGGAAAAAG-----ATTGCCAGAAAGAGAGCCGTAGAAAAATAAAAGAAC	2543
QY	1035	euLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrS	1055
DB	2544	ACAAACCAGAGTC-----	2557
QY	1055	erThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerA	1075
DB	2558	-----AACCATATGCCAACAGTGCACCAAGGTTTACATTTGATCACTATA	2603
QY	1075	laGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHiss	1095
DB	2604	GAGAA-----GAGGATGAAGACCAAGCACCCCTATC	2633
QY	1095	erProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyA	1115
DB	2634	CGCCTTTCGATGTG-----	2647


```
QY 1115 rgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyG 1135
Db 2648 -----CCAGTAGGGAA----- 2659
QY 1135 luGlyGlnGluSerGlnAspGluGluSerSerGluGluGluArgAlaSerProAlaG 1155
Db 2660 -----GAGGAAGAGGAGAGGAGGAGGATGAACCTGAGGTTCCTGCCG 2702
QY 1155 lySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuP 1175
Db 2703 GACCCCGTCTCGAAGGATCTCGAGGTGAACATGAAGGAAATAATTGCC---CCCATCC 2759
QY 1175 roAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerG 1195
Db 2760 CTGAAA-----GGGAGCGCT--- 2773
QY 1195 luHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProA 1215
Db 2773 ----- 2773
QY 1215 spAspProProLeuAspGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluA 1235
Db 2773 ----- 2773
QY 1235 rgValArgAlaTyrIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrps 1255
Db 2773 ----- 2773
QY 1255 exAlaTyrIlePheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrH 1275
Db 2774 --TTCCTCATCTTAGCAAGACCAACCCGATCCGCTGAGGCTGCCAAGCTCATCAACC 2831
QY 1275 isLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaM 1295
Db 2832 ACCACATCTTCACCAACTCATCTCTGCTTCATCATGCTGAGCAGCGCTGCCCG 2891
QY 1295 etGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnT 1315
Db 2892 CAGAGGACCC---ATCCGAGCCACTCTCTCCGGAACAGCATCTGGGTACTTGACT 2948
QY 1315 yrIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpC 1335
Db 2949 ATGCTTTCAGCAATCTTTACTGTGAGATCTGTGAAGATGACAACTTTTGGAGCTT 3008
QY 1335 ysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuVal 1355
Db 3009 TCCTCCACAAAGGGCTCTTCGAGGAACACTTCAATTTGCTGGATATGCTGTGGTTG 3068
QY 1355 euIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuG 1375
Db 3069 GGGTGTCTCTGGTGTCAATTTGGGATTCAA-----TCCAGTGGCATCT 3110
QY 1375 lyMetLeuArgValLeuArgLeuArgThrLeuArgProLeuArgValIleSerArgA 1395
Db 3111 CCGTTGTGAAGATCTGAGGGCTTTAAGGCTCTGCGTCCCTCAGGGCCATCAACAGAG 3170
QY 1395 laGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnI 1415
Db 3171 CAAAGGACTTAGACAGCTGGTTCAGTGGCTCTCTGCGGCATCCGGACCATCGGCAACA 3230
QY 1415 leValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheL 1435
Db 3231 TCATGATCGTCACTACCTCCTCGAGTTCATGTTTGCCTGATCGGGTCCAGTTGTTC 3290
QY 1435 ysglyLysPheValCysGlnGlyGluAspThrArgAsn----- 1448
Db 3291 AGGGGAAGTTCATCGCTGTACGGATGAAGCCAAAAGTAACTCGTAAGAATGACGGGAC 3350
QY 1449 -----IleThrAsnLysSerAspCysAlaGluAlaSerTyrArg-----TyrV 1463
Db 3351 TTTTTCATCTCTACAGGATGGGATGTTGACAGTCTCTGTGGTCCGTGAACGATCTGGC 3410
QY 1463 alArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuA 1483
```

```
Db 3411 AAAACAGTGTATTTCAACTTCGACAACTCTCTCTCTATGATGGCGCTCTTTCACAGTCT 3470
QY 1483 laSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspG 1503
Db 3471 CCAGTTTGGAGCTGGCGCTGCTGTATTAAGCCATCGACTCGAATGGAGAGAACA 3530
QY 1503 lnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuI 1523
Db 3531 TCGGCCCAATCTACAACCCAGCGGTGGAGATCTCCATCTTCTTTCATCATCTACATCATCA 3590
QY 1523 leValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysC 1543
Db 3591 TTCTAGCTTTCTTCATGATGAACATCTTGTGGCTTTGTTCATCGTTTACATTT--- 3643
QY 1543 ysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluGluLysArgLeuArgArgL 1563
Db 3644 -----CAGGNACAGGAGAAAAGAGATATAAGAACTGTGAG-----C 3680
QY 1563 euGlyLysLysArgArgLysAlaGlnCysLysProTyr----- 1575
Db 3681 TGGACAAAATCAGCGT-----CAGTGTGTTGAATACGCTTGAAGACAGCTCCCTTCG 3734
QY 1576 -----TyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisT 1594
Db 3735 GGAGATACATCCCAAAACCCCTACCACTACCAAGTTCTGCTACGTGGTGAACCTCTTCGC 3794
QY 1594 yrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluH 1614
Db 3795 CTTTCCAAATACATGATGTTTGTCTCATGCTCAACACACTGCTTGGCCATGTCAGC 3854
QY 1614 isTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrV 1634
Db 3855 ACTACGAGCAGTCCAAGATGTTCAATGATGCCATGGACATTTCTGAACATGGTCTTTCACCG 3914
QY 1634 alIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheG 1654
Db 3915 GGGTGTTCACCGTCGAGATGGTTTGAAGATCATCGCATTTAAGCCCTAAAGGGGTATTTTA 3974
QY 1654 lnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrL 1674
Db 3975 GTGACCCCTGGAAACACGTTTGACTCCCTCATGTAATCGGCAGCATTTATAGAGTGGCCC 4034
QY 1674 euGluGluIleGluValAsnAlaSer-----LeuProfile----- 1685
Db 4035 TCAGCGAAGCGGACCCCACTGAAAGTGAAATGTCCTCTGTCGCCAACTGCTACACCTGGGA 4094
QY 1686 -----AsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1701
Db 4095 ACTCTGAAGAGAGCAATAGAAATCTCCATCACCTTTTTCGCTCTTTTCCGAGTATGCGAT 4154
QY 1701 alLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMet--- 1719
Db 4155 TGTGTGAAGTCTCTCAGCAGGGGGAAGGATCGGACATTCGGCATTTGCTGGAGCTTTTATTAA 4214
QY 1720 -----GlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheI 1738
Db 4215 CCTTTTCAGGGCTCCCGTATGTG-----GCCCTCTCATAGCCATGCTGTTCTTCA 4265
QY 1738 lePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProC 1758
Db 4266 TCTATCGGTTCATTTGGCATGTCAGATGTTTGGGAAAGTTGCCATGAGAGATAACAACACAG- 4324
QY 1758 ysgLysGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuP 1778
Db 4325 -----ATCAATAGGAACAATACTCCAGACGTTTCCCCAGCGGTGCTGCTGCTCT 4376
QY 1778 heArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeu-----ArgA 1796
Db 4377 TCAGGTGTCAACAGGTGAGGCTGCGAGAGATCATGTGGCTGCTCTCCCAGGGAAGC 4436
QY 1796 spCysAspGlnGluSer-----ThrCysTyrAsnThrValI 1808
```

4437 TC TGTGACCTGAGTCAGATTACAACCCCGGGAGGAGTATACATGT---GGAGCAACT 4493
 1808 leSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValV 1828
 :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
 4494 TTGCCATTGCTATTTCATCAGTTTTTACATGCTCTGTGCATTTCTGTGATCATCATCTGT 4553
 1828 alleAlaValLeuMet----- 1833
 :::: :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4554 TTGTGGTGTCATCATGATAAATTCGACTATCTGACCCGGGAGCTGTCATTTTGGGGC 4613
 1934 --lysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluAlaGlu- 1852
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4614 CTCACCAATTTAGTAGAAATTC---AAAGAATATGTCAGAAATATGACCCTTGAGGAAGG 4670
 1853 -----LeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlys 1870
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4671 GAAGGATAAAACACCTTGATGTGTCACCTCTGCTTCGACGCATCCAGCCTCCCTGGGT 4730
 1870 erProPheLeuTrpPro-----GlyValGluGlyProA 1888
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4731 TTGGGAAGTTATGTCCACACAGGGGTAGCGTGCAAGAGATTAGTGGCATGAACATGCCTC 4790
 1881 spSerProAaspSerProLysProGlyAlaLeuHiProAlaAlaHisAlaArgSerAlas 1901
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4791 TCAACAGTCAGCGGACAGTCATGTTTAATGCAACCCCTGTTGCTTTGGTTGGAACGGCTC 4850
 1901 erHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeu----- 1917
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4851 TTAAGATCAAGACCGAAGGNACCTGGAGCAAGCTAAT--GAAGAACCTTCGGGCTGTGA 4907
 1918 -----ProG 1919
 4908 TAAAGAAAATTTGGAAGAAAAACAGCATGAAATTACTTGACCAAGTTGTCCCTCCAGCTG 4967
 1919 lyProAaspLeuLeuThrsValArgLys----- 1927
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 4968 GTGATGATGAGGTAAACCGTGGGGAAGTTCTATGCCACTTTCCTGTATACAGGACTACTTTA 5027
 1927 ----- 1927
 5028 GGAATTCAGAAAACGNAAGAACACAGGACTGGTGGGAAAGTACCTTCGGAAGAACACCA 5087
 1928 -----SerGlyValSerArgThrHisSerLeu----- 1936
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5088 CAATTGCCCTACAGCGGGATTAAGAGCACTGTCATGACATTTGGGCCAGAAATCCGGCGTG 5147
 1937 -----ProAsnAaspS 1940
 5148 CTATATCTGTGATTTCGACAGTACAGAGCTGAGGAACAAAACGAGAGACAGAGATG 5207
 1940 erTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyL 1960
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5208 ATGTGTTCAAAGAATAATGGTGCCTGCTTGAAACCATGTCAATCAT----- 5254
 1960 euProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAaspThrSerT 1980
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5255 -----GTTAATAGTATGATAGAGAGATTCCTCCTTC 5282
 1980 yIleLeuGlnLeuProLysaspAlaProHisLeuLeuGlnProHisSerAlaProThrT 2000
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5283 AGCAGACCAATACCAACCCAGCTCCCTCGATGTCCTCAAGGCCCTTCAATTCACCTCCAA 5342
 2000 rpGlyThr---IleProLysLeuProProGlyArgSerProLeu----- 2014
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5343 GTGATACTGAGAAACCGCTGTTTCTTCAGCAGGNAATTCGGTGTGTCAATCAACCATCAT 5402
 2015 -----AlaArgProLeuArgArgGlnAlaAlaIleArgThrAspS 2029
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5403 ACCATAATTTCCATAGGAAGCAAGTTCCCACCTCAACAAATGCCAATCTCAATAATGCCA 5462
 2029 erLeuaspValGlnGlyLeuGlySerArgGluAaspLeu-----LeuAlaGluValSer- 2046
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 5463 ATATGTCCAAGACTGCCCATGGAACCGGCCAGCATTTGGGAACCTTGAGGTGTGTGCTG 5522

Qy	2047	-----GlyProSerProp	2051
Db	5523	AAAATGGGCATCACTTCCCAACAGCATGACCGGAGCCTCAGAGAAGGTCAGAGTGA	5582
Qy	2051	roLeuAlaArgAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGln-----	2068
Db	5583	AAAGAACCCTATTATGAACCTTACATTAGTCCGACTCAGGAGATGAACAGCTCCCAA	5642
Qy	2069	--HisSerArgSerHisSerLysLysHisMetThrProProAlaProCysProG	2088
Db	5643	CTATTTCCGGGAAGACCCAGAGATACATGGCTATTTCAGGAGACCCC---C	5699
Qy	2088	lyProGlu-----ProAsnTrpG	2094
Db	5700	GGGAGCAGGAGTATTTAGTAGTGAAGATGTACAGGATGACAGCTGCCACCTCGA	5759
Qy	2094	lyLys-----GlyProProGluThrArgSerSerLeuGluLeuLeuAspThrGluLeuS	2111
Db	5760	CGAGCCAAACTATGGCTACTACAGCAGATACCCAGCGAGAAACATCGACTCTGAGAGGC	5819
Qy	2111	erTrpIleSerGlyAspLeuLeuProProGlyGlnGluProProSerProArgA	2131
Db	5820	CC-----CGAGGCTACCATCATCCCAAGGATTCTTGAGGACGATGACTCGCCC	5869
Qy	2131	spLeuLysLysCysTySerValGluAlaGlnSerCysGlnArgArg-----Prof	2148
Db	5870	-----GTTTGTATGAT---TCAGGAGATCTCCAAGGAGACGCTACTACCTCCCA	5918
Qy	2148	hrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlys	2168
Db	5919	CCCCA-----GCATCCACCGGAGATCCTCCTTCAACTTTGAGTGCCTGCG-CCGCGCAG	5971
Qy	2168	erGlnProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProG	2188
Db	5972	AGCAGCCAGGAAGAGTCCCGTCTCCCATCTT-----CCCCATCGCAGCGGCCCTG	6025
Qy	2188	lySer-----ArgProLysLysLysLeuSerP	2197
Db	6026	CCTCTGCATCTAATGACGACACAGATCATGGCAGTTCGCGGCTAGATTCAAGTAAGCC	6085
Qy	2197	roProSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProS	2215
Db	6086	CAGAAGTACTCACCGAGTCACTCGACCGGTGCTGGGCCACCCCTCCAGCAACCCCTCCC	6145
Qy	2215	erProGlyIle-----CysLeuArgArgAlaProSerSerAspSerLysAspProL	2233
Db	6146	TACCGGACTGGACACCGTGTACACCCCTTGATCCCAAGTGGAGCAGTCAGAGGCCCT-	6204
Qy	2233	euAlaSerGlyProProAspSerMetAlaAlaSerProSerPro-----L	2248
Db	6205	-----GGACCAAGGTGAACGGCAGCCTGCCCTCCTGCACCGCAGCTCCTGGTACACA	6256
Qy	2248	ysLysAspValLeuSerLeuSerGlyLeuSerSerAspProProAlaAspLeuAspPro	2266
Db	6257	GACGAGC-CCGACATCTCCTACCGGACTTTTCACACCAGCAGCCTGACTGTGCCCA	6311
RESULT 13			
US-11-313-450-11			
; Sequence 11, Application US/11313450			
; Publication No. US20060110778A1			
; GENERAL INFORMATION:			
; APPLICANT: Adorante, Joseph S.			
; APPLICANT: Ehring, George R.			
; TITLE OF INVENTION: High-Throughput Screens For Identifying			
; TITLE OF INVENTION: Selective Persistent Sodium Channels Channel Blockers			
; FILE REFERENCE: 17407 CIP (AP)			
; CURRENT APPLICATION NUMBER: US/11/313,450			
; CURRENT FILING DATE: 2005-12-19			
; PRIOR APPLICATION NUMBER: 09/989797			
; PRIOR FILING DATE: 2001-11-20			
; PRIOR APPLICATION NUMBER: 60/252771			
; PRIOR FILING DATE: 2000-11-22			

```
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5943
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-313-450-11

Alignment Scores:
Pred. No.:      2,19e-62      Length:      5943
Score:          1590.50      Matches:     568
Percent Similarity: 42.3%      Conservative: 380
Best Local Similarity: 25.3%      Mismatches:  799
Query Match:     13.4%      Indels:      498
DB:              8          Gaps:         80

US-09-611-257A-37 (1-2266) x US-11-313-450-11 (1-5943)
QY 28 AlaGlyGlyArgProGly---ProGlySerAlaGluLysAspProGlySerAlaAspSer 46
Db 132 TCGGGAGGAGCGATGAGGACAGCAAGCCCAAGCCCAACACAGCGACCTGGAAAGCAGGAAGAG 191
QY 47 GluAlaGluGlyLeu-----ProTyrProAlaLeuAla-ProValValPhePh 62
Db 192 TTTGCCCTTTCATCTACGGGACATCCCCCAAGCCCTGGTTCAGATTCCCTCGAGGACTT 251
QY 62 e-----TyrLeuSerGln-----66
Db 252 TGACCCATACATAITTCAGCGCAGAAACCTTTGTAGTATTAAACAGAGGGAACCTCTCTT 311
QY 67 -----AspSerArgPro-----ArgSerTr 73
Db 312 CAGATTAGTGCACCGCTCCCTGTACATTTTAAAGTCCTTTAAACCTGATAAGAAAT 371
QY 73 pCysLeuAlaThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeu 93
Db 372 AGCTATTAAATTTTGATACATCTCAGTATTAGCATGATCATTTAGTGCATCTTTTGAC 431
QY 93 uAsnCysValThrLeuGlyMetPheArgPro-----CysGluAspIleAlaCysAs 110
Db 432 CAACTGTGATTTCATGACTTTTAGTAACCTCTGACTGTGTCGAAGAAATGTG-----483
QY 110 pSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePhe-----AlaPhePheAl 129
Db 484 -----GAGTACACGCTTCACAGGGATTTATAC 509
QY 129 aValGluMetValValIysMetValAlaLeuGlyIlePheGlyLysCys-----146
Db 510 ATTTGAATCACTAGTGAAATCAATTGCAAGAGTTTC-----TGCATAGATGG 557
QY 147 -----TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMe 164
Db 558 CTTTACCTTTTACGGGATCCATGGAACTGGTTAGATTTTCAGTGTCTATCATGATGCGCTA 617
QY 164 tLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgVa 184
Db 618 TATAACAGAGATTGTAAACCTTAGCAATGTT-----TCAGCTCTACGCACTTTTCAGGCT 671
QY 184 lLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLe 204
Db 672 ACTGAGGGCTTTGAAACATATTTTGGTAAATCCCAAGCCCTGAACAAATTTGTGGTGGCTCCCT 731
QY 204 uLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 224
Db 732 GATTTCAGCTGTGAAGAACTGTGCAGATGTGATGATCCTGACAGTGTCTTGCCTGAGTGT 791
QY 224 ePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu-- 243
Db 792 TTTTGGCTTTCATCGGAGTGCAGCTGTTTCATGGGGAACCTTCGAAACAAGTGTGTGTGTG 851
QY 244 -ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln-----Th 261
Db 852 GCCCATAAACTTCAAC-----GAGAGCTATCTTTGAAATGGCAC 890
```

```
QY 261 rGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgse 281
Db 891 CAAAGGCTTTGATTGGGAAGAGTATATC-----AACATAAAACAAA 932
QY 281 rCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProPro-----CysGl 299
Db 933 TTTTCTACACAGTTTCCT-----GGCATGCTGGAACCTTTACTCTGTGG 974
QY 299 yLeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTy 319
Db 975 G-----AACAGTTCTGATGCTGGCAATGCCAGAGGATACACAG-- 1014
QY 319 rTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyValAlaIleAsnPheAspAs 339
Db 1015 -----TGTATCAAAGCAGGAAGAACCCCAACTATGTTTACACAAGTTTTCACAC 1064
QY 339 nIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIl 359
Db 1065 TTTTAGCTGGGCTTCTTGGCATTTATTCGCCTTATGACCCAGGACTATTGGGAAACTT 1124
QY 359 eMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIl 379
Db 1125 GTATCAATTGACTTTACGAGCAGCCGCGAAACATACATGATCTTCTGCTCTTGGTCAT 1184
QY 379 eIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPhe-- 398
Db 1185 CTTTGTGGGTCTTCTTCTATCTGTGTAACCTTGCTTGGCTGTGTCGCTCATGCTTATGA 1244
QY 399 -----SerGluThrLysGlnArgGluSerGlnLeuMe 409
Db 1245 AGAACAGATACAGGCAACACTCGAGAGGAGCAGAACAAAAAGAGCTGAATTTTAAAGCAAT 1304
QY 409 tArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluPr 429
Db 1305 GTTGGAGCACTTAAAGAACCAACAGGAAGGACAGGCTGTCGATGCCACTTCAGC 1364
QY 429 oGlySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaAr 449
Db 1365 AGGAACGTCTCAGAAGATGCCATAGAG-----1392
QY 449 gArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAl 469
Db 1393 -----GAAGAAGGTGAAGAAAGAGGAGGGGCTC 1418
QY 469 aProLeuGlyGlyGlnGluThrGlnProSerSerCysSerArgSerHisArgArgLe 489
Db 1419 CCTCGGAGCTCTTCTGAATCTCTTAACTCAGCTCAAAGAGTGCAAGAGAAAGAGCT-- 1476
QY 489 uSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHis 509
Db 1476 -----1476
QY 509 nGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlyse 529
Db 1477 -----AACAGAGAAAGAGAGGAAGCAAAAGGAACCTCTCTGAAGAGAGAGAGAAAGGGA 1532
QY 529 r-ArgArgLeuMetLeuProProSerThrProAlaLeuSerGlyAlaProProGly- 548
Db 1533 TCCCGAAGAGGTGTTTAAAGTCAGATCAGAAAGATGCCATGAGNAGGAAGGCCCTTTCGGCT 1592
QY 549 -----GlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisL 563
Db 1593 GCCAGACACAGAAATAGGAGGAAATTTTCCATCATGAATCAGTCAC-----TGCTCAG 1646
QY 563 euGluProValArgCysGlnAlaPro-----ProProArgSerProSerGluAlaSerG 581
Db 1647 CATCCAGGCTCGCCCTCTCTCCGCCACAAACAGAGAGAGAGCATCTTTCAGTTTCAG 1706
QY 581 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluT 601
Db 1707 GGGACCTGGGCGGTTCGAGAGACCCGGGCTCCGAGAAATGAGTTTCG-----C 1751
```


Db 3558 ----- 3558
Qy 1264 ArgPheArgLeuLeuLeuHisHisArgIleIleThrHisLysMetPheAspHisValValLeu 1283
Db 3559 ---CTGGGAAACCTGCTTCTCCTCATCGTGGAGCACAACCTGGTTGGAGACCTTCATCATC 3615
Qy 1284 ValIleIlePheLeuLeuHisHisArgIleIleThrIleAlaMetGluArgProLysIleAspProHis 1303
Db 3616 TTCATGATTCTGTGAGCAGTGGCGCCCTCGCCCTTCGAGGACATCTACATTGAGCAGAGA 3675
Qy 1304 SerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAla 1323
Db 3676 AAGACCATCCGACCATCTCGGAATATGCTGCAAAAGTCTTCACCTATATCTTCATCCTG 3735
Qy 1324 GluMetThrValLysValAlaLeuGlyTyrPheGlyGluGlnAlaTyrLeuArg 1343
Db 3736 GAGATGTGCTCAAGTGGAGCAGCTATGGCTTCGTC-----AAGTTCCTCACC 3783
Qy 1344 SerSerTrpAsnValLeuLeuAspGlyLeuLeuValLeuLeuSerValIleAspIleLeuVal 1363
Db 3784 AATGCCTGTGTGGCTGGACTTCTCATTTGGTGTCTCTTAGTCAGCCTTATAGCT 3843
Qy 1364 SerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeu 1383
Db 3844 AATGCCCTG-----GGCTACTCGAACTAGGTGCCATAAAGTCCCTTAGGACCCCTA 3894
Qy 1384 ArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlu 1403
Db 3895 AGAGCTTTGAGACCTTATAGACCTTATCAGATTGTAAGGATGAGGGTGGTGGTGAAT 3954
Qy 1404 ThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleValIleCysCysAlaPhePhe 1423
Db 3955 GCCTTGGTGGCGCCATCCCTCCATCATGAATGTCTGTGTGTCTCTCTCTCTCTCTG 4014
Qy 1424 IleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGly 1443
Db 4015 CTGATTTTCAGCATATGGAGGTAACTGTTTTCGGGAAAGTACCACCTACTGCTTTAAT 4074
Qy 1444 Glu-----AspThrArgAsnIleThrAsnLysSerAspCysAlaGlu 1457
Db 4075 GAGACTTCTGAATCCGATTTGAAATGAGATGTCAACATATAAACTGAATGTGAAAG 4134
Qy 1458 -----AlaSerTyrArgTTPValArgHisLysTyrAsnPheAspAsn 1471
Db 4135 CTTATGGAGGGAAACAATACAGAGATCAGATGAAGAACCTGAAGATCAACTTTGACAT 4194
Qy 1472 LeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIle 1491
Db 4195 GTTGGGCGGAGTACCTGGCCCTTCTCAAGTAGCAACCTTCAAAAGGCTGGATGGACATC 4254
Qy 1492 MetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPro 1511
Db 4255 ATGTATGACAGTGTAGATTCCCGAAGCCTGATGACGACCTTAAGTATGAGGACAATATC 4314
Qy 1512 TrpMetLeuLeuTyrPheIleSerPheLeuIleValAlaPhePheValLeuAsnMet 1531
Db 4315 TACATGTACATCTATTTGTTCATCTTCATCATCTTCGGCTCCTTCTTCACCTGGAACCTG 4374
Qy 1532 PheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGlu 1551
Db 4375 TTCAATTTGGTGTATCATCTTGAATCAATCAACAAAAGTTCGAGGCTCAGGAC 4434
Qy 1552 AlaArgArgGluGlu-----LysArgLeuArgLeuGluLysLysArgGlyLys 1569
Db 4435 ATCTTCATGACCAAGACAGAAAGTACTCAATGCCATGAAAAGCTGGGCTCAAAAG 4494
Qy 1570 AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeu 1589
Db 4495 AAGCCACAGAAACCATTCCTCCCGCCCTTGAACAAAATCCCAAGGAATCTCTTTGATTTT 4554
Qy 1590 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609
Db 4555 GTCACTCAGCAAGCCCTTTGACATTTGTTATCATGATGCTCATCTGCTTAAACATGGTGACA 4614

Qy 1610 MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629
Db 4615 ATGATGGTGGAGACACACTCAAGCAAGCAGATGGAGAACATCTCTACTGGATTAAAC 4674
Qy 1630 TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe 1649
Db 4675 CTGGTGTGTTGTTATCTTCTTCCCTGAGTGTGCTCAAAATG-----TTTGCCTTG 4728
Qy 1650 ArgArg---PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSer 1668
Db 4729 AGGCATCTACTTACCTACCATTTGGCTGGAACATCTTCGACTTCGTGGTAGTCATCTCTCC 4788
Qy 1669 IleMetGlyIleThrLeuGluGluIleGluValAlaAsnAlaSerLeuProIleAsnProThr 1688
Db 4789 ATTTGGGAATGTCTTGGCAGATATA-----ATTGAGAAATACTTTGTTTCCCAACC 4842
Qy 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708
Db 4843 CTATTCCGAGTCAATCGATTGGCCCGTATTGGCGCATCTTGGCTGTGATCAAAAGCGCC 4902
Qy 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
Db 4903 AAAGGATTCGATCCCTGCTCTTGCCTTAATGATGCTTGCCTGCTCTGCTTCAACATC 4962
Qy 1729 GlyLeuLeuPheMetLeuLeuPheIlePheAlaLeuGlyValGluLeuPheGly 1748
Db 4963 GGCTTCTGCTCTTCTGTCATGTTCACTTCTTCCATTTTGGGATGTCATTTTGA 5022
Qy 1749 AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg 1768
Db 5023 TATGTGAAGCACAG-----GCTGGTATCGATGACATGTTCAACTTTTGAG 5067
Qy 1769 AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrClyAspAsnTrpAsnGly 1788
Db 5068 ACATTTGGCAACAGCATGATGCTGCTGTTTCAAAATCACAACCTCAGCTGCTGGGATGC 5127
Qy 1789 IleMetLysAspThrLeuArg-----AspCys-----AspGlnGlu----- 1800
Db 5128 CTGCTGCTCCCATCTTAACCGCCCTGACTGAGCTAGTAGAAGAACACCCAGGG 5187
Qy 1801 -----SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPhe 1816
Db 5188 AGTGGCTTTAAGGGAGATTGTGGAAACCCCTCAGTGGGCATCTTCTTCTTTGTAAGCTAC 5247
Qy 1817 ValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeu 1836
Db 5248 ATCATCATCTCTTCTTAATTCGTGAACATGTACATTCGCCATCATCTCTGGAGAACTTC 5307
Qy 1837 GluGluSerAsnLysGluAlaLysGlu-----GluAlaGluLeuGluAlaGluLeu 1853
Db 5308 AGTGTAGCCACAGAGAAAGTCCAGACCCCTCTGAGTGAGATGACTTTGAGACCTTCTAT 5367
Qy 1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873
Db 5368 GAG-----ATC 5373
Qy 1874 TrpProGlyValGluGluProAspSerProAspSerProLysProGlyAlaLeuHisPro 1893
Db 5374 TGGGAGAAAGTTCCGAC---CCCGATGCCACCCAGTTCATTGAGTACTGTAAAGTGGCAGAC 5430
Qy 1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913
Db 5431 TTTGAGATGCTC-----TTGGAGATCTCTCCGAGTGGCCCAAG 5469
Qy 1914 ProThr-----GluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSer 1931
Db 5470 CCAATACCATTTGAGCTCATCGCTATGGATCTGCCAATGGTG-----AGCGG---GAT 5520
Qy 1932 ArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGly 1951
Db 5521 CGCATCCACTGTCTTG-----GACATCCT-TTTTGCCTTCCACCAAGCG-----GGT 5564

Db 1363 CTTTGTGGGTTCTTTCTATCTGGTGAACCTGATCTGGCTGTGGTGGCCATGGCTTATGA 1422
Qy 399 -----SerGluThrLysGlnArgGluSerGlnLeuMe 409
Db 1423 AGAACAAGAAATCAGCAACACTGGAGGAGGAGCAAAAGAGGCTGAATTTAAAGCAAT 1482
Qy 409 tArgGluGlnArgValArgPheLeuSerAenAlaSerThrLeuAlaSerPheSerGluPr 429
Db 1483 GTTGGAGCAACTTAAGAAGCAACAGGAGAGGACAGGCTGCTCGATGGCCACTTCAGC 1542
Qy 429 oGlySerCysTyGluGluLeuLeuLysTyLeuValTyIleLeuArgIysAlaAlaA 449
Db 1543 AGAAGCTCTCAGAGATGCCATAGAG----- 1570
Qy 449 gArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAl 469
Db 1571 -----GAAGAAGGTGAAGAAGGAGGGGGCTC 1596
Qy 469 aProLeuGlyGlyGlnGluThrGlnProSerSerCysSerArgSerHisArgArgLe 489
Db 1597 CCCTCGGAGCTCTTCTGAAATCTCTAAACTCAGCTCAAGAGTGCAAGAGGAAAGAGCT-- 1654
Qy 489 uSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHis 509
Db 1654 ----- 1654
Qy 509 nGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySe 529
Db 1655 ----AACAGGAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1710
Qy 529 r-ArgArgLeuMetLeuProProProSerThrProAlaLeuSerGlyAlaProProGly- 548
Db 1711 TCCCGAGAGAGGTGTTAAAGTCAGAGTCAGAGATGGCATGAGAAGGAGGAGGAGGAGGAG 1770
Qy 549 -----GlyAlaGluSerValHisSerPheTyHisAlaAspCysHisL 563
Db 1771 GCAGACAACAGAAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1824
Qy 563 euGluProValArgCysGlnAlaPro-----ProProArgSerProSerGluAlaSerG 581
Db 1825 CATCCAGGCTCGCCCTCTCTCTCCGCCACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1884
Qy 581 lyArgThrValGlySerGlyLysValTyProThrValHisThrSerProProProGluTr 601
Db 1885 GGCAGCTGGCGGCTCCGAGACCCGGCTCCGAGATGAGTTCC-----C 1929
Qy 601 hrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThrs 621
Db 1930 GGATGACGACAGCAGCAGCGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1982
Qy 621 erLeuAsnIleProProGlyProTyxSerSerMethHisLysLeuLeuGluThrGlnSerT 641
Db 1983 -----TCATCCCATCCGGGCGCCGAGCGCC-----GGAGCAGCTA 2019
Qy 641 hrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGlyA 661
Db 2020 CAGCGGCTACAGCGGCTACAGCCAGGCGAGCGGCTCT-----CGCGCATCTTCCCGCAG 2073
Qy 661 laCysGlyPro-----AspSerCysProTyCysAlaArgA 673
Db 2074 CTTGCGGCGGCGGCTGAAGGCGCAACGACGCGTGAGCTGCAACGGCGGTGGTCTCCCTCAT 2133
Qy 673 laGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla- 692
Db 2134 CGCGCGCGCGGCTCC-CACATCGCGGCGGTCTCTCGCAGAGGCTACAACTGAGGTGG 2192
Qy 693 -----ValTyGluPheThrGlnAspAlaGlnHis- 702
Db 2193 AAATTAAGAAGAAAGCCCTGGATCTCTTTAGTTTCCATGGACCAATAGCCCTCTCAGC 2252
Qy 703 -----SerAspLeuArgAspProH 709
Db 2253 GCGGGAAGGACAGAAATCAACAGTATAATAGTGTTGTTTACAATAACACTAGTAGAAGAAC 2312

Qy 709 isSerArgArgGlnArgSerLeuGlyPro----- 718
Db 2313 TGGAAAGAGTCTCAGAGAAAGTGCCTCCATGCTGGTATAAATTTGCCAACACTTTCTCCTCA 2372
Qy 719 -----AspAlaGluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheA 737
Db 2373 TCTGGAGAGTGCACCC-----TACTGGATAAAACTGAAGAGATTGTGA 2417
Qy 737 rGlyLysIleValAspSerLysTyPheGlyArgGlyIleMetIleAlaIleValAsnT 757
Db 2418 ACTGTAGTATTGACCCCTTTTGTGGATTAGCCATCACCATCTGCATCGTCTCTGAATA 2477
Qy 757 hrLeuSerMetGlyIleGluTyHisGluGlnProGluLeuLeuThrAsnAlaLeuGluI 777
Db 2478 CACTGTTTATGGCAATGGAGCACCATCTATGACACACCAATTTGAACATGTCTTGCGTG 2537
Qy 777 leSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValT 797
Db 2538 TAGGAAATCTGGTTTTTCACTGGAAATTTTACAGCGGAAATGTTCTTGAAGCTCATAGCCA 2597
Qy 797 yrGlyProPheGlyTyIleLysAsnProTyAsnIlePheAspGlyValIleValI 817
Db 2598 TGGATCCCTACTATTATTTCCAAAGAGGTGGAAACATTTTGGCGATTATTGTCTCCC 2657
Qy 817 leSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheA 837
Db 2658 TCAGTTTAAATGGAACACTGAGTGTAGCAGACGTGGAGGGCTTTTCAGTGCTCGCATCTTCC 2717
Qy 837 rGluMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValV 857
Db 2718 GATTGTCCGAGTCTTCAAAATTTGGCCAAATCTCTGGCCACCCTGAACATGCTAAAGA 2777
Qy 857 alLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheTrleP 877
Db 2778 TTATGGAAATTCAGTGGGTGGCTGGGCAACCTGACACTGGTGCTGGCCATATTGTCT 2837
Qy 877 heIlePheSerIleLeuGlyMetHisLeuPheGly-----CysL 890
Db 2838 TCATCTTTCCCGTGGTGGGATGATCACTCTTTGGAAAAAGCTACAAAGAGTGCTGTGCA 2897
Qy 890 yPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuL 910
Db 2898 AGATCAACACGAGCATGTGAA-----CTCCCT---CGCTGCATATGTCATGACTTTT 2945
Qy 910 euTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuT 930
Db 2946 TCATTTCTCTCTCATTGTTCTTCGAGTGTGTGGCGGAG---TGGATTGACCATGT 3002
Qy 930 yrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyPheIleAlaLeuMetT 949
Db 3003 GGGACTGTCATGGAAGTGGCAGGCCAGGCCATGTGCTCCTATTGCTTTATGATGGTCATGG 3062
Qy 949 hrPheGlyAsnTyValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 969
Db 3063 TGATTGGCAACTTGGTGGTGTGCAACCTGTTTGGCCCTTGTCTCTGAGCTCCTCAGTG 3122
Qy 969 laGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProV 989
Db 3123 CAGACAACTGGCTGCCACAGATGAC---GATGGGGAATGAACAACTCCAGATCTCAG 3179
Qy 989 alAspSerGlnGlyGlyAspAlaAlaAsnLysSerGluSerGluProAspPhePheSerProS 1009
Db 3180 TGATCCGT----- 3187
Qy 1009 erLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHis- 1028
Db 3188 -----ATCAAGAGGGTGTGGCTTGGACCAAACTAAAAGGTGCACG 3227
Qy 1029 ProGluLeuArgLysSerLeuLeuProProLeuIleIle----- 1041
Db 3228 CCTTCATGACGCGCCCACTTTAAGCAGCGTGTAGGCTGTATGAGGTGAAGCCCTCTGGATGAGT 3287

QY 1042 -----HisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGly 1057
Db TGTATGAAAGAGGCAACTGTATGCCAATCACA---CCAGTGCAGACATCCACCGGA 3344
QY 1058 LeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluPro 1077
Db ATG-----GTGACTCCAGAGAAGATGGCA-----ATGGCACAACCA 3380
QY 1078 GlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrp 1097
Db CGCGCA----- 3386
QY 1098 SerAlaAlaSerSerTrp-----ThrSerArgArgSerSerArgAsnSerLeuGlyArg 1115
Db ---TTGCGACAGCGTGGAGAGTACATCATT-GATGAGGACCACATGCTCTTCATCAAC 3442
QY 1116 AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu 1135
Db AACCCTCAACTGACTGTACCGGTACCC-----ATTGCTGTGGCGGAG 3484
QY 1136 GlyGln---GluSerGlnAspGluGluLysSerSerGluGluGluAlaSerProAla 1154
Db TCTGACTTTGAGAACTCAACACAGAGAGTGTAGCAGCGAG-----TCGGATCCTGAA 3538
QY 1155 GlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeu 1174
Db GGCAGCAAAAGATAAATACTAGATGACACAGCTCTCTCGAAGGA---AGCACCATGATATC 3595
QY 1175 ---ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAla 1193
Db AAACCAAGATGAGAGAGTCCCT----- 3619
QY 1194 SerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArg 1213
Db GTGAA 3625
QY 1214 ProAspAspProProLeuAspGlyAspAspAlaAspAspGluGly----- 1228
Db CAGCCTGAGGAATACTTGGATCCAGATGCCTGCTTCACAGAGGTGTGTCCAGCGGTTTC 3685
QY 1229 -----AsnLeuSerLysGlyGluArgValArgAlaAlaTrpIleArgAlaArg 1243
Db AAGTGCTGCCAGGTCAACATCGAGAAGGGCTAGCAGAGCTTGGTGGATC----- 3736
QY 1244 LeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProProGlnSer 1263
Db 3736 ----- 3736
QY 1264 ArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeu 1283
Db ---CTGGCGAAACCTGCTCTCATCGTGAGCACAACCTGGTTTGAGACCTTCATCATC 3793
QY 1284 ValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHis 1303
Db TTCATGATCTCGTAGAGCGGGCCCTGCGCTCGAGGACATCTACATTTGACAGAGA 3853
QY 1304 SerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAla 1323
Db AAGACCATCCGACCATCTCGAATATGCTGACAAAGTCTTCACCTATATCTTCATCTG 3913
QY 1324 GluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArg 1343
Db GAGATGTTGCTCAAGTGACAGCCTATGCGCTTCGTC-----AAGTTCTTCACC 3961
QY 1344 SerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleVal 1363
Db AATGCTGCTGTGGCTGGACTTCTCATTTGCTGCTGCTCTTTAGTCAGCCTTATAGCT 4021
QY 1364 SerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeu 1383
Db AATGCCCTG-----GGCTACTCGGAACCTAGGTGCCATAAAGTCCCTTAGGACCCTA 4072
QY 1384 ArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlu 1403

Db AGAGCTTTGAGACCCCTTAAGACCTTATCACCATTTCAGAGGATGAGGGTGGTGAAT 4132
QY ThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePhe 1423
Db GCCTTGGTGGGCGCATCCCTCCATCATGAATGTGCTGCTGTGCTCATCTTCTGG 4192
QY IleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGly 1443
Db CTGATTTTCAGCATCATGGAGTTAACTTGTTCGGGAAGTACCACCTACTGCTTTAAT 4252
QY Glu-----AspThrArgAsnIleThrAsnLysSerCysAlaGlu 1457
Db GAGACTTCTGAAATCCGATTTGAAATGGAAGTGTCAACAATAAACTGAAATGTAAG 4312
QY 1458 -----AlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsn 1471
Db CTTATCGAGGGGAAACAATACAGAGATCAGATGGAAGACGTGAAGATCAACTTTGACAAT 4372
QY 1472 LeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIle 1491
Db GTTGGGCGAGGATACCTGGCCCTTCTCAAGTAGCAACCTTCAAAGCTGGATGGACATC 4432
QY 1492 MetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPro 1511
Db ATGTATGCACTGTAGATTCCCGGAAGCCTGATGAGACCTTAAGTATGAGGACAATATC 4492
QY 1512 TrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPheValLeuAsnMet 1531
Db TACATGTACATCTATTTGTCTCATCTTCGGCTCTCTTTCACCTGGAACCTG 4552
QY 1532 PheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGlu 1551
Db TTCAATGGTGTCACTATTGATAACTCAATCAAAAGAAAAAGTTCCGAGGTCCAGAC 4612
QY 1552 AlaArgArgArgGluGlu-----LysArgLeuArgLeuGluLysLysArgLys 1569
Db ATCTTCATGACCCAGACAGACAGAGAGTACTACAATGCCATGAAAAAGCTGGGTCAAAG 4672
QY 1570 AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeu 1589
Db AAGCCACAGAAACCCATTTCCCGCCCTTGAACAAAAATCCCAAGAAATCGCTTTGATTTT 4732
QY 1590 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609
Db GTCACTCAGCAAGCCTTTGACATTTGATGCTCATCTGCTTACCTTTACATGCTGACA 4792
QY 1610 MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629
Db ATGATGCTGGAGACAGACACTCAAAGCAAGCAGATGGAGAACATCTCTACTGGATTAAAC 4852
QY 1630 TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe 1649
Db CTGCTGTTTGTATCTTCTTCCCTGTGAGTGTGCTCAAAATG-----TTTGCCTG 4906
QY 1650 ArgArg---PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSer 1668
Db AGGCATCTACTTTCACCATTTGGCTGGAAACATCTTCGACTTCGTGGTAGTACTCTCTCC 4966
QY 1669 IleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThr 1688
Db ATTGTGGGAATGTTCTTGGCGCATCTTGGCGCATCTTGGCTGCTGATCAAGAGGCC 5020
QY 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708
Db CTAATCCGAGTCATCCGATTTGGCGCATCTTGGCGCATCTTGGCTGCTGATCAAGAGGCC 5080
QY 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
Db AAAGGGATTCGTACCTTCTTGGCTTAAATGATGCTTCTTGGCTGCTGCTTCAACATC 5140
QY 1729 GlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValGluLeuPhe 1749

Db 2658 TCAGTTTAAAGAACTGAGTCTAGCAGACGTGGAGGGGCTTTAGTCTGCGAFTTTTCC 2717
Qy 837 rglLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValV 857
Db 2718 GATTGCTCCGAGTCTTCAATTGGCCAAATCTCGCCACCTCGAAACATGCTAATCAAGA 2777
Qy 857 alLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIleP 877
Db 2778 TTATTGGAAATTACGTGGGTGCCCTGGGCAACCTGACACTGGTCTGGCCATTTATGCT 2837
Qy 877 heilePheSerIleLeuGlyMetHisLeuPheGly-----CysL 890
Db 2838 TCATCTTTGGCGTGGGTGGGATGCAACTTTTGGAAAAGCTACAAAGAGTGTCTGCA 2897
Qy 890 ysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuL 910
Db 2898 AGATCAACCAAGACTGTGAA-----CTCCCT---CGCTGCATATGCATCACTTTT 2945
Qy 910 euTrpAlaIleValThrPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuT 930
Db 2946 TCCATTCTCTCTCATTTGCTCTTCGAGTGTGTGGGGAG---TGGATTGAGACCATGT 3002
Qy 930 yrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 949
Db 3003 GGGATCGCATGGAAGTGGCAGCGCCAGCCATGTCCCTCATTTGTTATGATGTCATGG 3062
Qy 949 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 969
Db 3063 TGATTGGCAACTGGTGTGCTGAACCTGTTCGCTTCTGGCTTCTCTGAGCTCTTCAGTG 3122
Qy 969 laGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProv 989
Db 3123 CAGACAACCTGGCTGCCACAGATGAC---GATGGGGAATGACAACCTCCAGATCTCAG 3179
Qy 989 alAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPheSerProS 1009
Db 3180 TGATCCGT----- 3187
Qy 1009 erLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHis- 1028
Db 3188 -----ATCAGAAAGGTGTGGCTCGAGGTGATGAGGTGAAGCTCTCGATGAGT 3227
Qy 1029 ProGluLeuArgLysSerLeuLeuProLeuIleIle----- 1041
Db 3228 CCTTCATGCAGCCCACTTTTAAGCAGTGTGAGGTGATGAGGTGAAGCTCTCGATGAGT 3287
Qy 1042 -----HisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGly 1057
Db 3288 TGTATGAAAAGAGCCCAACTGTATCGCCAAATCACA---CGGTGCGACACATCCACCGGA 3344
Qy 1058 LeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluPro 1077
Db 3345 ATG-----GTGACTTCCAGAAAGATGGCA-----ATGGCAACCA 3380
Qy 1078 GlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrp 1097
Db 3381 GCGGCA----- 3386
Qy 1098 SerAlaAlaSerSerTrp-----ThrSerArgArgSerSerArgAsnSerLeuGlyArg 1115
Db 3387 ---TTGGCAGCAGCGGTGGGAAGTACATCATTT-GATGAGGACCACATGCTCTTCATCAAC 3442
Qy 1116 AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu 1135
Db 3443 AACCCCAACTTGACTGTACGGGTATCCC-----ATTGCTGTGGCGAG 3484
Qy 1136 GlyGln---GluSerGlnAspGluGluSerSerGluGluGluArgAlaSerProAla 1154
Db 3485 TCTGACTTTGAGAACTCAACACAGAGGATGTAGACCGAG-----TCGGATCCTGAA 3538
Qy 1155 GlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeu 1174
Db 3539 GGCAGCAAGATAAACTAGATGACACCACTGCTCTGAAGGA---AGCACCATTGATATC 3595

Qy 1175 ---ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAla 1193
Db 3596 AAACACAGAACTAGAGAGGTCCCT----- 3619
Qy 1194 SerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArg 1213
Db 3620 -----GTGAA 3625
Qy 1214 ProAspAspProProLeuAspGlyAspAlaAspAspGluGly----- 1228
Db 3626 CAGCTGAGGAATACTTGGATCCAGATGCTGCTTTCACAGAGGTTGTGTCCACGGGTTTC 3685
Qy 1229 -----AsnLeuSerLysGlyGluArgValArgAlaIlePheIleArgAlaArg 1243
Db 3686 AAGTGTGTCAGGTCACATCGAGGAAGGCTAGGCAAGTCTTGGTGGATC----- 3736
Qy 1244 LeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePheProGlnSer 1263
Db 3736 ----- 3736
Qy 1264 ArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeu 1283
Db 3737 ---CTGCGGAAAACCTCTCTCTCATCTCGAGGACACAACTGGTTTGAGACCTTCATCATC 3793
Qy 1284 ValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHis 1303
Db 3794 TTCATGATTCTGCTGACAGCTGGCGCCCTCGAGGACATCTACATTGAGCAGAGA 3853
Qy 1304 SerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAla 1323
Db 3854 AAGACCATCGCACCATCTCGAATATGCTGACAAAGTCTTCACCTATATCTTCATCCTG 3913
Qy 1324 GluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArg 1343
Db 3914 GAGATGTGCTCAAGTGGACAGCCTATGGCTTCTGTC-----AAGTCTTCACC 3961
Qy 1344 SerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuVal 1363
Db 3962 AATGCTGTGTGTGGCTGGACTTCTCATTTGTGCTGTCTTCTTAGTCAGCCTTATAGCT 4021
Qy 1364 SerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeu 1383
Db 4022 AATGCCCTG-----GGCTACTCGGAACCTAGGTGCCATAAAAGTCCCTTAGGACCCCTA 4072
Qy 1384 ArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlu 1403
Db 4073 AGAGCTTTGAGACCTTAAGAGCCCTTATCAGATTGAAGGATGAGGTTGGTGAAT 4132
Qy 1404 ThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePhe 1423
Db 4133 GCCTTGTGGGCGCCATCCCTCCATCATGAATGTGCTGTGTGTGTCTCATCTCTTCG 4192
Qy 1424 IleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGly 1443
Db 4193 CTGATTTTTCAGCATCATGGGAGTTAACTTTGTCGGGAAAGTAGTACCCTACTGCTTTAAT 4252
Qy 1444 Glu-----AspThrArgAsnIleThrAsnLysSerAspCysAlaGlu 1457
Db 4253 GAGACTTCTGAAATCCGATTTGAAATGAAGATGTCAACATAAACTGAATGTGAAAG 4312
Qy 1458 -----AlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsn 1471
Db 4313 CTTATGAGGGGAACAATACAGAGATCAGATGGAAGAACGCTGAAGATCACTTTGACAAT 4372
Qy 1472 LeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIle 1491
Db 4373 GTTGGGCGAGGATACCTGGCCCTTCTTCAAGTAGCAACCTTCAAAAGGCTGATGACATC 4432
Qy 1492 MetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPro 1511
Db 4433 ATGTATGACGCTGTAGATATCCCGGAAGCCTGATGAGCAGCCTTAAGTATGAGGACATATC 4492

Qy	1512	TrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMet	1531
Db	4493	TACATGTACATCTATTATTGTCATCTTTCATCATCTTCGGTGCTCTTCTTCAACCTGAACCTG	4552
Qy	1532	PheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluGlu	1551
Db	4553	TTCAATTGGTGTCATCATTTGATAATCTTCAATCAACAAAAGAAAAGTTCGGAGGTCCAGGAC	4612
Qy	1552	AlaArgArgArgGluGlu-----LysArgLeuArgLeuGluGluLysLysArgArgLys	1569
Db	4613	ATCTTCATGACCAAGAACAGAGAGAGTACTCAATGCATGAAAAGCTGGCGCTCAAG	4672
Qy	1570	AlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeu	1589
Db	4673	AAGCCACAGAAACCCATTCCCGCCCTTGAAACAAAATCCAAGGAATCGTCTTTGATT	4732
Qy	1590	CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr	1609
Db	4733	GTCACTCAGCAAGCCTTTGACATTGTATTATCATGATGCTCATCTGCTTAACTATGTTGACA	4792
Qy	1610	MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn	1629
Db	4793	ATTGATGTGAGACAGACACTCAAGCAAGCAGCATGGAGACAATCTCTACTGGATTAA	4852
Qy	1630	TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe	1649
Db	4853	CTGGTGTTGTTATCTTCTTTCACCTGTGAGTGTGTCTCAAAATG-----TTTGC	4906
Qy	1650	ArgArg---PhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuSer	1668
Db	4907	AGGCACCTACTACTTACCAATTTGCTGGAACATCTTCGACTTCGTGTAGTACTCTCTC	4966
Qy	1669	IleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThr	1688
Db	4967	ATTGTGGGAATGTTCTCGGCAGATATA-----ATTGAGAAATACTTGTGTTCCCA	5020
Qy	1689	IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAla	1708
Db	5021	CTATTCCGAGTCATCCGATTGGCCGCTATTATGGGCGCATCTTGGCTGTGATCAAA	5080
Qy	1709	ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu	1728
Db	5081	AAAGGGATTGCTACCCCTGCTTTTGCCCTTAATGATGTCTTGCTGCTGCCCTGTTC	5140
Qy	1729	GlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGly	1748
Db	5141	GGCCTTCTGCTTCTCCGGTCATGTTCACTCTCCATTTTGGGATGTCCTCAATTGCA	5200
Qy	1749	AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg	1768
Db	5201	TATGTGAAGCACGAG-----GCTGGTATCGATCAGATGTTCAACTTTTGAG	5245
Qy	1769	AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGly	1788
Db	5246	ACATTTGGCAACAGCATGATCTGCTCTTTCAAATCACAACTCAGCTGGTGGGATGGC	5305
Qy	1789	IleMetLysAspThrLeuArg-----AspCys-----AspGlnGlu-----	1800
Db	5306	CTGCTGTGCCCATCTTAAACCGCCCCCTGACTGCAGCCTAGATAGGAACACCCAGGG	5365
Qy	1801	-----SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPhe	1816
Db	5366	AGTGGCTTTAAGGAGATTGTGGAAACCCCTCAGTGGGCATCTTCTTTGTAAGCTAC	5425
Qy	1817	ValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeu	1836
Db	5426	ATCATCATCTCTTTTCCCTAAATTTGCTGAACATGTACATTGCCATCATCTCTGGAGA	5485
Qy	1837	GluGluSerAsnLysGluAlaLysGlu-----GluAlaGluLeuGluAlaGluLeu	1853
Db	5486	AGTGTAGCCACAGGAAGTGGACCCCTCTGAGTGAGGATGATCTTTGAGACCTCTAT	5545
Qy	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873

Db	5546	 GAG-----	5551	 -----ATC
Qy	1874	TtrProGlyValGluGlyProAspSerProLysProGlyAlaLeuHisPro	1893	 -----
Db	5552	TGGAGAGTTGCAC---CCCGATGCCACCGACTTCATTGAGTACTGTAGCTGGCAGAC	5608	 -----
Qy	1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis	1913	 -----
Db	5609	TTTGCAGATGCC-----TTGAGCATCCTCTCCGAGTGCACAAG	5647	 -----
Qy	1914	ProThr-----GluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSer	1931	 -----
Db	5648	CCAAATACCAATCAGCTCATCGCTATGGATCTGCCAAATGGTG-----ACCGGG---	5698	 -----GAT
Qy	1932	ArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGly	1951	 -----
Db	5699	CGCATCCACTGCTTG-----GACATCCT-TTTTGCTTCCACCAAGCG-----GGT	5742	 -----
Qy	1952	ProLeuGlyHisArgGlyTrrPglyLeuProLysAlaGlnSerGlySerValLeuSerVal	1971	 -----
Db	5743	CCTGGGAGATAGCGGGAGTTGGACATCCTCGCGCAGACAGATGGAAGAGCGGTTC--GTG	5800	 -----
Qy	1972	HisSerGlnProAlaaspThrSerTyrIleLeuGlnLeuProLysaspAlaProHisLeu	1991	 -----
Db	5801	GCATCCAAATCCTTCCAAAGTGCTTAC-----	5827	 -----
Qy	1992	LeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArg	2011	 -----
Db	5828	-----GAGCCAATCACACACACTGCGTCGCAAGCAGGAGGAGGTATCT	5872	 -----
Qy	2012	SerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArg-----	2026	 -----
Db	5873	GCAGTGGTCTCGACGCTGCTACTCCGGGGACATTTGGCAAGCGGGGCTTCATCTGCAAA	5932	 -----
Qy	2027	---ThrAspSerLeuaspValGlnGlyLeuGlySerArgGluaspLeuAlaGluVal	2045	 -----
Db	5933	AAGACAACCTTCTAATAAGCTGGAGATGGAGGGCACACCCGGGAG-----AAAAAAGAG	5986	 -----
Qy	2046	SerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGln	2065	 -----
Db	5987	AGCACCCCATCTACAGCCTCCCTCCGTCCTATCACAGTGTAACTAAACCTGAAAGAGG	6046	 -----
Qy	2066	AlaGlnGlnHisSer-----ArgSerHisSerLysIleSerLysHisMet	2080	 -----
Db	6047	AAACAGACGGCGGACAGAGGAGGAAGGAAGGAAAGCCTAAACACAAAAAGAGGCT	6103	 -----

Search completed: July 10, 2006, 20:42:20
Job time : 780.108 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 10, 2006, 06:41:34 ; Search time 807.259 Seconds
(without alignments)
7878.383 Million cell updates/sec

Title: US-09-611-257A-37

Perfect score: 11904

Sequence: 1 MDEEDGAGAEAGSQPRSPM.....PKXDVLSGLSLSDPADLDP 2266

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Fgapop 10.0 , Fgapext 0.5

Dgapop 6.0 , Dgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09611257/runat_10072006_064119_6880/app_query.fasta_1
-DB=issued Patents NA -QMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs804 -USER=US09611257 @CGN 1 1140 @runat_10072006_064119_6880
-NCPU=6 -ICPU=3 -NO_WMAP -NEG_SCORES=0 -WAIT -DEPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*

1: /EMC_Celerra_SIDS3/ptodata/2/ina/1/COMB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5/COMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A/COMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B/COMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7/COMB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H/COMB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS.COMB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP.COMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE.COMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	11877.5	99.8	6822	3	US-09-426-998-3 Sequence 3, Appli
2	11877.5	99.8	7741	3	US-09-426-998-4 Sequence 4, Appli
3	11241	94.4	7405	3	US-09-949-016-3859 Sequence 3859, Ap
4	6315.5	53.1	2993	3	US-09-398-522-51 Sequence 51, Appl
5	6214.5	52.2	7898	3	US-08-984-709A-49 Sequence 49, Appl
6	5492.5	46.1	6816	3	US-09-404-650-1 Sequence 1, Appli
7	5492.5	46.1	6816	3	US-09-935-541-1 Sequence 1, Appli
8	5492.5	46.1	6816	3	US-10-425-800-1 Sequence 1, Appli

9	5484	46.1	6855	3	US-09-404-650-3 Sequence 3, Appli
10	5484	46.1	6855	3	US-09-935-541-3 Sequence 3, Appli
11	5484	46.1	6855	3	US-10-425-800-3 Sequence 3, Appli
12	5418.5	45.5	6503	3	US-09-404-650-12 Sequence 12, Appl
13	5418.5	45.5	6503	3	US-09-935-541-12 Sequence 12, Appl
14	5418.5	45.5	6503	3	US-10-425-800-12 Sequence 12, Appl
15	2237	18.8	70308	3	US-09-949-016-15601 Sequence 15601, A
16	1971.5	16.6	1669	3	US-08-984-709A-51 Sequence 51, Appl
17	1786.5	15.0	7376	5	US-09-268-163-3 Sequence 3, Appli
18	1786.5	15.0	7376	5	US-10-033-026-3 Sequence 3, Appli
19	1784.5	15.0	7362	2	US-08-455-543A-7 Sequence 7, Appli
20	1784.5	15.0	7362	2	US-08-193-078B-7 Sequence 7, Appli
21	1784.5	15.0	7362	2	US-08-223-305C-7 Sequence 7, Appli
22	1784.5	15.0	7362	2	US-08-149-097D-7 Sequence 7, Appli
23	1784.5	15.0	7362	2	US-08-949-386-7 Sequence 7, Appli
24	1784.5	15.0	7362	3	US-08-450-562-7 Sequence 7, Appli
25	1784.5	15.0	7362	3	US-08-984-709A-7 Sequence 7, Appli
26	1784.5	15.0	7362	3	US-08-450-272-7 Sequence 7, Appli
27	1784.5	15.0	7362	3	US-08-450-273-7 Sequence 7, Appli
28	1784	15.0	7266	3	US-08-713-118-1 Sequence 1, Appli
29	1784	15.0	7266	3	US-09-452-007-1 Sequence 1, Appli
30	1782.5	15.0	7364	3	US-09-268-163-5 Sequence 5, Appli
31	1782.5	15.0	7364	5	US-10-033-026-5 Sequence 5, Appli
32	1778	14.9	7175	2	US-08-455-543A-8 Sequence 8, Appli
33	1778	14.9	7175	2	US-08-193-078B-8 Sequence 8, Appli
34	1778	14.9	7175	2	US-08-223-305C-8 Sequence 8, Appli
35	1778	14.9	7175	2	US-08-149-097D-8 Sequence 8, Appli
36	1778	14.9	7175	3	US-08-949-386-8 Sequence 8, Appli
37	1778	14.9	7175	3	US-08-450-562-8 Sequence 8, Appli
38	1778	14.9	7175	3	US-08-984-709A-8 Sequence 8, Appli
39	1778	14.9	7175	3	US-08-450-272-8 Sequence 8, Appli
40	1778	14.9	7175	3	US-08-450-273-8 Sequence 8, Appli
41	1776	14.9	7177	3	US-09-268-163-7 Sequence 7, Appli
42	1776	14.9	7177	5	US-10-033-026-7 Sequence 7, Appli
43	1728.5	14.5	7011	3	US-09-268-163-9 Sequence 9, Appli
44	1728.5	14.5	7011	5	US-10-033-026-9 Sequence 9, Appli
45	1711.5	14.4	5975	2	US-08-404-354B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3

Alignment Scores:
Pred. No.: 0
Score: 11877.50
Percent Similarity: 99.6%
Best Local Similarity: 99.6%
Query Match: 99.8%
DB: 3
Length: 6822
Matches: 2264
Conservative: 1
Mismatch: 1
Indels: 7
Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-426-998-3 (1-6822)

Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGGACGAGGAGGATGAGCGGGCCCGGAGGATCGGACACGCCCGGAGCTTCATG 60
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CGGCTCAACGACCTGTGCGGGGCGGGGCGGGCGGGGCGGGGTGACGAGAAAAGGAC 120
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGACAGCGGACTCCGAGCGGAGGGGTGCGCTACCGGGGCGTGGCCCGGTGGTT 180
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuAsnThrValCysAsn 80
Db 181 TTCCTTCTACTTGAGCCAGACAGCGCGCGGGAGCTGGTGCTCCGCACCGGTCTGTAAAC 240
Qy 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCCTGGTTTGAGCGCATCAGCATGTGTGTCATCTTCTCAACTGGTGACCCCTGGGCATG 300
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCGGCCATGCGAGCATCGCTGTGACTCCACAGCGCTGCGGATCCTGACGAGCCCTT 360
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTTCATCTTTGGCTTCTTCCCGTGAGATGGTGGTGAAGATGGTGGCCCTTGGGC 420
Qy 141 IlePheGlyLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160
Db 421 ATCTTTGGGAAAAAGTGTACTCTGGAGACACTTGGAACCGGCTTGACTTTTCATCGTC 480
Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATCGAGGGATGCTGGAGTACTCGTGACCTGCAGACAGTGCAGCTTCTCAGCTGTCAAG 540
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTCTCGACCGCTCAGGGCCATTAAACCGGGTGCCGAGATGCGCATCTCTT 600
Qy 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTACAGTTGCTGCTGGATACGCTGCCATGCTGGGCAACGCTCTGCTGCTTCTTCTTC 660
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTCTTCATCTTCGGCATCTCGGGCTCCAGCTGTGGGCAGGCTGCTTCGGAACCGA 720
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCTCACTACCTGAGAAATTCAGCTCTCCCTCGAGCGTGAGCTTGAGCGCTATTACCAG 780
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGAACAGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGACGGCATGCGG 840
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTCGAGAAGCTGCCACGCTGCGGGGAGCGGGGCGGTGGCCACCTTGGCGTCTG 900
Qy 301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGCGCTACAAACAGCTCCAGAACACCACTGTGTCAACTGGAACCACTACTAC 960
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyValaIleAsnPheAspAsnIle 340
Db 961 ACCAACTGCTCAGCGGGGAGGACAAACCCCTTCAGAGGGGCCCATCACTTTGACCAACTT 1020
Qy 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
Db 1021 GGCTATGCTGGATCGCCATCTTCCAGGTTCATCAGCTGGAGGGCTGGGTTCGACATCATG 1080

Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1081 TACTTTGTGATGATGCTCATTTCTTCTACAAATTCATCTACTTTCATCTCTCATCATC 1140
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGCTCTCTTCTCATGATCAACCTGTGCTGGTGTGATTCGACGACAGTTCTCTCAGAG 1200
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAGCAGCGGAAAGCCAGCTGATCGGAGCAGCGTGTGCGGTTCCTGTCCACGCC 1260
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1261 AGCACCTTGGCTAGCTTCTGTAGCCCGCAGCTGTATGAGGAGTGTCTCAAGTACCTG 1320
Qy 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACATCTCTTAAGGAGCAGCCCGCAGGCTGAGTCTCTCGGGCAGCAGGTGTG 1380
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CGGTTGGGCTGTCTCAGAGCCCGCAGCCTCTCGGGGCGCAGGAGACCCAGCCAGCAGC 1440
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHisHisHis 500
Db 1441 AGCTGTCTCTGCTCCACCGCGCTATCGTCCACACCTGGTGACACCCACCACCAC 1500
Qy 501 HisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CATCACCACTTACCCTGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 1560
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1561 ATCCAGGACAGGATGCCAATGGGTCCCGCAGGCTCATGCTGCCACACCTCTCAGCGCT 1620
Qy 541 AlaLeuSerGlyAlaProProGlyValAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1621 GCCCTCTCCGGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 1680
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTAGAGCCAGTCCGCTGCGAGGCGCCCTCCACAGTCCCTCCATCTGAGGCATCC 1740
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
Db 1741 GGCAGGACTGTGGGCGCGGGAAGGTGATCCCACCGTGACACACGAGCCCTCCACCGGAG 1800
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ACGCTGAAGGAGAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGGGCCCCCAACCTCACC 1860
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1861 AGCTTCAACTCCACCCCGGCCCTTACAGCTCCATGTCACAAAGCTGCTTGAGACACAGAGT 1920
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACAGTGTGCTGCAAAAGCTCTTTGAAGATCTCCAGCCCTTGCTTGAAGACAGACAGTGA 1980
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeu 680
Db 1981 GCCTGTGTTCAGACAGCTGCCCTTACTGTGCCCGGGCGGGGACAGGAGGTGGAGCTC 2040
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCGGACCGTGAATGCCCTGACTCAGACAGCAGGAGGAGTTTATGAGTTTCCACAGAGATGCC 2100
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2101 CAGCACGCGACCTCCGGGACCCCCACAGCGCGGGCAACGAGGCTGGGCCACAGATGCA 2160
Qy 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740

Db ||||| 2161 GAGCCAGCTCTGTGCTGGCCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
Qy ||||| 741 AspSerLysTyrPheGlyArgGlyLeuMetIleAlaIleLeuValAenThrLeuSerMet 760
Db ||||| 2221 GACAGCAAGTACTTTGGCCGGGGAATCATGATGCCATCTCTGGTCAACACACTCAGCATG 2280
Qy ||||| 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db ||||| 2281 GGCAATCAATACACAGCAGCAGCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340
Qy ||||| 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPhe 800
Db ||||| 2341 GTCTTCAAGCTCTTTGCCCTGGAGATGCTGTAAGCTGCTTGTATGTGTCCTTT 2400
Qy ||||| 801 GlyTyrIleLysAenProTyrAsnIlePheAspGlyValIleValValIleSerValTyr 820
Db ||||| 2401 GGCTTACATCAAGATCCCTACCAATCTTGTATGGTGTCAATGTGGTCATCAGCGTGTGG 2460
Qy ||||| 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db ||||| 2461 GAGATCGTGGCCACAGCGGGGGCGGCTGTGCGTGTGCGGACCTTCCGCTGATGCGT 2520
Qy ||||| 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db ||||| 2521 GTGCTGAAGCTGTGTGCGCTTCTGCGCGCGCTGCGAGCGGAGCTGTGTGCTCATGAAG 2580
Qy ||||| 861 ThrMetAspAenValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db ||||| 2581 ACCATGACACACGTGGCCACCTCTGCAATGCTGCTTATGCTCTTCATCTTTCATCTT 2640
Qy ||||| 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db ||||| 2641 ATCTTGGCATGCACTCTTCTGGCTGCAAGTTTGCCTCTGAGCGGGATGGGACACCTG 2700
Qy ||||| 901 ProAspArgLysAenPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db ||||| 2701 CCAGACGGGAAGATTGTAATCTGCTTGGGCCATCTGCTCACTGTCTTTCAGATCCTG 2760
Qy ||||| 921 ThrGlnGluAspTrpAenLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla 940
Db ||||| 2761 ACCCAGAGGACTCGAACAAGTCTCTACAAATGGTATGGCTCCACGTCGTCCTGGCG 2820
Qy ||||| 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAenTyrValLeuPheAenLeuVal 960
Db ||||| 2821 GCCCTTATTTATGTCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTGCTGTC 2880
Qy ||||| 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
Db ||||| 2881 GCCATTCTGGTGGAGGCTTCCAGCGAGGAAATCAGCAAAACGGGAAGATGCGAGTGA 2940
Qy ||||| 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAenLysSerGlu 1000
Db ||||| 2941 CAGTTAAGCTGTATTCAGCTGCTGTGCTGATCCAGGGGGAGATGCCAACAAAGTCCGAA 3000
Qy ||||| 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu 1020
Db ||||| 3001 TCAGAGCCCGATTTCTTCTCACCCAGCTGATGCTGATGGGACAGAGAGTGTG 3060
Qy ||||| 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProProLeuIle 1040
Db ||||| 3061 GCCTTGTGTCTCTGGGAGACACCCGAGCTGGGGAAGAGCCTGCTGCCCTCTCATC 3120
Qy ||||| 1041 IleHisThrAlaAlaThrProMetSerLeuProLysThrSerThrGlyLeuGlyGlu 1060
Db ||||| 3121 ATCCACACGGCCGCCACACCATGTGCTGCCAAGACACACAGCGGGCTGGGCGAG 3180
Qy ||||| 1061 AlaLeuGlyProAlaSerArgThrSerSerGlySerAlaGluProGlyAlaAla 1080
Db ||||| 3181 CGCTTGGCCCTTGTGCTGCGCGCGCACCGACAGCGGGTGGCAGAGCTTGGGGCGGCC 3240
Qy ||||| 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
|||

Db ||||| 3241 CACGAGATGAAGTCAACGCCCGCCGCGAGCTCTCCGCACAGCCCTCGAGCGCTGCA 3300
Qy ||||| 1101 SerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db ||||| 3301 AGCAGCTGGACACAGCAGCGCTCCAGCCGGAACAGCTCTCGCCGTGACCCAGCTGAAG 3360
Qy ||||| 1121 ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGluGlyGlnGluSerGln 1140
Db ||||| 3361 CGGAGAAGCCCAAGTGAGAGCGCGCTCTGTGTGCGGAGAAGGCCAGGAGAGCCAG 3420
Qy ||||| 1141 AspGluGlnSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db ||||| 3421 GATCAAGAGAGAGCTCAGAAAGAGGAGCGGCCAGCCCTCGGGCAGTGACCATCGCCAC 3480
Qy ||||| 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db ||||| 3481 AGGGGTCTCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTCAGGTG 3540
Qy ||||| 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db ||||| 3541 CCAGGGTGCATCGCACTGCCAGTGGCGGAGGCTCTGCTTCTGAGCACACGAGCTGCAAT 3600
Qy ||||| 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db ||||| 3601 GGCAAGTCGGCTTCAGGGCGCTGGCCCGGGCCCTGCGGCTGATGACCCCTACTGGAT 3660
Qy ||||| 1221 GlyAspAspAlaAspAspGlyGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db ||||| 3661 GGGATGACGCCGATGACGAGGGCACTGACGAAAGGGGNAACGGGTCCGCGCTGGATC 3720
Qy ||||| 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db ||||| 3721 CGAGCCGACTCTCTGCTGCTCGCTCGAGCGAGACTCTCTGGTCAGCTACATCTTCCCT 3780
Qy ||||| 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db ||||| 3781 CCTCAGTCCAGTTCGCCCTCTCTGTGTACCGGATCATACCCCAAGATGTTTCAGCCAC 3840
Qy ||||| 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db ||||| 3841 GTGTCCTTGTTCATCTCTTCTTAACTGTCATCACCATCGCCATGGAGCGCCCAAAAT 3900
Qy ||||| 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db ||||| 3901 GACCCCCACAGCGCTGAACGCACTCTCTGACCCCTCTCCAATTACATCTTTCACCGCAGTC 3960
Qy ||||| 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
Db ||||| 3961 TTTCTGGCTGAAATGACAGTGAAGGTGTGGCACTGGGCTGGTCTTTCGGGGAGCAGCGC 4020
Qy ||||| 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db ||||| 4021 TACTCGCGAGCAGTTGGAAACGTGTGGAACGGCTGTGGTGTCTCATCTCCGTTCATCGAC 4080
Qy ||||| 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db ||||| 4081 ATTCTGTGTCCATGCTCTCTGACAGCGGCAACCAAGATCTCTGGCATGCTGAGGTGTG 4140
Qy ||||| 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db ||||| 4141 CGGCTGTGCGGACCTTGCCTGCGCTCAGGGTGTATCAGCGGGCGGAGGGCTGAAGCTG 4200
Qy ||||| 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db ||||| 4201 GTGGTGGAGACGTGATGCTCTCTCACTGAACCCCATCGGCAACATTTGTAGTCATCTGCTGT 4260
Qy ||||| 1421 AlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db ||||| 4261 GCCTTCTTTCATCTTTCGGCATCTTGGGGGTGCGAGCTCTTCAAAGGGAAGTTTTCGTG 4320
Qy ||||| 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
Db ||||| 4321 TGCCAGGGCGAGGATACAGGAACATCACCAATAAATCGGACTGTGCGGAGGCCAGTTAC 4380

1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db |||||
4381 CGTGGGFCGCGCAAAAGTAACTTTGACAACTTGGCCAGGCCGCGTATCTCCCTGTTT 4440
Qy |||||
1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
Db |||||
4441 GTTTTGGCTCCAAAGGATGGTTGGTGACATCATGTACGATGGCTGGATGCTGTGGGC 4500
Qy |||||
1501 ValAspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
Db |||||
4501 GTGGACAGCAGCCCATCATGAACACCAACCCCTGGATGCTGTACTTTCATCTCGTTC 4560
Qy |||||
1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlyAsnPhe 1540
Db |||||
4561 CTGCTCAVTTGGCTCTCTTTGCTCGTGAACATGTTTGGTGTTGGTGGAAGAACTTC 4620
Qy |||||
1541 HisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLeu 1560
Db |||||
4621 CACAAGTGTGGCAGCACAGAGGAAGAGAGGCCCGCGCGGGAGGAGAGGCCCTA 4680
Qy |||||
1561 ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys 1573
Db |||||
4681 CGAAGACTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCTGAAGCCAGTGCATA 4740
Qy |||||
1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLysCysThrSerHis 1593
Db |||||
4741 CCTTACTACTCCGACTACTCCCGCTTCGCGCTCTCGTCCACCACTTGTGCACAGCCAC 4800
Qy |||||
1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613
Db |||||
4801 TACCTGGACCTTCTCATCACAGGTGTCTATCGGGCTGAACGTGGTCACCATGGCCATGGAG 4860
Qy |||||
1614 HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr 1633
Db |||||
4861 CACTACCAAGCAGCCACAGATTCTGGATGAGGCTCTGAAGATCTGAAGATCTGCACATCTTCACT 4920
Qy |||||
1634 ValliePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgPhePhe 1653
Db |||||
4921 GTCACTTTTGTGTGAGTCAAGTTTCAAACCTTGGGCTTTTGGTTTCCGTCGGTCTTTC 4980
Qy |||||
1654 GlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673
Db |||||
4981 CAGNACAGGTGGAACACAGCTGGACCTGGCCATTGTGCTGCTGTCCATCATGGGCATCAG 5040
Qy |||||
1674 LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693
Db |||||
5041 CTGGAGGAAAATCGAGGTCACAGCCTCGCTGCCATCAACCCACCATCATCGGCATCATG 5100
Qy |||||
1694 ArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAla 1713
Db |||||
5101 AGGGTGTGCGCATTTGCCGAGTGTCTGAAGCTGTGAAGATGGCTGTGGGCATTCGGGCG 5160
Qy |||||
1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733
Db |||||
5161 CTGCTGGACACGGTGATGACGGCCCTGCCAGGTGGGGAACCTTGGGACTTCTCTTCATG 5220
Qy |||||
1734 LeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753
Db |||||
5221 TTGTTGTTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTTGGAGACCTGGAGTGTGAC 5280
Qy |||||
1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773
Db |||||
5281 GAGACACACCCCTGTGAGGGCTGGGCGGTATGCCACCTTTTCGGAACCTTTGGCATGGCC 5340
Qy |||||
1774 PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr 1793
Db |||||
5341 TTCTTAACCTTCTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATTTATGAAGACACCC 5400
Qy |||||
1794 LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe 1813
Db |||||
5401 CTCCGGGAGCTGTGACAGAGTCCACCTGCTACAAACACGGTCATCTCGCCTACTTACTTT 5460

1814 ValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMet 1833
Db |||||
5461 GTGTCTTGTGCTGACGGCCAGTTGTGCTAGTCAACGTGGTGTATCGCGTCTGATG 5520
Qy |||||
1834 LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeu 1853
Db |||||
5521 AAGCACCTGGAGGAGAGCAACAAGAGAGCCCAAGAGGAGGCGGAGCTAGAGGCTGAGCTG 5580
Qy |||||
1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873
Db |||||
5581 GAGCTGGAGATGAAGACCTCAGCCCCCAGCCCACTCGCCACCTGGGCAGCCCTTCCTC 5640
Qy |||||
1874 TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro 1893
Db |||||
5641 TGGCTTGGGTCTGAGGGCCCCGACAGCCCCACAGCCCCCAAGCCTTGGGGCTCTGCACCCA 5700
Qy |||||
1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913
Db |||||
5701 GCGSCCCACGCGAGATCAGCCCTCCACTTTTTCCTGGAGCACCCACGATCGACGCCAC 5760
Qy |||||
1914 ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr 1933
Db |||||
5761 CCCACGGAGCTGCCAGACCAGACTTACTGACTGTGCGAAGTCTGGGGTCTGAGCGAACG 5820
Qy |||||
1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu 1953
Db |||||
5821 CACTTCTGCCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCCGAGGGGCCCTG 5880
Qy |||||
1954 GlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973
Db |||||
5881 GGACACAGGGGCTGGGGCTCCCAAGCTCAGTCAGGCTCCGTCCTGCTGCTGCTCACTCC 5940
Qy |||||
1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993
Db |||||
5941 CAGCAGCAGATACCACTACATCTCAGCTTCCCAAGATGACCTCTCATCTGCTCCAG 6000
Qy |||||
1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerPro 2013
Db |||||
6001 CCCACAGCGCCCAACCTGGGGCACCATCCCCAAACTGCCCCACAGGAGCTCCCT 6060
Qy |||||
2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033
Db |||||
6061 TTGGCTCAGAGGCCACTCAGCGCCAGCAGCAATAAGGACTGACTCTCTTGACGCTTCAG 6120
Qy |||||
2034 GlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAla 2053
Db |||||
6121 GGTCTGGGCACTCCGGGAAGACTCTGTCGAGAGGTAGTGGGCTCTCCCGCCCTGGCC 6180
Qy |||||
2054 ArgAlaTyrSerPheTrpGlyGlnSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
Db |||||
6181 CCGGCTTACTCTTTCTGGGGCCAGTCAAGTACCAGGCACAGCAGCACTCCCGCAGCCAC 6240
Qy |||||
2074 SerLysIleSerLysHisMetThrProAlaProCysProGlyProGluProAsnTrp 2093
Db |||||
6241 AGCAAGATCTCCAAGCACATGACCCCGCAGCCCTTCCCGAGGCGCCAGAACCTGG 6300
Qy |||||
2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113
Db |||||
6301 GGCAGGGCCCTCCAGAGACCAGAGAGCTTAGAGTTGGACACGGAGCTGAGCTGGATT 6360
Qy |||||
2114 SerGlyAspLeuLeuProProGlyGlnGluProProSerProArgAspLeuLys 2133
Db |||||
6361 TCAGGAGACCTCTGCCCCCTGGCGCCAGGAGGAGCCCCCATCCCCACGGACCTGAAG 6420
Qy |||||
2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153
Db |||||
6421 AAGTGCTACAGCTGGAGGCCAGAGCTGCCAGCGCGGCTTACGCTCTGCTGGATGAG 6480
Qy |||||
2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
Db |||||
6481 CAGAGGAGACACTCTATCCCGCTGAGTCTCTGGACAGCGGCTCCCAACCCACCTGGGC 6540
Qy |||||
2174 ThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2193

```
Db 6541 ACAGACCCCTAACTTGGGGGCGAGCCTTGGGGGCGCGGAGCGCGCCCAAGAAA 6600
Qy 2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213
Db 6601 AAATCTAGCCCGCTAGTATCACCATAGACCCCGGAGAGCCCAAGGTCTCGGACCCCG 6660
Qy 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
Db 6661 CCCAGCCCTGGTATCTGCCCTCCGAGGAGGGCTCCGTCCAGCGACTCCAGGATCCCTTG 6720
Qy 2234 AlaSerGlyProProAspSerMetAlaAlaSerProProSerProLysLysAspValLeuSer 2253
Db 6721 GCCTCTGCCCGCCCTGACAGCATGGCTCGCCTCGCCCTCCCCCAAGAAAAGATGTCTGAGT 6780
Qy 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6781 CTCTCCGGTTTATCCTCTGACCCAGCAGACCTGGACCCC 6819

RESULT 2
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAVASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426.998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-4

Alignment Scores:
Pred. No.: 0 Length: 7741
Score: 11877.50 Matches: 2264
Percent Similarity: 99.6% Conservatives: 1
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.8% Indels: 7
DB: 3 Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-426-998-4 (1-7741)
Qy 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 523 ATGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGACAGCCCGGAGCTTCATG 582
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyClyArgProGlyProGlySerAlaGluLysAsp 40
Db 583 CGGCTCAACGACCTGTTCGGGGGGCGGGGGCGGGGGCGGGGGTCAGCAGAAAAGGAC 642
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProValVal 60
Db 643 CCGGGCAGCGGGACTCCGAGCGGGAGGGGTGCCGTACCCGGCGCTGGCCCGGTGGTT 702
Qy 61 PhePheTyLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 703 TCTCTACTTGTAGCAGACAGCCCGCGCGGAGCTGGTGTCTCCGACCGCTCTGTAAC 762
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 763 CCCTGGTTGAGCGCATCAGCATGTGTGTCATCCTTCTCAACTCGCTGACCCCTGGGCATG 822
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
```

```
Db 823 TTCGGGCATCGGAGGACATCGCTGTGACTCCCGAGCGCTGCCGATCCTCGAGCGCCTTT 882
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 883 GATGACTTTCATCTTTTGGCTTCTTTTGGCGTGGAGATGGTGGTGAAGATGGTGGCCTTGGGC 942
Qy 141 IlePheGlyLysLysCysTyLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 943 ATCTTTGGGAAAAGTGTACCTGGGAGACACATTGGAACCGGCTTGACTTTTTCATCGTC 1002
Qy 161 IleAlaGlyMetLeuGluTyLeuSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 1003 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCGAGAACGTCAGCTTCTCAGCTGTCTCAGG 1062
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 1063 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATCGGCATCCTT 1122
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 1123 GTCAGTTGCTGTGGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTGCTCTCTCTTC 1182
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1183 GTCTTCTTCTTTCGGCATCGTCGGGTCGAGCTGTGGGCGAGGCTGCTTCGGAACCGA 1242
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyLeuGln 260
Db 1243 TGCTTCTTACTGAGAAATTTTCAGCTCCCTCGAGCTGGACCTGGAGCGCTATTACCCAG 1302
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1303 ACAGAGAACCGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACCGAGAACCGCATCGGG 1362
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
Db 1363 TCCTGCAAGACGTCGCCCGCTGCGGGGACCGGGGCGGTGGCCCACTTGGCGGTCTG 1422
Qy 301 AspTyLeuAlaTyLeuAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyTrp 320
Db 1423 GACTATGAGGCTTACAAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCATGACTATC 1482
Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 1483 ACCAACTGCTCAGCGGGGAGCACAAACCTTCAAGGGCGCCATCACTTTGACAAACATT 1542
Qy 341 GlyTyAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
Db 1543 GGCTATGCTGGATCGGCATCTTCCAGGTATCATCAGCTGAGGGGCTGGGTGACATCATG 1602
Qy 361 TyrPheValMetAspAlaHisSerPheTyLeuAsnPheIleTyPheIleLeuLeuIleIle 380
Db 1603 TACTTTGTGATGGATGCTCATTTCTTCAAAATTCATCTACTCTCTCTCTCTCTCTCTCTCT 1662
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1663 GTGGGCTCCTTCTTTCATGATCAACCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1722
Qy 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1723 ACCAAGCAGCGGGAAGCCAGCTGATCGGGAGCAGCGGTGTGCGGTCTCTGTCCAACGCC 1782
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyLeuGluLeuLeuLysTyLeu 440
Db 1783 AGCACTTGGCTAGCTTCTCTGAGCCCGAGCTGCTATAGAGGAGCTGCTCAAGTACCTG 1842
Qy 441 ValTyIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1843 GTGTACATCTTCTGTAAGGAGCCCGCAGGCTGCTCAGGTCTCTCGGGCAGCAGGTGTG 1902
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
```

Db 1903 CGGCTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGC 1962
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 500
Db 1963 AGCTGCTCTCGCTCCCAACCGCGGCTATCCGTCACACCACTGTGGTGCACCAACCAAC 2022
Qy 501 His 520
Db 2023 CATCACCAACCACTACCACTGGCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG 2082
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 2083 ATCCAGGACAGGGATGCCAATGGGTCCCGCAGGCTCATGCTGCCACCACTCCAGCGCT 2142
Qy 541 AlaleuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheThrHisAlaAsp 560
Db 2143 GCCCTCTCCGGGGCCCCCTCGTGGCGCAGAGTCTGTGCACAGCTTCTACCAATGCCGAC 2202
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 2203 TGCCACTTAGAGCCAGTCCGCTGCAGCGGCCCTCCAGGTCCCAATCTGAGGCATCC 2262
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 2263 GGCAGGACTGTGGCAGCGGGAAGGTGTATCCACCGTGACACACAGCCCTCCACCGGAG 2322
Qy 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 2323 ACGCTGAAGGAGAGGCACTAGTAGAGGTGCTGCCAGCTCTGGGGCCCCCAACCTCACC 2382
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2383 AGCTTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAGT 2442
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2443 ACAGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA 2502
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2503 GCCTGTGCTCCAGACAGCTGCCCCCTACTGTGCCCGGGCCGGGCGAGGAGGTGGAGCTC 2562
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2563 GCCGACCGTGAATGCCCTGACTCAGACAGCAGGCGAGTTATGATTTACACAGGATGCC 2622
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2623 CAGCACAGCACTCCGGGACCCCCACAGCGCGGCAACGAGGCTTGGGCCACAGATGCA 2682
Qy 721 GluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2683 GAGCCACAGCTCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACCTTCGAAAGATTGTG 2742
Qy 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2743 GACACAAGTACTTTGGCGGGGAATCATGATCGCCATCTGGTGCACACACTCAGCATG 2802
Qy 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuLeuIleSerAsnIle 780
Db 2803 GGCATCGAATACCAAGCAGCGCCGAGGAGCTTACCAACGCGCTAGAAATCAGCAACATC 2862
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPhe 800
Db 2863 GTCTTTCACAGCTCTTTTGCCCTGGAGATGCTTGCTGAAGCTGCTTGTGTATGGTCCCTTT 2922
Qy 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr 820
Db 2923 GGCTACATCAAGAATCCCTACAAACATCTTCGATGGTGTCAATGTGCTCATCAGCGTGTGG 2982
Qy 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2983 GAGATCGTGGGCCAGCAGGGGGGGCGCTGTGCGTGCTGCGGACCTTCCGCTGTATGCGT 3042

Qy 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 3043 GTGCTGAAGCTGGTGGCCCTTCTGCCGGCGCTGCAGCGGAGCTGTGGTGTCTCATGAAG 3102
Qy 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
Db 3103 ACCATGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTTCTTCACTTTCATCTTCAGC 3162
Qy 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3163 ATCTTGGCGATGATCTCTTTCGGTGCAGTTTGCCTCTGAGCGGAGTGGGACACCCCTG 3222
Qy 901 ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu 920
Db 3223 CCAGACCGAAGAATTTTGACTCTCTGCTCTGGGCCATCTGCTACTGTCTTTCAGATCTCTG 3282
Qy 921 ThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 3283 ACCCAGGAGGACTGGAACAAGTCTCTACAAATGGTATGGCTCCACGTCGCTCGTGGGCG 3342
Qy 941 AlaleuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 3343 GCCCTTTATTTCATTGCCCCTCATGACCTTCGGCAACTACGTCCTTCAATTTGCTGGTC 3402
Qy 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
Db 3403 GCCATTCTGGTGGAGGCTTCCAGCGGAGGAATACAGAAACGGGAAGATGCCAGTGA 3462
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
Db 3463 CAGTTAAGCTGTAATTCAGCTGCTGTCGACTCCCGAGGGGGAGATGCCAACAAAGTCCGAA 3522
Qy 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3523 TCAGAGCCCGATTTCTTCTCACCCAGCTGTGATGGTGTATGGGGACAGAAAGTGGTTG 3582
Qy 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
Db 3583 GCCTTGTGTCTCCCTGGGAGAGACCCCGAGCTCGGGAAGAGCTGTCTGCCCTCTCATC 3642
Qy 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3643 ATCCACAGCGCCGCCACACCCATGCTGCTGCCAACAGACACAGCAGCGGCTTGGCGAG 3702
Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3703 CGCTTGGGCCCTGCGTCCGCCGCCACACGACGACGCGGTCTGGCAGAGCCTTGGGGCGGCC 3762
Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla 1100
Db 3763 CACGAGATGAAGTCAACGCCCGAGCGCCGAGCTCTCCGCACAGCCCCCTGGAGCGCTGA 3822
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3823 AGCAGTGGACACAGCAGCGCGCTCCAGCGGAACAGCCTCGGCGGTGACCCAGCGCTGAAG 3882
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGluSerGln 1140
Db 3883 CGGAAGACCCCAAGTGGAGAGCGCGGTCCCTGTGTCTGGGAGAGGCGCAGAGAGCCAG 3942
Qy 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3943 GATGAAGAGAGAGCTCAGAAGAGAGCGGCCAGCCCTCGCGGAGTGACCATCGCCAC 4002
Qy 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 4003 AGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCACAGACACACTGCAGGTG 4062
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 4063 CCAGGGCTGCATCGCACTGCCAGTGGCGGCGGTCTGTCTTGAGCACACAGGACTGCAAT 4122

Qy	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	4123	GGCAAGTTCGGCTTCAGGGCGCTTGGCCCGGCGCTGCGGCTGATGACCCGCCCATGGAT	4182
Qy	1221	GlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
Db	4183	GGGATGACCGCGATGACGAGGGCACTGAGCAAGGGAAACGGTCCCGGTGGATC	4242
Qy	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
Db	4243	CGAGCCCGACTCCCTGCCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCTTCCCT	4302
Qy	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	4303	CCTCAGTCCAGGTTCCGCTCTGTGTACCGGATCATCACCACAAAGATGTTTCGACCAC	4362
Qy	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	4363	GTGTCTCTGTGCATCATCTTCTTAACTGCATCACCATCCCATGGAGCGCCCAAAATT	4422
Qy	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Db	4423	GACCCCCACAGCGCTGAACGATCTTCTGNACCTCTTCCAATTACATCTTCGCGCAGTC	4482
Qy	1321	PheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAla	1340
Db	4483	TTTCTGCTGAAATGCACAGTCAAGGTGTGGCACTGGGCTGGTCTTCGGGAGCAGCGC	4542
Qy	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleIleSerValIleAsp	1360
Db	4543	TACCTGGGAGCAGTTGGAACGTGCTGGACGGGCTGTGTGGTGTCACTCCGTCATCGAC	4602
Qy	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4603	ATTCTGTTGTCATGGTCTCTGACAGCGGCACCAAGATCTTGGGCATGCTGAGGGTCTG	4662
Qy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	4663	CGGCTGTGGACCTCTGCGCCCTCAGGGTGATCAGCGGGCGCAGGGGCTGCAAGCTG	4722
Qy	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4723	GTGTGGAGACGCTGATGTCTACTGAAACCCATCGGCACCATGTGATGTCATCTGCTGT	4782
Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
Db	4783	GCCCTTCTCATCTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGAGGAAGTTTTTCGT	4842
Qy	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4843	TGCCAGGGCGAGGATACACAGAACATCACCAATAAATCGGACTGTGCCGAGGCCAGTTAC	4902
Qy	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4903	CGGTGGGTTCGGCAACAAGTCAACCTTTGACAACTTCGCCACGGGCCCTTGATGTCCTGTC	4962
Qy	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4963	GTTTTGGCCTCAAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTGTGGGC	5022
Qy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	5023	GTGGACCAGCAGCCCATCATGAACCAACCCCTGGATGCTGCTGTACTTTCATCTCGTTC	5082
Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	5083	CTGCTCATTTGGGCTTCTTTGTCTGAACTATGTTTGGGTGTGGGTGGAGAACTTC	5142
Qy	1541	HisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLeu	1560
Db	5143	CACAAGTGTGGCAGACCAAGAGAGAGGAGGCCCGCGCGGGAGGAGAGCGCCTA	5202
Qy	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573

Db	5203	CGAAGACTGGAGAAAAGAGAAAGGATGAGGAGAACGACAGATGGCTGAAGGCCCCAGTGCAAA	5262
Qy	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuValHisHisLeuCysThrSerHis	1593
Db	5263	CCTTACTACTCCGACTACTCCCGCTTCGGCTCCTCGTCCACCACCTGTGCACACGACC	5322
Qy	1594	TyrLeuAspLeuPheLeThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	5323	TAGCTGGACCTCTTCATCACAGGTGTTCATCGGGCTGAACGTGGTCAACATGGCCATGGAG	5382
Qy	1614	HisTyrClnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	5383	CACCTACAGCAGGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCAC	5442
Qy	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	5443	GTCACTTTTGTCTGGAGTCAGTTTCAAACTTGTGGCCCTTTGGTCTTCGTCGGTCTTC	5502
Qy	1654	GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	5503	CAGGACAGGTGGAAACAGCTGGACCTGGCCATCTGTCTGTCTCCATCATGGGCATCAGC	5562
Qy	1674	LeuGluClnIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	5563	CTGGAGAAATCAGAGTCAACGGCTCGCTGCCCATCAACCACCATCATCCGCATCATG	5622
Qy	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5623	AGGGTGTGGCATTTGCCCGAGTGCTGAAGCTGCTGAAGATGGCTGTGGGCATCGCGCG	5682
Qy	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5683	CTGCTGGACACGGTGATGACAGGCCCTGCCCCAGGTGGGGAACCTGGGACATCTCTTC	5742
Qy	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5743	TTGTGTGTTTTCATCTTTGAGCTCTGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGAC	5802
Qy	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	5803	GAGACACACCCCTGTGAGGGCCCTGGGCGCTGACCCACCTTTCCGAACTTTGGCATGCC	5862
Qy	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	5863	TTCTAACCTCTTCGAGTCTCCACAGGTGACAAATTGGAATGGCATATGGAAGGACACC	5922
Qy	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5923	CTCCGGGACTGTGACACAGGAGTCCACCTGTCTACAAACGGTGCATCTCGCTATCTACTTT	5982
Qy	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5983	GTGTCTTCGTGTGACGGCCCGAGTTCGTGCTAGTCAACGTGTGATGCGCGTGTGATG	6042
Qy	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuAlaGluLeu	1853
Db	6043	AAGCACCTGGAGGAGAGACAAAGGAGGCCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTG	6102
Qy	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
Db	6103	GAGCTGGAGATGAAGACCCCTCAGCCCCCAGCCCCACCTCGCCACTTGGGACGCCCTCTC	6162
Qy	1874	TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro	1893
Db	6163	TGGCTCGGGTTCAGGGCCCCGACAGCCCCGACAGCCCCAAGCTCTGGGGCTCTGCACCCA	6222
Qy	1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis	1913
Db	6223	CGGCCCCACGCGAGATCAGCCTCCCACTTTTCCCTGGAGACACCCACGATGTCAGCCCC	6282
Qy	1914	ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr	1933

Db 6283 CCCACGGAGTGCACGAGCAGACTTACTGACTGTGCGGAAGTCTGGGGTCAGCCGAACG 6342
Qy 1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu 1953
Db 6343 CACTCTCTGCCAATGACAGCTACTATGTCTCGGATGGGAGCACTGCGGAGGGGCCCTG 6402
Qy 1954 GlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973
Db 6403 GGACACAGGGGCTGGGGCTCCCAAGCTCAGTCAGGCTCCGTCTGTGCGTTCATCC 6462
Qy 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuGln 1993
Db 6463 CAGCAGCAGATACAGCTATCTCTGAGCTTCCCAAGATGACACCTCATCTCTGCTCAG 6522
Qy 1994 ProHisSerAlaProThrTTPGlyThrIleProLysLeuProProGlyArgSerPro 2013
Db 6523 CCCACAGCGCCCAACCTGGGGCACCATCCCAAACTGCCCCACAGGACGCTCCCT 6582
Qy 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033
Db 6583 TTGGCTCAGAGCCACTCAGCGGCGCAGCAGCAATAGGACTGACTCTTGGAGCTTCAG 6642
Qy 2034 GlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAla 2053
Db 6643 GGTCTGGCAGCGCGGAAGACTCTGTGGCAGAGGTGAGTGGGCCCTCCCCGCCCTGGCC 6702
Qy 2054 ArgAlaTyrSerPheTTPGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
Db 6703 CGGGCCCTACTCTTCTGGGGCCAGTCAAGTAGTACCAGGACAGCAGCACTCCCGCAGCCAC 6762
Qy 2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp 2093
Db 6763 AGCAGATCTCCAGCACATGACCCCGCCAGCCCTTGGCCAGCGCCAGAACCACTGG 6822
Qy 2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113
Db 6823 GGCAAGGGCCCTCCAGAGACCAGAACGACGTTAGAGTTGGACACGGAGCTGAGCTGGATT 6882
Qy 2114 SerGlyAspLeuLeuProProGlyGlyGlnGluProProSerProArgAspLeuLys 2133
Db 6883 TCAGGAGACCTCTCTGCCCCCTGGGGCCAGGAGAGCCCTATCCCCACGGGACCTGAAG 6942
Qy 2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153
Db 6943 AAGTGCTACAGCTGGAGGCCAGAGCTGCCAGCGCCGCTACGCTCTGCTGATGAG 7002
Qy 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
Db 7003 CAGAGGAGACACTCTATCGCGCTCAGCTGCTGGACAGCGGCTCCCAACCCACCTGGGC 7062
Qy 2174 ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2193
Db 7063 ACAGACCCCTCTAACCTTGGGGCCAGGCTCTTGGGGGGCCCGGAGCGGCCCAAGAAA 7122
Qy 2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213
Db 7123 AAACCTACCCCGCCCTAGTATCACCATAGACCCCGCCAGAGCAAGGTCTCGGACCCCG 7182
Qy 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
Db 7183 CCCAGCCCTGTATCTGCTCCGAGGAGGGCTCCGTCAGCGACTCCCAAGGATCCCTTG 7242
Qy 2234 AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLeuAspValLeuSer 2253
Db 7243 GCCTCTGGCCCCCTTGACAGCATGGCTGCCCTCCCAAAAGAAAGATGTGCTGAGT 7302
Qy 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7303 CTCCTCGGTATCTCTTGACCCAGCAGACCTGGACCCC 7341

RESULT 3

US-09-949-016-3859

; Sequence 3859, Application US/09949016

; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3859

Alignment Scores:

Pred. No.: 0 Length: 7405
Score: 11241.00 Matches: 2162
Percent Similarity: 95.1% Conservative: 1
Best Local Similarity: 95.1% Mismatches: 1
Query Match: 94.4% Indels: 110
DB: 3 Gaps: 4

US-09-611-257A-37 (1-2266) x US-09-949-016-3859 (1-7405)

Qy 1 MetAspGluGluAspGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGGACGAGGAGGAGTGGAGCGGGCCGAGAGTGGGACAGCCCGGAGGTTCTATG 432
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACGACCTGTTCGGGGCGGGGGCGGGCGGGCGGGGTGAGCAAGAAAGGAC 492
Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 493 CCGGGCAGCGCGGACTCCGAGGCGAGGGGTGCGGTACCCGGCGCTGGCCCCGGTGGTT 552
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 553 TTCTTCTACTTGACCAAGACAGCCGCGCGGAGCTGGTGTCTCCGACCGGTCTGTAAAC 612
Qy 81 Pro---TrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGly 99
Db 613 CCTACCTGGTTTGAGCGCATCAGCATGTTGTCATCTCTCAACTGCGTGACCTGGGC 672
Qy 100 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 119
Db 673 ATGTTCCGGCCATCCGAGGACATCCCTGTGTACTCCAGCGCTGCGGATCCTGAGGCC 732
Qy 120 PheAspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeu 139
Db 733 TTTGATGACTTCATCTTTGGCTTCTTTGGCTGGAGATGGTGGTGAAGATGGTGGCCTTG 792
Qy 140 GlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIle 159
Db 793 GGCATCTTTGGAAAAAGTGTGTACTCTGGGACACTTGGAAACCGGCTTGACTTTTTCATC 852
Qy 160 ValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaVal 179
Db 853 GTCATCCGAGGATGCTGGAGTACTCGCTGACCTGCAGAACGTCAGCTTCTCAGCTGTC 912
Qy 180 ArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIle 199
Db 913 AGGACAGTCCGTGTGCTGGACCGCTCAGGGCCATTAAACCGGGTCCCGCAGCATGGCATC 972
Qy 200 LeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 219

Db	973	CTTGTCAAGTTGCTGGATACGCTGCCATGCTGGCAACGTCCTGCTGCTCTGCTTC	1032
Qy	220	PheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsn	239
Db	1033	TTGCTCTTCTTCATCTTCGGCATCGTCGGCGTCAGCTGTGGCAGGGCTGCTTCGGAAC	1092
Qy	240	ArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyr	259
Db	1093	CGATGCTTCTACTGAGATTTTCAGCCTCCCTCTGAGCGTGGACCTGGAGCGCTATTAC	1152
Qy	260	GlnThrGluAsnGluAspGluSerPropheIleCysSerGlnProArgGluAsnGlyMet	279
Db	1153	CAGACAGAGAACGAGGATGAGAGCCCTTCACTCTGCTCCAGCCACGCGAGAAACGGCATG	1212
Qy	280	ArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGly	299
Db	1213	CGGTCTTCAGAACGCTGCCCGCTCGCGGGGACCGGGGGCGTGGCCCACTTCGCGGT	1272
Qy	300	LeuAspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyr	319
Db	1273	CTGGACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCAACTGGAAACAGTAC	1332
Qy	320	TyrThrAsnCysSerAlaGlyGluHisAsnPropheIysGlyAlaIleAsnPheAspAsn	339
Db	1333	TACACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCATCACTTTGACAAAC	1392
Qy	340	IleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIle	359
Db	1393	ATTGGCTATGCTGGATTCGGCATCTTCCAGGTATCATCGCTGGAGGGCTGGGTGCACATC	1452
Qy	360	MetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle	379
Db	1453	ATGTACTTTGTGATGATGTCTCATCTCTTACAAATTCATCTACTTCATCTCTCTCATC	1512
Qy	380	IleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSer	399
Db	1513	ATCGTGGGCTCTTCTTCATGATCAACCTGTGCTGGTGGTGGTATGGCCACGAGTTCTCA	1572
Qy	400	GluThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsn	419
Db	1573	GAGACCAAGCAGCGGGAACCCAGCTGATCGGGAGCAGCGTGTGCGGTTCTGTCCAAAC	1632
Qy	420	AlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyr	439
Db	1633	GCCAGCACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTAC	1692
Qy	440	LeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGly	459
Db	1693	CTGGTGTACATCTTCTGTAAGGCAGCCCGCAGCGCTGCTCAGGTCTCTCGGGCAGCAGGT	1752
Qy	460	ValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSer	479
Db	1753	GTGCGGGTTGGGTGCTCAGCAGCCCAAGCACCCTCTCGGGGGCCAGGAGACCCAGCCAGC	1812
Qy	480	SerSerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis	499
Db	1813	AGCAGCTGCTCTCGCTCCCAACCGCGCTATTCGCTCCACCCTGGTGGACCAACCCAC	1872
Qy	500	HisHisHisHisIstYrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerPro	519
Db	1873	CACCATCACCACTACCACTGGGCAATGGGAGCTCAGGGCCCCCGGGCCAGCCCG	1932
Qy	520	GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThr	539
Db	1933	GAGATCCAGGACAGGGATGCCAATGGGTCCCGCGCTCATGTGCTCCACCACTCTCGACG	1992
Qy	540	ProAlaLeuSerGlyAlaProProGlyGlyValaGluSerValHisSerPheTyrHisAla	559
Db	1993	CTTGCCCTCTCCGGGGCCCCCTTGGTGGCGAGAGTCTGTGCACAGCTTCTACCATGCC	2052
Qy	560	AspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAla	579

Db	2053	GACTGCCACTTAGAGCAGTCCGCTGCCAGGCGCCCTCCAGGTCCTCCCATCTGAGGCA	2112
Qy	580	SerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProPro	599
Db	2113	TCGGGCAGGACTGTGGGCAGCGGGAAGGTGATCCCAACCGTGACACACCCCTCCACCG	2172
Qy	600	GluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeu	619
Db	2173	GAGACGCTGAAGGAGAAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTC	2232
Qy	620	ThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGln	639
Db	2233	ACCAGGCTCAACATCCACCCGGGCTTACAGCTCCATGTCACCAAGCTGTGGAGACAG	2292
Qy	640	SerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLysLeuAlaAspSer	659
Db	2293	AGTACAGGTGCTGCCAAGACTTTGCAAGATCTCCAGCCCTTGTGTAAGGACAGAGT	2352
Qy	660	GlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGlu	679
Db	2353	GGAGCCTGTGGTCCAGACAGTGCCTTACTGTGCCCGGGCGGAGGAGGTGGAG	2412
Qy	680	LeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAsp	699
Db	2413	CTCGCCGACCGTGAAATGCTGACTCAGACAGCGAGGCAGTTTATGAGTTTCACACAGAT	2472
Qy	700	AlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAsp	719
Db	2473	GCCACGACAGCACTCCGGGACCCCAACAGCGGGCAACGAGCCTGGGCCCNAGAT	2532
Qy	720	AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle	739
Db	2533	GCAGAGCCCGACTCTGTGTGGCTTCTGGAGGCTAATCTGTGCACACCTTCCGAAAGATT	2592
Qy	740	ValAspSerIstYrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer	759
Db	2593	GTGGACAGCAAGTACTTTGGCCGGGAATCATATGCCATCTCGTCAACACACTCAGC	2652
Qy	760	MetGlyIleGluTyrHisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsn	779
Db	2653	ATGGGATCGAATACCAGCAGCAGCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAAC	2712
Qy	780	IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro	799
Db	2713	ATCGTCTTCCACAGCCTTTCCTGCTGGAGATCGTCTGAAGCTGCTGTGTATGTGTC	2772
Qy	800	PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal	819
Db	2773	TTTGGGTACATCAAGAATCCCTACAACATCTTCGATGGTGTCAATGTGGTCAACAGCGT	2832
Qy	820	TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet	839
Db	2833	TGGGAGATCGTGGGCAGCAGGGGGCGGCTCTGCGTGTCTGGGACCTTCCGCTCATG	2892
Qy	840	ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet	859
Db	2893	CGTGTCTGNAGCTGTGTGGCTTCTTCCCGCGCTGCGCGGCGAGCTGGTGGTCTCATG	2952
Qy	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe	879
Db	2953	AAGACCATGGACAACCTGGCCACCTTCTGCATGCTGCTTATGCTTTCATCTTCATCTTC	3012
Qy	880	SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899
Db	3013	AGCATCTGGGCATGATCTCTTTCGGCTGCAAGTTTTCCTCTGAGCGGATGGGACACC	3072
Qy	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919
Db	3073	CTGCCAGACCGGAAGATTTTGACTCTTGTCTCTGGGCCATCTGCTACTGCTTTCAGATC	3132
Qy	920	LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp	939
Db	3133	CTGACCCAGGAGACTGGAAACAAAGTCTCTACAATGGTATGGCCTCCACGTCGTCCTGG	3192

Qy 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
Db 3193 GCGGCCCTTTATTTCATGTCCTCATGACCTTCGCGCAACTACGTGCTCTTCAATTGCTG 3252
Qy 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979
Db 3253 GTCGCCATTCTGGTGGAGGGCTTCCAGCGGAG----- 3285
Qy 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSer 999
Db 3286 -----GGAGATGCCAAACAGTCC 3303
Qy 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019
Db 3304 GAATCAGAGCCCGATTCTTCTTCCACCCAGCCTGGATGGTGTATGGGACAGGAAGAAGTGC 3363
Qy 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu 1039
Db 3364 TTGGCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAGCCTGTGCCGCCCTCTC 3423
Qy 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059
Db 3424 ATCATCCACAGCGCGCCACACCCATGTGCTGCCCAAGAGCACAGCAGCGGCCCTGGGC 3483
Qy 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGluProGlyVala 1079
Db 3484 GAGCGCTGGGCCCTCGTCCGCGCGCCACAGCAGCAGCGGGTGGCAGAGCCTTGGGGCG 3543
Qy 1080 AlaHisGluMetLysSerProProSerAlaArgSerProHisSerProTrpSerAla 1099
Db 3544 GCCCAGAGATGAAGTCCACCGCCAGCGCCCGCAGCTCTCCGCACAGCCCTGGAGCGCT 3603
Qy 1100 AlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeu 1119
Db 3604 GCAAAGCAGCTGGACAGCAGCGCTCCAGCGCGAACAGCCTCGCGCGTGCACCCAGCCTG 3663
Qy 1120 LysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSer 1139
Db 3664 AAGCGGAGAACCCNAAGTGGAGAGCGCGCGTCCCTTGTGTGGAGAAAGCCAGAGAGC 3723
Qy 1140 GlnAspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArg 1159
Db 3724 CAGGATGAAGAGGAGAGCTCAGAAGAGAGCGGGCCAGCCCTCGCGGCGAGTGACCATCGC 3783
Qy 1160 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGln 1179
Db 3784 CACAGGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTGTACCTGCCACAGACACTGCGAG 3843
Qy 1180 ValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCys 1199
Db 3844 GTGCCAGGGCTGCATCGCAGCTGCCAGTGGCCGAGGGTCTGTCTCTGAGCACAGGACTGC 3903
Qy 1200 AsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu 1219
Db 3904 AATGCAAGTCCGCTTCAGGCGCGCTGCCCGGGCCCTCGCGCCTGTATGACCCGCCACTG 3963
Qy 1220 AspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrp 1239
Db 3964 GATGGGGATGACCGCGATGACAGGGCAACCTGAGCAAAAGGGGAACGGGTCCGCGCGTGG 4023
Qy 1240 IleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhe 1259
Db 4024 ATCCAGGCCCGACTCCCTCGCTGCTGCTGCGCGAGACTCCTGGTTCAGCCTACATCTTC 4083
Qy 1260 ProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAsp 1279
Db 4084 CCTCCTCAGTCCAGGTTCGCGCTCCTGTGTACCGGATCATCACCCACAAAGATGTTGCAC 4143
Qy 1280 HisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLys 1299
Db 4144 CACGGGGTCTTGTTCATCTCTTAACTGTCATCACCATCGCCATCGCCAGCGGCCCAAA 4203

Qy 1300 IleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAla 1319
Db 4204 ATTGACCCCCACAGCGCTGAACGATCTTCTGACCCCTCTCCAATTACATCTTCCACGCA 4263
Qy 1320 ValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGln 1339
Db 4264 GTCTTTCTGGCTGAATGACAGTGAAGTGGTGGCACTGGGCTGTCTTCGGGGAGCAG 4323
Qy 1340 AlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIle 1359
Db 4324 GCGTACTTCGGAGCAGTTGGAACGTGCTGACGGGCTGTGTGCTCACTTCCTCGTCATC 4383
Qy 1360 AspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal 1379
Db 4384 GACATTCGTGTCCATGGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTCAGGGTG 4443
Qy 1380 LeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLys 1399
Db 4444 CTGCGGCTGTGCGGACCTTCGCGCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAG 4503
Qy 1400 LeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCys 1419
Db 4504 CTGGTGTGGAGAGCGCTGATGTCTCACTGAACCCATCGGCAACATTTAGTCACTGTC 4563
Qy 1420 CysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePhe 1439
Db 4564 TGTGCCCTTCTTCATCATTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAAGGAAAGTTTTC 4623
Qy 1440 ValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSer 1459
Db 4624 GTGTGCCAGGCGGAGGATACAGGAACATCACCATAAATCGGACTGTGCCGAGGGCAGT 4683
Qy 1460 TyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeu 1479
Db 4684 TACCGTGGGTCCGGCACAGTACAACTTTGACAACTTGGCCAGGGCCTGATGTCCCTG 4743
Qy 1480 PheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaVal 1499
Db 4744 TTCGTTTTGGCCTCCAAGGATGTTGGTGGTGCATCATCATGATGGCTGGATGCTGTG 4803
Qy 1500 GlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSer 1519
Db 4804 GGCGTGCACGAGCAGCCCATCATGAACCAACCCCTGGATGCTGCTGTACTTTCATCTCG 4863
Qy 1520 PheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsn 1539
Db 4864 TTCTCTCATTTGGGCTTCTTGTCTGNAACATGTTTGGGGTGTGGTGTGGAGAAC 4923
Qy 1540 PheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArg 1559
Db 4924 TTCCACAAGTGTGCGCAGCACAGAGAGAGAGGAGGCCCGCGCGGAGAGAGAGCGC 4983
Qy 1560 LeuArgArgLeuGluLysLysArgArg-----LysAlaGlnCys 1572
Db 4984 CTACGAAGACTGGAGAAAAAGAGAGAGGTAAAGAGAGCAGATGGCTGAAGAGCCAGTGC 5043
Qy 1573 LysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSer 1592
Db 5044 AAACCTTACTACTCCGACTACTCCCGCTTCGCGCTCCTCGTCCACCATCTTGTGCACAC 5103
Qy 1593 HisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMet 1612
Db 5104 CACTTACCTGGACCTTTCATCACAGGTGTATCGGGCTGAACGCTGGTCAACATGGCCATG 5163
Qy 1613 GluHisTyrGlnGlnProGlnIleLeuAspGluAlaIleLysIleCysAsnTyrIlePhe 1632
Db 5164 GAGCACTACCAAGAGCCCCAGATTCGTGATGAGGCTCTGAAGATCTGAACACTACATCTTC 5223
Qy 1633 ThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhe 1652
Db 5224 ACTGTCTCTTGTCTGGAGTCAGTTTCAAACTTGTGGCTTTGGTTTCCGTCGGTTC 5283
Qy 1653 PheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIle 1672

```
Db 5284 TTCCAGGACAGGTGGAAACAGCAGCTGGACCTGGCCATTGTGTGCTGTCCATCATGGGCATC 5343
Qy 1673 ThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIle 1692
Db 5344 ACGCTGGAGGAATCAGAGGTCAACGCTCGCTGCCATCAACCCACCATCATCCGCATC 5403
Qy 1693 MetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArg 1712
Db 5404 ATGAGGGTGTGGCATTGGCCGAGTCTGAAGCTGCTGAAGATGGCTGTGGGCATCGG 5463
Qy 1713 AlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPhe 1732
Db 5464 GCGCTGTGGACACGGTATGACAGCCCTGCCCCAGGTGGGAAACCTGGGACTTCTCTTC 5523
Qy 1733 MetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCys 1752
Db 5524 ATGTGTGTGTTTTTCATCTTTTCAGCTCTGGGCGTGAGCTCTTTGGAGACCTGGAGTGT 5593
Qy 1753 AspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMet 1772
Db 5584 GACGAGACACACCCTGTGAGGGCTGGGCGCTCATGCCACCTTTTCGGAACCTTTGGCATG 5643
Qy 1773 AlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAsp 1792
Db 5644 GCCTTCTCAACCCCTCTCCAGTCTCCACAGGTGACAAATTGGAAATGGCATTTATGAAGAC 5703
Qy 1793 ThrLeuArgAspCysAspGlnGluSerThrCysTrpAsnThrValIleSerProIleTrp 1812
Db 5704 ACCCTCGGGACTGTGACAGGAGTCCACCTGCTACAAACAGCGTCATCTCGCCTATCTAC 5763
Qy 1813 PheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeu 1832
Db 5764 TTTGTGCTCTGCTGTCAGCGCCAGTTCGTGTAGTCAACGTGGTGATCGCGCTGCTG 5823
Qy 1833 MetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGlu 1852
Db 5824 ATGAAGCACCTGGAGGAGAGCAACAGAGGCCAAGGAGGAGGCCGAGCTAGAGGCTCAG 5883
Qy 1853 LeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPhe 1872
Db 5884 CTGGAGCTGGAGATGAAGACCTCAGCCCCCAGCCCCCAGCTCGCCACCTGGGGCAGCCCCCTC 5943
Qy 1873 LeuTrpProGlyValGluGlyProAspSerProLysProLysProGlyValAlaLeuHis 1892
Db 5944 CTCTGGCTGGGGTTCGAGGGCCCCGACAGCCCCCAGCCCCCAGAGCTCGGGCTCTGCAC 6003
Qy 1893 ProAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnPro 1912
Db 6004 CCAGCGGCCACGCGAGATCAGCTCCACCTTTTCCCTGGAGCACCCCCACGATCGAGCCC 6063
Qy 1913 HisProThrGluLeuProGlyProAspLeuThrValArgLysSerGlyValSerArg 1932
Db 6064 CACCCACGAGCTGCCAGGACAGACTTACTGATGTGGGAAAGTCTGGGGTCAAGCCGA 6123
Qy 1933 ThrHisSerLeuProAsnAspSerTrpMetCysArgHisGlySerThrAlaGluGlyPro 1952
Db 6124 ACGCACTCTCTGCCCAATGACAGCTACATGTGTGGCATGGAGCACTGCCGAGGGGCC 6183
Qy 1953 LeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis 1972
Db 6184 CTGGGACACAGGGGTGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCTTGTCCGTTTAC 6243
Qy 1973 SerGlnProAlaAspThrSerTrpIleLeuGlnLeuProLysAspAlaProHisLeuLeu 1992
Db 6244 TCCAGCCAGCAGATACACAGCTACATCTCGAGCTTCCCAAAGATGCACTCATCTGCTC 6303
Qy 1993 GlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSer 2012
Db 6304 CAGCCCCACAGCGCCCCCAACTGGGGCACCATTCGCCAACTGCCCCCCACAGGAGCTCC 6363
Qy 2013 ProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAspSerLeuAspVal 2032
```

```
Db 6364 CTTTGGCTCAGAGGCCACTCAGGCGCCAGGCAATAAGGACTGACTCTCTTGGAGCTT 6423
Qy 2033 GlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeu 2052
Db 6424 CAGGGTCTGGGACAGCCGGGAAGACCTCTCTGGCAGAG----- 6459
Qy 2053 AlaArgAlaTrpSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSer 2072
Db 6459 ----- 6459
Qy 2073 HisSerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsn 2092
Db 6459 ----- 6459
Qy 2093 TrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrp 2112
Db 6459 ----- 6459
Qy 2113 IleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeu 2132
Db 6460 -----GAGGAGCCCCCATCCACCGGACCTG 6486
Qy 2133 LysLysCysTrpSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAsp 2152
Db 6487 AAGAAGTGTACAGCGTGGAGGCCAGAGCTGCCAGCGCCGCCACCTCTCTGGCTGGAT 6546
Qy 2153 GluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeu 2172
Db 6547 GAGCAGAGGAGACACTCTATCGCGCTCAGCTGCTGGACAGCGGCTCCCAACCCACCTG 6606
Qy 2173 GlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySerArgProLys 2192
Db 6607 GGCACAGACCCCTTAACCTTGGGGGCGAGCTCTTGGGGGGCTTGGGAGCGGCCCAAG 6666
Qy 2193 LysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThr 2212
Db 6667 AAAAACTCAGCCCGCTAGTATCACCATAGACCCCCCAGAGCCCAAGTCTCTCGGACC 6726
Qy 2213 ProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspPro 2232
Db 6727 CCGCCAGACCTGGTATCTGCTCCGAGGAGGGCTCCGTCACGACTCCCAAGGATCCC 6786
Qy 2233 LeuAlaSerGlyProProAspSerMetAlaAspSerProSerProLysLysAspValLeu 2252
Db 6787 TTGGCTCTGGCCCCCTGACAGCATGGCTCGCTCGCCCTCCCAAGAAAGATGTGCTG 6846
Qy 2253 SerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6847 AGTCTCTCCGGTTTATCTCTGACCCAGAGACCTGGACCCCC 6888
```

RESULT 4

```
US-09-398-522-51
; Sequence 51, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (373)....(3993)
; US-09-398-522-51
```

Alignment Scores:				
Pred. No.:	0	Length:	3993	
Score:	6315.50	Matches:	1207	
Percent Similarity:	98.1%	Conservative:	0	
Best Local Similarity:	98.1%	Mismatches:	0	
Query Match:	53.1%	Indels:	23	
DB:	3	Gaps:	1	
US-09-611-257A-37 (1-2266) x US-09-398-522-51 (1-3993)				
Qy	1	MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20	
Db	373	ATGACGAGGAGGAGGATGGAGCGGCCCGGAGGTCGGACACCCCGGAGCTTCATG	432	
Qy	21	ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40	
Db	433	CGGCTCAACGACCTGTGCGGGGCGGGGCGGGCGGGGCGGGGTCAGCAGAAAAGGAC	492	
Qy	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60	
Db	493	CCGGGACGCGGACTCCGAGCGGAGGGGCTGCGGTACCCGGGCGTGGCCCGGTGGTT	552	
Qy	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80	
Db	553	TTCTTTCTACTTGAGCCAGGACAGCCGCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	612	
Qy	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100	
Db	613	CCCTGGTTTGAGCGCATCAGCATGTGTTGTCATCTCTTCTCAACTGCGTGACCTGGGCATG	672	
Qy	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120	
Db	673	TTCCGGCCCATGCGAGGACATCGCCTGTGACTCCAGAGCGCTCCGGGATCCTCGAGGCCCTTT	732	
Qy	121	AspAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGly	140	
Db	733	GATGACTTCATCTTTCCTTTCCTGCGTGAGATGGTGGTGAAGATGGTGGCTTGGGC	792	
Qy	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160	
Db	793	ATCTTTGGGAAAAAGTGTACTCGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTC	852	
Qy	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180	
Db	853	ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAACCGTCAGCTTCTCAGCTGTACGG	912	
Qy	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200	
Db	913	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGGTGCCAGCATGGCATCCTT	972	
Qy	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220	
Db	973	GTCAGTTGCTGCTGGATACGTGCCCATGTGTTGGGCAACGTCCTGCTGCTGCTTCTTC	1032	
Qy	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240	
Db	1033	GTCCTTCTTCATCTTCGGCATGCTCGCGCTGCTGAGCTGTGGGAGGGGCTGCTTCGGHAACCGA	1092	
Qy	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260	
Db	1093	TGCTTCTTCTACCTAGAAATTCAGCCCTCCCGCTGAGCGTGGACCTGGAGGGCTATTACCA	1152	
Qy	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280	
Db	1153	ACAGAGAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACGCGAAGCGGATGCGG	1212	
Qy	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300	
Db	1213	TCCTCAGAAGCGTCCCAACGCTGCGGGGAGCGGGGCGGGGCGGGGCTGCTGCGGCTCTG	1272	
Qy	301	AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320	

Db	1273	GACTATGAGGCTACAACAGCTCCAGCAACACCACTGTGTCAACTGAGTGAACCACTACTAC	1332	
Qy	321	ThrAsnCySerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340	
Db	1333	ACCAACTGCTCAGCGGGGAGCAACCCCTTCAAGGGCGCCATCAACTTTGACCAACAT	1392	
Qy	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360	
Db	1393	GGCTATGCTGGATCGGCATCTTCCAGGTCAACGCTGAGGGGCTGGTGGATCATATG	1452	
Qy	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380	
Db	1453	TACTTTGTGATGGATGCTCATTCCTTACAAATTTCTACTTCTATCTCTCTCATCATC	1512	
Qy	381	ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu	400	
Db	1513	GTGGGCTCTCTTCTCATGATCAACCTGTGCTGGTGTGATTTGCCAGCGAGTTCTCAGAG	1572	
Qy	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420	
Db	1573	ACCAAGCAGCGGGAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTTCTCTTCCCAACGCC	1632	
Qy	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrIleu	440	
Db	1633	AGCACTCTGGCTAGCTTCTCTGAGCCGCGAGCTGTCTATGAGGAGCTGTCAAGTACCTG	1692	
Qy	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460	
Db	1693	GTGTACATCTTCTTAAGGAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG	1752	
Qy	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480	
Db	1753	CGGGTTGGGCTGCTCAGCAGCCAGCACCCCTCTCGGGGCGCAGGAGACCCAGCCAGCAGC	1812	
Qy	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500	
Db	1813	AGCTGCTCTCGCTCCCAACCGCGCTATCGCTCCACCACTGTGTGCACACCAACCCACAC	1872	
Qy	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520	
Db	1873	CATCACCACCACTACCACTGGGCAATGGGACGCTCAGGGGCCCCCGGGCGAGCCCGGAG	1932	
Qy	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540	
Db	1933	ATCCAGGACAGGATGCCATGGTCCCGCGGCTCATGCTGCCACCACTCTGACGCGCT	1992	
Qy	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560	
Db	1993	GCCCTCTCCGGGGCCCCCTTGTGGGCGAGAGTCTGTGCACAGCTTCTACCATGCCGAC	2052	
Qy	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580	
Db	2053	TGCCACTTAGAGCAGATCCGCTGCCAGGCGCCCTCCAGGTCCCATCTGAGGCATCC	2112	
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600	
Db	2113	GGCAGGACTGGGCGGCGGAGGTGTATCCCACTGTCACACGAGCCCTCCACCGGAG	2172	
Qy	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620	
Db	2173	ACGCTGAAGGAGAAGGCACTAGTAGAGTGGCTGCCAGCTCTGGGCCCCCAACCCCTCAC	2232	
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640	
Db	2233	AGCTTCAACATCCCAACCGGGCCCTTACAGCTTCCATGCAAGCTGTCTGGAGACACAGAGT	2292	
Qy	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660	
Db	2293	ACAGGTGCTCGCAAAAGCTCTTGAAGATCTCCAGCCCTTGTCTTGAAGAGCAGACAGTGA	2352	
Qy	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680	
Db	2353	GCCTGTGGTCCAGACAGCTGCCCTTCTGTGCCCGGGCGGGGAGGGAGGTGGAGCTC	2412	

Db 1991 CATAGAGGGCCGAGAGAGGGCCCGGTGGGCATATGCCGACGACCACTGCCGCTGCCAG 2050
Qy rGlyArg---ThrValGlySerGlyLysVal---TyrProThrVal----- 593
Db 2051 CCTCAGGCTGGCCACAGGGGTGGGCACCATGAACCTACCCACGATCCTGCGCTCAGGGGT 2110
Qy 594 -----HisThrSerPro-----ProPr 599
Db 2111 GGGCAGCGGCAAGAGCAGCACCAGCCCGGACCAAGGGGAAGTGGGCGGTGGACCGCC 2170
Qy 599 oGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLe 619
Db 2171 AGGCACC-----GGGGGACCGCGCCGTTGAGCTT 2200
Qy 619 uThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrG1 639
Db 2201 GAACAGC-----CCTGATCCCTACGAGAAGATCCCGCATGTGTCGGGGAGCA 2248
Qy 639 nSerThrGlyAlaCysGlnSer-----SerCysLysIleSerSe 652
Db 2249 TGGACTGGGCAGGCCCTCGCCATCTGTGGGGCTCAGTGTGCCCTCGCCCTGCCCCAG 2308
Qy 652 rProCysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaAr 672
Db 2309 CCCC-----CCAGCGGGCACACTGACCTGTGAGCTGAAGAGCTGCCCGTACTGCACCCG 2362
Qy 672 gAla---GlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerG1 691
Db 2363 TGGCCTGGAGACCCGAGGGTGAAGCTCAGCGGCTCGGAAGTGGAGACTCAGATGGCCG 2422
Qy 691 uAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro----- 708
Db 2423 TGGCGTCTATGAATTACGACGAGACGTCCGGCACGTGCGTGGGACCCACCGCAGCC 2482
Qy 709 -----HisSerArgArgGlnArgSe 715
Db 2483 ACCCGTGGCAGCAGACACACAGGCCCGCAGGCCAGGCCCGCGGGGACAGCA 2542
Qy 715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspTh 735
Db 2543 GAGGGACCCCGGGCAGCCAGGCTGGATGGGCGGCTCTGGGTTACCTTCAGCGGCAA 2602
Qy 735 rPheArgLysIleValAspSerTyrPheGlyArgGlyIleMetIleAlaIleLeuVa 755
Db 2603 GCTGCGCGCATCTGTGACAGCAAGTACTTCAGCGGTGGCATCATGATGGCCATCTTGT 2662
Qy 755 lAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLe 775
Db 2663 CAACACGCTGAGCATGGGCGTGGAGTACCATGACAGCCCGGAGAGCTGACTAATGCTCT 2722
Qy 775 uGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLe 795
Db 2723 GGAGATCAGCAACATCTGTTCCACCATGTTTCCCTGGAGATGCTGTGAAGCTGCT 2782
Qy 795 uValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVa 815
Db 2783 GGCCTGCGGCGCTCTGGGCTACATCCGGAACCCGTACAACATCTTCAGCGCATCATCT 2842
Qy 815 lValIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgTh 835
Db 2843 GGTATCAGCGCTCGGGAGATCGGGGCGGCGGCGGCGGTGGCTGTGTGCTGGCGCAC 2902
Qy 835 rPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLe 855
Db 2903 CTTCCGGCTGCTGCTGTGCTGAAGCTGTGTGGCTTTCTTGCACGCCCTTGGCGGCCAGCT 2962
Qy 855 uValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPh 875
Db 2963 CGTGGTCTGTGAAGACCATGGACACAGCTGGCTACCTTCTGCACGCTGTCTCATGCTCTT 3022
Qy 875 eilePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluAr 895
Db 3023 CATTTTCATCTTCAGCATCCTGGGCATGCACCTTTTCGGCTGCAAGTTTCAGCTGAAGAC 3082

Qy 895 gAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleVa 914
Db 3083 AGACACCGGAGACACCGTCTGCACAGGAAGAACTTCGACTCCCTGCTGTGGGCATCGT 3142
Qy 914 lThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAl 934
Db 3143 CACCGTGTTCACATCTGACCAGGAGGACTGAAGCTGGTCTGTGTACACGCGCATGGC 3202
Qy 934 aSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVa 954
Db 3203 CTCACCTCTCTCTGGCGCCCTCTACTTCTGTGGCCCTCATGACCTTCGGCAACTATGT 3262
Qy 954 lLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLy 974
Db 3263 GCTCTTCAACCTGCTGTGGCCATCTCTGTGGAGGGCTTCAGGCGGAG----- 3311
Qy 974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyG1 994
Db 3312 -----GG 3313
Qy 994 YAspAlaAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAsp-- 1013
Db 3314 CGATGCCACAGATCCGACACGAGGAGCAAGAGCTCGTCCACTTCGAGGAGGACTT 3373
Qy 1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerLe 1025
Db 3374 CCACAAGCTCAGAGAACTCCACACACAGAGCTGAAGATGTTCCTCGCGCTGACCCC 3433
Qy 1025 uGlyGluHisProGluLeuArgLysSerLeuProProLeuIleIleHisThrAlaAl 1045
Db 3434 CAACGGGACCTCGAGGGACGAGGACGCTGCCCTCCCTCATCATGTGCACAGCTGC 3493
Qy 1045 aThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyAlaLeuGlyProAl 1065
Db 3494 CAGCCCATGCTTACCCCAAGAGCTACCATTTCTCTGGATGCAGCCCCCGCTCCAGCA 3553
Qy 1065 aSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysSe 1085
Db 3554 CTCTCGCGCTGGCAGCAGCAGCTCCGGGGACCGGCCA-----CTGGGAGACCAAGAGCC 3607
Qy 1085 rProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105
Db 3608 TCCGGGCGAGCTCCGAAGTTCTCCCTGTGCCCTTGGGGCCCGCAGTGGCGCTCGAGCAG 3667
Qy 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerSerLeuLysArgArgSerProSe 1125
Db 3668 CCGCGCTCCAGCTGGAGCAGCTGGGCGCTGCCCCAGGCTCAAGCGCCCGGCCAGTG 3727
Qy 1125 rGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSe 1145
Db 3728 TGGGAACGTGAGTCCCTGCTGTCTGGCGAGGGCAAGGGCAGCACCGACGACGAA----- 3782
Qy 1145 rSerGluGluGluArgAlaSerProAla-----GlySerAspHisArgHisArgGlySe 1163
Db 3783 -GCTGAGGAGCGGCGGCGCGCGCGCGCGCGCGCTGCACCCCGCAGTGGCGGGCGGAGTC 3841
Qy 1163 rLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu----- 1178
Db 3842 CTTGGACCCACGGCCCTGGCGGGCGGCGGCTCCCGCTTACCAAGTGCCTCGCATCGCGA 3901
Qy 1179 -----ArgThrAlaSerGlyArgGlySe 1192
Db 3902 CGGCGAGGTGGTGGCCCTGCCAGCGACTTCTTCTGCGCATCGACAGCCACCGCTGAGGA 3961
Qy 1192 rAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLe 1212
Db 3962 TGCAGCGAGCTTGACGACGACTCGGAGGACAGCTGCTGCTCCGCTCGCATNAAGTCT 4021
Qy 1212 uArgProAspAspProProLeuAspGlyAspAlaAspAspGluGlyAsnLeuSerLy 1232
Db 4022 GGAGCCCTACAAGCCC----- 4037

Qy 1232 sGlyGluArgValArgAlaThrIleArgAlaArgLeuProAlaCysTyrLeuGluArgAs 1252
Db 4038 -----CAGTGGTCCGGAGC-----CGGA 4057
Qy 1252 pSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeuCysHisArgII 1272
Db 4058 GGCCTGGGCCCTTACCTTCTCCCCACAGAACCGGTTCGGCGTCTCCTGCCAAGGT 4117
Qy 1272 eIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleTh 1292
Db 4118 CATCACACACAGATGTTGATACAGTGGTCTCTCTTCACTCTCTCAACTCGCTAC 4177
Qy 1292 rIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLe 1312
Db 4178 CATCGCCTCGAGAGGCTGCATTTGACCCCGGACGACCGAGCGGTCTTCTCAGCGT 4237
Qy 1312 uSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLe 1332
Db 4238 CTCCAATTACATCTTACGGCCATCTTCGTGGCGGAGATGATGTGAAGGTGGTGGCCCT 4297
Qy 1332 uGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLe 1352
Db 4298 GGGCTCTGTCTCCCGCAGACGCTTACCTGCAGACAGCTGGAACTGCTGGATGGCT 4357
Qy 1352 uLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLy 1372
Db 4358 GCTGGTGTGTCTCGCGGTCTCTGCTCGGACCTCGGCTCGGCTGGTGGCGCAA 4417
Qy 1372 sIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIl 1392
Db 4418 GATCCTGGTGTCTCGCGGTCTCTGCTCGGACCTCGGCTCGGCTGGTGGCGCAA 4477
Qy 1392 eSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIl 1412
Db 4478 CAGCGGGCGCCGGCCCTCAAGCTGGTGGAGACGCTGATATCGTCTCAGGCCCAT 4537
Qy 1412 eGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGl 1432
Db 4538 TGGGAACATCGTCTCATCTCTCGCGCTCTCTTCATCATTTTGGCATCTTGGGTGTGCA 4597
Qy 1432 nLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLy 1452
Db 4598 GCTCTTCAAGGGAAGTTCTACTACTCGAGGGCCCGCACACAGGAACATCTCCACAA 4657
Qy 1452 sSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLe 1472
Db 4658 GGCACAGTGGCGGCCGCCCACTACCGCTGGGTGCGACGCAAGTACAACTTCGACAACT 4717
Qy 1472 uGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe 1492
Db 4718 GGGCCAGGCCCTGATGTCTGTCTGTCTGTCTATCCAGGATGGATGGGTGAACATCAT 4777
Qy 1492 tTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTr 1512
Db 4778 GTACGACGGGCTGATGCGGTGGTGTGCGACACGACGCTGTGCAGAACCAACCCCTG 4837
Qy 1512 pMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPh 1532
Db 4838 GATGCTGTGTACTTATCT 4897
Qy 1532 eValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAl 1552
Db 4898 CTTGGGCTGTGTGTGAGAACTTCCACNAGTGGCGGACGACCCAGAGGGCGGAGGAGGC 4957
Qy 1552 aArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArg----- 1568
Db 4958 CGCGCGCGCAGAGAGAAGCGCTCGCGCGCTAGAGAGGAGCGCGCAGGACATTTTCCC 5017
Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuVa 1586
Db 5018 CAGCCCAAGAGCCCGCGCCCTACTATGCGACTACTGCGCCCGCGCCCTCCAT 5077
Qy 1586 lHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAs 1606

Db 5078 TCATCTGCTGTGCACGACCATATCTCGACCTTCTCATCACCTTCTCATCTGTGCAA 5137
Qy 1606 nValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLy 1626
Db 5138 CGTCATCACCATGTCCATGGAGCATAATAACCAACCAAGTCGTGGACGGCCCTCAA 5197
Qy 1626 sIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAl 1646
Db 5198 GTACTGCACCTACGTCTTACCATCTCGTGTGTGTCTTCGAGGCTGCACCTGAAGCTGTGAGC 5257
Qy 1646 aPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLe 1666
Db 5258 ATTGGGTTCGTGGTCTTCAAGACAGTGGAAACACAGCTGGACCTGGCCATCGTGCT 5317
Qy 1666 uLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAs 1686
Db 5318 GCTGTCACTCATGGCATCAGCTGGAGGAGATAGATGAGCGCCGCTGCCCATCAA 5377
Qy 1686 nProThrIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLy 1706
Db 5378 CCCACCATCATCCGCATCATCGCGTCTTCGCAITTCGCCGTGTCTGAAGCTGTCTGAA 5437
Qy 1706 sMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGl 1726
Db 5438 GATGGCTACGGCATCGCGCCCTGCTGGACACTGTGTGTCGAAGCTCTCCCCAGGTGGG 5497
Qy 1726 yAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValGluLe 1746
Db 5498 GAACTTGGGCTCTTCTTTCATGCTCTGTGTTTTTATCTATGCTGCGTGGAGTGGAGCT 5557
Qy 1746 uPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaTh 1766
Db 5558 GTTCGGAGGCTGGAGTGCAGTGAAGACAACCCCTCGAGGGCTTGAGAGGACGCCAC 5617
Qy 1766 rPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTr 1786
Db 5618 CTTCAGCAACTTCGGCATGGCTTCTCACGCTGTTCCGCGTGTCCACGGGGACAACCTG 5677
Qy 1786 pAsnGlyIleMetLysAspThrLeuArgAspCys-----AspGlnGluSerThrCy 1803
Db 5678 GAACTGGATCATGAAGACACGCTGCGCGAGTGTCTCCGTGAGGACAAGCACTCCCTGAG 5737
Qy 1803 sTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheVa 1823
Db 5738 CTACTCCCGGCCCTGTGCGCCGTCTACTTCTGACCTTCTGTGTGTGGCCCCAGTTCTGT 5797
Qy 1823 lLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAl 1843
Db 5798 GCTGTGAACGTGGTGGTGGCCGTGCTCATGAAGCACCTGGAGGAGAGCAACAAGGAGGC 5857
Qy 1843 aLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProGl 1863
Db 5858 ACGGAGAGTCCGGAGTGGACGCCGAGATCGAGTGGAGATG----- 5900
Qy 1863 nProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerPr 1883
Db 5901 -----CGCAGGCGCCCGGAGTGC 5920
Qy 1883 o-----AspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAl 1900
Db 5921 ACGCCGGTGGACCGGACAGGCCT----- 5945
Qy 1900 aSerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGly-- 1919
Db 5946 -----CCCTGCCCGCAGAGAGTCCGGCGC 5971
Qy 1920 -----ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLe 1936
Db 5972 CAGGATGCCCAACCTGGT---GCACGCAAGGTGTCGTGTCCAGGATGCTCTCGCT 6028
Qy 1936 uProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyPro----- 1952

Db 6029 GCCAACACGACGCTACATGTTCCAGGCCCCGTGGTGCCTCGCGCGCCCCACCCCGCCCC 6088
Qy 1953 -----LeuGlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySe 1967
Db 6089 GCTGAGGAGTGGAGTGGAGACCTATGGGGCGGACACCC-----TTGGGCTC 6139
Qy 1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAs 1987
Db 6140 CGTTGCCTGTGCTACCTCTCGCGCGGACAGTCTGTGCTCTCCAGATCCCA----- 6194
Qy 1987 pAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuPr 2007
Db 6195 -----CTGGCTGTGTCTGCCACGAGCGGAGCGGAGCCCTCCACGCGCTGTC 6244
Qy 2007 oProProGly-----ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaLail 2025
Db 6245 CCTCGGGGACAGCCCGCTCCCGGCTCTCAGCGGCTCTCTGACAGAGGAGGCTGT 6304
Qy 2025 eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu-----Al 2043
Db 6305 GCACACCGATTCTTGAAGGGAAG---ATTGACAGCCCTAGGACACACCTGGATCCTGC 6361
Qy 2043 aGluValSerGlyProSerPro-----ProLeuAlaArgAlaTyrSerPheTrpGly-- 2060
Db 6362 AGAGCCTGTGTAGAAAACCCCGGTGAGCGCGGTGACCCAGGGGGCTCCCTGCAGTCCCC 6421
Qy 2061 ----GlnSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHi 2079
Db 6422 ACCACGCTCTCCCGCGCCCGGCGGCTCGGACCTCTGTAAGCATACC---TTGGACAGCA 6478
Qy 2079 sMetThrProProAlaPro---CysProGlyProGluProAsnTrpGlyLysGlyProPr 2098
Db 6479 CTGGCTCCAGCGCGCGCGGCGGCGGAGAG----- 6515
Qy 2098 oGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLe 2118
Db 6516 -GAGCGCGAGCCTCGGACCCAGCCGAGGAGGAGGTGAGCCATCACCAGCTCCGCGCTG 6574
Qy 2118 uPro-----ProGlyGlyGlnGluGluProPro-----SerPr 2129
Db 6575 CCCCTGGGAGCCACAGCGGAGCCCATGGCCCCGAAAGCCTCTCCGTGGCGCGCGGGA 6634
Qy 2129 oArgAspLeuLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSe 2149
Db 6635 CGCGGACTCGCAGGCTCTACACGCTGGAGCTCAGGCTCTCTGGACAAAGCG---GG 6691
Qy 2149 rTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGl 2169
Db 6692 CCGGCGACAGCAGCAGTGGCGGCGCTCGCGGAGCTGGGAGCGGAGCGCTGGGAGGC 6751
Qy 2169 nProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySe 2189
Db 6752 GAAGCCTGGGGCCCTCAG-----GCCGAGGCC-----GCTTGGGTGC 6790
Qy 2189 rArgProLysLysLysLeuSerProProSerIleIleAspProPro---GluSerGl 2208
Db 6791 GCGCAGAAAGAGAGATGAGCCCCCTCGATCTCGGTGGAACCCCTCGGAGGAGCA 6850
Qy 2208 nGlyProArgThrProProSerPro-----GlyIleCysLeuArgArgAlaPr 2225
Db 6851 GGGCTCTGGCGGCGCTCGCGGAGAGGGCGGAGCACCACACTGAGGCGCAGGACCCC 6910
Qy 2225 oSerSerAspSerLys----- 2230
Db 6911 GTCTGTGAGGCCACGCTCACAGGGAATCCTTGAGGCCACAGAGGCTCAGGGCGGG 6970
Qy 2231 ---AspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLy 2249
Db 6971 GGGGACCTCTGACGCAAGGGGGGAGCTGGGGGCCAGGCC-----TCTTCCCGGGC 7021
Qy 2249 sAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeu----- 2264
Db 7022 TGAGCACCTGACCTGCCAGCTTTTGCTTTGAGCGCGTGGACCTCGGGGTCCCGAGTGG 7081

Qy 2265 -AspPro 2266
Db 7082 AGACCT 7088

RESULT 6

US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.3% Conservative: 213
Best Local Similarity: 51.4% Mismatches: 506
Query Match: 46.1% Indels: 449
DB: 3 Gaps: 55

US-09-611-257A-37 (1-2266) x US-09-404-650-1 (1-6816)

Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 264 CAGCCGGACCCCGGAGCCCCCATCTCCCGCGAGCCTGGAGAGCCTCTGGATGA 323
Qy 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTCCACACCCAGACCTGGCGCTATTGCTTCTTCTGCTCGACAG 383
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 384 ACCACAGCCCCCGAACTGGTGCATCAAGATGGTGTGCAACCCCGTGGTTTGAATGTGTC 443
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGATGTGTGTGATCTCTGTAAGTGTGACATCTGGCATGTGACAGCGCTGCGACGAC 503
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGGACTGCTGTCCGACCGCTGCAGATCTCGAGGTCTTTGATGACTTCATCTTTATC 563
Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 564 TTCTTTCCCATGGAGATGGTGTCTCAAGATGGTGGCTGGGGATTTTGGCAAGAAGTGC 623
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTCGGGACACATGGACCGCTGATTTCTTCATCGTCATGGCAGGATGTGTCGAG 683
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGGACCTTCAGAACATCAACCTGTGCACCATCCGACCGCTGCGCGTCTCTGAGG 743
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAsp 206
Db 744 CCCCCTCAAGGCCATCAACCCCGCTGCCAGTATGCGGATCTCTGGTGAACCTCTCTCTGAC 803

Db 2490 AAGAACTTCGACTCCCTGCTGGGCCATGTCATGTTCCAGATCCTCACCCAGGAG 2549
Qy 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr 943
Db 2550 GACTGGAACTCGTCTCTACAAATGGCATGGCTCCCACTTCTCCCTGGGCTCCCTCTAC 2609
Qy 944 PheLeuAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaLeuLeu 963
Db 2610 TTTGTGGCCCTCATGACCTTCGGCAACTATGTCTTTCAACCTGCTGGTGGCCATCCTG 2669
Qy 964 ValGluGlyPheGlnAlaGluGluLysSerLysArgGluAlaSerGlyGlnLeuSer 983
Db 2670 GTGGAGGGCTTCAGGGCGGAG----- 2690
Qy 984 CysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTACGCCAAATCGCTCTCTACCTCGGACGAG 2720
Qy 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACCAGAGCTCATCCAACATAGAAGAGTTTGATAAGCTCCAGGAAGGCTTGACAGCAGC 2780
Qy 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGCAC----- 2825
Qy 1034 SerLeuLeuProLeuLysIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
Db 2826 -----CTGGACCC-----AGTCTCCCACTGGGT 2849
Qy 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGCACCTAGGTCTCTGGGGCTCGGGACCTGCCCCGACTCTCACTGCACCCGGAC 2909
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGTGGCCCTGGGCTCCCGAAAGACAGTGTCTCTAGGAGGATGAGC 2969
Qy 1081 HisGluMetLysSerProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATGACAGCCGCTCCCTGCTCCAGTCCCGAGCTCTACTACGGGCCATGGGGCCGAGC 3029
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 GCGSCCTGGGCCACCGCTGCTCCAGCTGGAAC-----AGCCTCAAG 3071
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu-----GlyGlnGluSer 1139
Db 3072 CACAAGCCGCGTGGCGGAGCATGAGTCCCTGCTCTGCGGAGCGCGCGCGCGGCC 3131
Qy 1140 GlnAspGluGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGTCTGCGAGGTGTCGGCGGAGGAGGGCCGCGCGCGCGCGCGCGCGCGCGCCCA 3191
Qy 1158 His-----ArgHisArgGly 1162
Db 3192 CACGCCCCACCATTCATCAGGSCCCCATCTGCGCGCACCGCCACCGCCCGCGG 3251
Qy 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACGTGTCTCTCGACAAACAGGAGCTCGTGACCTGCGCGGAGTGTGGTGGCGGCGG 3311
Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCCACCCTGGGCGGCTGGAGGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCAAT 3371
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220
Db 3372 GGCAGGAT-GCCACAGCATCGC---CAAAGAGCTCTTACCAGAGATGGCGGCCGCGGGA 3427
Qy 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 1240 -----

Db 3428 TCGGCGGAGGATGAGGAGGAAATCGACTACACCCCTGTGCTTCCGCGCTCCGCAAGATGAT 3487
Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluAlaArgAspSerTrpSerAlaTyrIlePhePr 1260
Db 3488 CGACGTCTATAAGCCCACTGGTGGAGGTCGCGAAGACTGGTCTGTCTACCTCTTCTC 3547
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAGAACAGGTTCCGGGTCTGTGTGCAGACCATATTGCCCCACAAACTCTTCGACTA 3607
Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3608 CGTCTGCTGGCTTCATCTTTCTCAACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3667
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 3668 CGAGCGCGGACGACCCAGACGATCTTTCTCACCCTGTCCAACTACATCTTCACGGCCAT 3727
Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
Db 3728 CTTCTGGCGGAGATGACATTGAAGGTAGTCTCGCTGGCCCTGTACTTCGCGCAGCAGGC 3787
Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLeuLeuValIleAs 1360
Db 3788 GTACCTACGACGACGCTGGAAACGCTGTGGATGGCTTTCTTGTCTTCGTTCATCATCGA 3847
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
Db 3848 CATGCTGTGTCTCTCGCTCAGCGGGGAGGCCAAGATCTTTGGGGTCTCTCCAGTCTT 3907
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGCTCTCTCGCACCTACGCCCTCGCTGTGTATCAGCGCGCGCGCGGSCCTGAAGCT 3967
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGTGGAGACATCATCTCTCTCCCTCAAGCCCATCGCAACATCGTGTCTCATCTGCTG 4027
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4028 TGCTTCTCATCATCTTTGGCATCTTGGGAGTGCAGCTCTTCAAGGCGAAGTCTTACCA 4087
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGGCGTGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCGCGCAACTA 4147
Qy 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGCTGGGTCCATCACAAATACAACTTCGACAACTTCGAGCCAGGCTCTGTATGCTCCTT 4207
Qy 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAlaValG1 1500
Db 4208 TGTCTGGCATCAGAGTGTGGGTGAACATCATGTACAATGGATGGATGTGTGTTC 4267
Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520
Db 4268 TGTGGACACAGCCTGTGACCAACCAACCCCTGGATGCTGTGTACTTCTCTCTT 4327
Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
Db 4328 CTTCTCATCTCATCTCTTTTGTGTCTCAACATGTTTGTGGGTGTCTGTGGAGAACTT 4387
Qy 1540 eHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCACAGTGGCGGACGACCCAGGAGGCTGAAGAGCCAGCGCGCTGAGGAGAACCGCT 4447
Qy 1560 uArgArgLeuGluLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580
Db 4448 GCGCGCTCTGAGAGAGAGCGCGGAGGCGCCAGCGCTGCCCTACTATGCCACTATTG 4507
Qy 1580 rArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600
Db 4508 TCACCCCGGCTGTCTATCCTCCTCCATCTGTCACGACCACTACCTGGACATCTTTCATCAC 4567


```
Db 6518 CAGCTGGCCGCCCCCGCCGCCCCACGCGCGCCCTGGCCACCGCCTGGCCCGGAG 6577
Qy 2244 rProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264
Db 6578 CCCTCTGGCCCGCGGAC-----CGCAGCAAGGACCCCGCCGCGG 6619
Qy 2264 uAspPro 2266
Db 6620 GGCACCG 6626

RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.3% Conservative: 213
Best Local Similarity: 51.4% Mismatches: 506
Query Match: 449 Indels: 449
DB: 3 Gaps: 55

US-09-611-257A-37 (1-2266) x US-09-935-541-1 (1-6816)
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 264 CAGCCCGGACCCCGGAGCCCGCCATCCTCCCGCCAGCCCTGGAGAGCCCTCTGGATGA 323
Qy 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTGCCACACCCAGACCTGGCCCTATTGCCCTTCTTCGCTCGCGACAG 383
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 384 ACCACCGACCCCGGAACTGGTGATCAAGATGGTGCAACCGCGTGTGATGTGTC 443
Qy 87 SerMetLeuValLeuLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGTGTGTGATCTCTGCTGAACCTGGCATGACCTTGGCATGTACCAAGCGCTGCGACG 503
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPhePheAla 126
Db 504 ATGGAAGTCTGTCTCCGACCGCTGCAAGATCTGAGGTCTTGTGATGACTTCATCTTTATC 563
Qy 127 PhePheAlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysCys 146
Db 564 TTCTTTGCCATGGAGATGGTGCTCAAGATGGTGCCCTGGGATTTTGGCAAGAGTGC 623
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValLeuAlaGlyMetLeuGlu 166
Db 624 TACCTCGGGACACATGGAACCGCCTGGATTTCTTCATCGTTCATGGCAGGATGGTCGAG 683
```

```
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGGACCTTCAGAAACATCAACCTCTCAGCCATCCGACCGTGCCTCTGAGG 743
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
Db 744 CCCCTCAAAGCCATCAACCGCTGCCGATCGGATCGGATCGGTAACCTGCTCTCGAC 803
Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhePheIlePheGly 226
Db 804 ACACTGCCCATGTGGGAATGCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 863
Qy 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 864 ATCATAGGTGTGAGCTCTGGCGGCTCTCGTAACCGCTCTCTCTCTCTCTCTCTCTCT 923
Qy 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTrpGlnThrGluAsnGluAspGlu 266
Db 924 TTCACCATCAAGGGATGTGGCTTGGCCCATCTACTACCGCGGAGGAGGATGATGAG 983
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 984 ATGCCCTTTCATCTGCTCCCTGTCGGCGCAATGGGATAATGGCTGCCATGATATCCCC 1043
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1044 CCGCTCAAGGAGCAG-----GGCGTGAGTGTGCTGCTCCCAAGGACGAGCTCTAC 1094
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
Db 1095 GACTTTGGGGGGGGGGCCAGGACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGT 1154
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 1155 TACTCAATGTGTGCCGACGCGGCGCAACCCCAAGGCTGTCATCAACTTTGAC 1214
Qy 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
Db 1215 AACATCGGTATGCTTGGATGTTCATCTCCAGGTGATCACTCTGGAAGGCTGGTGGAG 1274
Qy 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeu 378
Db 1275 ATCATGTACTACGTGATGATGCTCTCTTCAAACTTCATCTACTTCTCTCTCTCTCT 1334
Qy 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
Db 1335 ATCATAGTGGCTCTCTTTCATGATCAACCTGTGCTCTGTTGTATAGGACCCAGTTC 1394
Qy 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1395 TCGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAGCGGACGCTACCTCTCC 1454
Qy 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys 438
Db 1455 ---TCCACAGCGGTGGCAGCTACCGGAGCTGGGAGCTGTACGAGGAGATCTTCCAG 1511
Qy 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaAla 458
Db 1512 TATGTCTGCCACATCTCGGCAAGGCCAAGCGC-----CGCGCCCTG 1553
Qy 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnThrGlnPro 478
Db 1554 GGCTCTACCGCCCTGCGAGCGCGGCGCGCCCTGGC----- 1595
Qy 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisLeuValHisHis 498
Db 1595 ----- 1595
Qy 499 HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518
Db 1595 ----- 1595
```


Db 3312 GCCCACCCCCGGGGCGGCTGTGAGGGCGGCGAGCCCGGGCCCCCGGGGCATGAGGACTGCAAT 3371
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220
Db 3372 GGCAGGAT-GCCAGCATCGC--CAAGAGCGTCTTCACCAAGATGGCGGACCGCGGGA 3427
Qy 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpI 1240
Db 3428 TCGCGGGAGGATGAGGAGGAATCGACTACACCTGTGCTTCGCGCGTCGCGCAAGATCAT 3487
Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260
Db 3488 CGAGCTCTAAGCCCGAGCTGTCGAGGTCGCGGAGAGCTGGTCTGTCTACCTCTCTTC 3547
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAGAACAGGTTCCGGGTCTGTGTCAGACCATATTGCCCCACAACTCTTCGACTA 3607
Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI 1300
Db 3608 CGTCGCTCGGCTTCATCTTTCTCAACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3667
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 3668 CGAGCGCGGAGACACCGAAGCGCATCTTCTCACCCTGTCCAACTACATCTTCACGGCCAT 3727
Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAl 1340
Db 3728 CTTGCTGGCGAGATGACATTGAAGTAGTCTCGCTGGGCTGTACTTCGGCGAGCAGGC 3787
Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLeuSerValIleAs 1360
Db 3788 GTACCTACCGAGCAGCTGGAACGTGCTGGATGGCTTCTTGTCTTCGTCCATCATCGA 3847
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal 1380
Db 3848 CATCGTGGTGTCTTGGCTCAGCCGGGGAGCGCAAGATCTTGGGGGTCTCCGAGTCTT 3907
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 CGGCTCTCTGGCACCTTACGCCCCCTCGGTGTGTATCAGCGGGCGCGGCGCTGAAGCT 3967
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGGTGAGACATCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGCTG 4027
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVa 1440
Db 4028 TGCCTTCTTCATCATCTTGGCATCTCTGGGAGTGCAGCTCTTCAAGGGCAAGTTCTACCA 4087
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGGCTGGACACCGCAACATCATCCNACCGCTCGGACTGCGATGGCGGCCAACTA 4147
Qy 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGTGGGTCCATCACAATAACAATCTCGAACCTGGGCCAGGCTCTGTATGTCCCTCTT 4207
Qy 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValG 1500
Db 4208 TGTCTGGCATCCCAAGATGGTGGGTGAACATCATGTATGATGGATGGATGGTGTGTTC 4267
Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520
Db 4268 TGTGGACAGCAGCTGTGTGACCAACCAACCCCTGGATGCTGTGTACTTCTCTCTT 4327
Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh 1540
Db 4328 CTTCTCATCTGCTCAGCTCTTTGTGCTCAACATGTTTGTGGGTGCTGTGGTGGAGAACTT 4387
Qy 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCACAAGTGGCGGAGCACCAAGGAGGCTGAAGAGGCAAGGCGGCGGTGAGGAGAAAGCGGCT 4447

Qy 1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580
Db 4448 GCGCGCGCTGTGAGAAAGCGCGGAAGGCCAGCGGCTGCCTTACTATGCGCACTATTG 4507
Qy 1580 rArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLysLeuAspLeuPheIleTh 1600
Db 4508 TCACACCCGGCTGTCTACCTCCATCCATGTGTCCACGACCACTTACCTGGACATCTTTCATCAC 4567
Qy 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI 1620
Db 4568 CTTTCATCATCTGCTCAACGTGTGTCCACCATGTCCCTGGAGCACTACAACTCAGCCACGTC 4627
Qy 1620 eLeuAspGluAlaLeuLysLysCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640
Db 4628 CTTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCCACCACTGTCTTGTGTGTGGAGGC 4687
Qy 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660
Db 4688 TGTGCTGAAGCTGGTGGCATTTGGTCTGAGCGCGCTTCTTCAAGGACCGATGGAAACCACT 4747
Qy 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
Db 4748 GGAACCTGGCCATTGTGCTACTGTGCTGATGGGCATCACCCTGGAGGAGATCGAGATCAA 4807
Qy 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TCGCGCCCTCCCATCATCAATCCACCATCATCCGCATCATGAGGGTTCTTGGCGATGGCCG 4867
Qy 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG 1720
Db 4868 AGTGTGAAGCTGTGTAAGATGGCCACAGGAATCGCGGCGCTTGTGGACACGGTGGTGCA 4927
Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740
Db 4928 AGCTTTGCCCGAGGTGGGCAACCTGGGCGCTTCTTTCATGCTGCTCTTCTTCTCATCTATGC 4987
Qy 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG 1760
Db 4988 TGCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGTCGAGGG 5047
Qy 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780
Db 5048 CATGAGCGGCATCGCCACCTTCGAGAACTTCGCGCATGGCGCTTCTCATCTTCTTCTTCCAGGT 5107
Qy 1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspG 1799
Db 5108 CTCCACGGGTGCAACCTGGAAACGGGATCATGAAGGACACCGCTGCGGAGCTGCACCCACGA 5167
Qy 1799 nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa 1817
Db 5168 CGAGCGCAGCTGCTGAGCAGCTGCGAGTTTGTGTCGCGCTGTACTTCTGTGAGCTTCGT 5227
Qy 1817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG 1837
Db 5228 GCTCACCGCGCAGTTCGTGCTCATCAACGTGGTGGTGTGTGCTCATGAAGACCTTGA 5287
Qy 1837 uGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuGluMe 1857
Db 5288 CGACGCAACAGAGCGCGGAGGACCGCGAGATGGATGCGAGCTTCGAGCTGGAGAT 5347
Qy 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG 1876
Db 5348 GGGCCCATGGCTGGGCCCTGGCCCGAGGCTGCCTACCGGCTCCCCGGGGCGCC---CCTGG 5404
Qy 1876 yValGluGlyProAspSerProAsp----- 1884
Db 5405 C---CGAGGGCGCGGAGGGCGGCGCGCGGCGGCGACACCGAGGCGGCTTGTGCCGCGC 5461
Qy 1885 -----SerProLysProGlyAlaLeu----- 1891
Db 5462 CTGCTACTCGCTCCCGCAGGACTCTTTGGAGGGGGAGGAGCTGACCATCATCGAACACCTGTC 5521


```
Qy 1892 -----HisProAlaAlaHisAla----- 1897
Db 5522 GGGCTCCATCTTCACCACTACTCTCGCTGCCGGTGCAGAGTGTCCACGACAA 5591
Qy 1898 -----ArgSerAlaSe 1901
Db 5582 GCAAGAGTGCAGCTGGTGAGACGGAGCCTTCTCCTGTAACCTCAGACAGGTCTCGTC 5641
Qy 1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
Db 5642 CATCCTGCTGGTGACGACCTGAGTCTCGAGAGCCCCACACGCTGCCCGCA 5701
Qy 1913 -----HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929
Db 5702 GGACAGCAGGTGAGTGGACCCACCTGAGCCCATGGGTGTGGAGACCTGGGCGAATG 5761
Qy 1930 -----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHi 1945
Db 5762 CTTCTCCCTTGTCTCTACGGCGGTCTCGCGGATCCAGAGAACTTCTGTGTGAGAT 5821
Qy 1945 sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe 1965
Db 5822 GGAGGAGATCCCATCAACCCGTG-----CGTCTCTGG-----CTGAACATGACAG 5869
Qy 1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr 1985
Db 5870 CAGTCAAGCACCACCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCTGCCCATGCC 5929
Qy 1985 oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999
Db 5930 AGCCGAGTGTCTTCACCCCTGCAGTGTCTGCAGCCAGAAAGGCCAGAAAGGCACTGG 5989
Qy 1999 rTrpGlyThrIleProLysLeuProProGly-----ArgSerProLe 2014
Db 5990 CACTGGAACCTCCCAAGATTTCGCGGTCTCGAGGGTCTCTGGGCATCTCTGCGGTCAACCAAG 6049
Qy 2014 uAlaGluArgProLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGl 2034
Db 6050 GGTCAACTGTACTCTCTCCGGAGGCCACCGGAGGACGACGTCGCTGGAC----- 6101
Qy 2034 yLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAlaAr 2054
Db 6102 -----GCCAGCCCCAGCAGCTCCGCGGGCAG 6127
Qy 2054 gAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSe 2074
Db 6128 CTGCAGACCACTCGTCCGAGCAGCCTGACCTGACGACAGCCCGCGGTGCC----- 6182
Qy 2074 rLysIleSerLysHisMetThrProAlaProCysProGlyProGluProAsnTrpGl 2094
Db 6183 -----CTGGGGCGCCCGCCCTGTCTCCAGACCCCGGGCGCGCTGTCTC 6226
Qy 2094 yLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe 2114
Db 6227 C-----CCCGCGCTCGCGCGCTCAGCCTG----- 6254
Qy 2114 rGlyAspLeuLeuProProGlyGlyGlnGluProProSerProArgAspLeuLysLy 2134
Db 6255 -----CGCGCGCGCGCGCTTTTCAG 6274
Qy 2134 sCysTySerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGl 2154
Db 6275 CTGCGGGGGTGGGGCG-----CATCA 6298
Qy 2154 nArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyTh 2174
Db 6299 GCGCAGCCACAGCAGCGGGCTCC-----ACCAGCCCGGCTGCACCCACACGACTCCAT 6355
Qy 2174 rAspProSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgPr 2191
Db 6356 GGACCCCTCGACGAGGAGGCCGCGGTGGCGCGGGCGGGGGCGCGGACGACGA 6415
Qy 2191 oLysLysLysLeuSerProProSerIleThr-----IleAspProProGluSerGl 2208
```

```
Db 6416 CTGGAGACCTCAGCAGCCTCTCGCTCACCTCCCTCTTCTGCGCGCGCC----- 6467
Qy 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6468 -----CCGCGCGCAGCCCGCGCTCAGCCCGCAGGAAGTTCAGCAGCACGAG 6517
Qy 2228 pSer-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSe 2244
Db 6518 CAGCTGCGCGCGCGCGCGCCACCGCCCGCTGGCCCGCTGGCCCGGAG 6577
Qy 2244 rProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264
Db 6578 CCCCCTGTCGGCGCGCGGAC-----CGCAGCAAGGACCCCGCGCGCG 6619
Qy 2264 uAspPro 2266
Db 6620 GGCACCG 6626

RESULT 8
US-10-425-800-1
; Sequence 1, Application US/10425800
; Patent No. 6893842
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-10-425-800-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.3% Conservative: 213
Best Local Similarity: 51.4% Mismatches: 506
Query Match: 46.1% Indels: 449
DB: 3 Gaps: 55

US-09-611-257A-37 (1-2266) x US-10-425-800-1 (1-6816)
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 264 CAGCCCGGAGCCCGGAGCCCGCCATCTCCCGCGAGCGCTGGAGGACCTCTGATGGA 323
Qy 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTCCACACCCAGACCTGGCGCTATTGCTTCTTCTGCTGCGACAG 383
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 384 ACCACCGAGCCCGGAACTGGTGCATCAGATGTTGTGCAACCCCGTGGTTGAATGTGTC 443
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGTGTGTGATCTCTGCTGAACCTGGACCTTGGCATGTACCAGCCGTCGACGAC 503
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGGACTGCCTGTCGAGCCGCTGCAAGATCCTGAGGCTTTTGTATGATCTTATCTTATC 563
```

Qy	127	PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys	146
Db	564	TTCTTTGCCATGAGATGGTGCTCAAGATGGTGGCCCTGGGGATTTTTTGGCAAGAAGTGC	623
Qy	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGlu	166
Db	624	TACCTCGGGGACACATGAACCGCTGGATTCTTCATGCTCATGGTGAAGGTGGTCGAG	683
Qy	167	TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg	186
Db	684	TACTCCCTGGACCTTCAGAACATCAACCTGTACGCATCCGCACCGTGC CGCTCTCTGAGG	743
Qy	187	ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp	206
Db	744	CCCCTCAAAGCCATCAACCGCGTCCCGATGTCGGATCCTGGTGAACCTGTCTCTGGAC	803
Qy	207	ThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	226
Db	804	ACACTGCCCATGCTGGGGAATGCTCTGCTCTGCTTCTTCTTCTTCTTCTTCTTCTTGGC	863
Qy	227	IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn	246
Db	864	ATCATAGTGTGACGCTCTGGGGGGCTGCTGCTTAACCGCTGCTTCTTCTTCTTCTTCTTGGAGAGAAC	923
Qy	247	PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu	266
Db	924	TTCAACCATCAAGGGGATGTGGCTTGCCCCCATACTACCAGCGGAGGAGGATGATGAG	983
Qy	267	SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro	286
Db	984	ATGCCCTTCATCTGCTCCCTGCTGGGGGCAATAGGGATAATGGGCTGCCATGAGATCCCC	1043
Qy	287	ThrLeuArgGlyAspGlyGlyGlyProCysGlyLeu-----	300
Db	1044	CCGCTCAAGGAGCAG-----GGCCGTGAGTGTGCTGCTGCCAAGGACGAGTCTAC	1094
Qy	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln	318
Db	1095	GACTTTGGGGGGGGCCAGGACCTCAATGCCAGCGCCCTCTGTGTCACTTGGAACTGGACCGT	1154
Qy	319	TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp	338
Db	1155	TACTACAATGTGTCCGACCGGCGAGCCGCAACCCCCACAAAGGTGCCATCACTTTTGAC	1214
Qy	339	AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp	358
Db	1215	AACATCGGTTATGCTTGGATTGTATCTCCAGGTGATCATCTCGAAGGCTGGGTGGAG	1274
Qy	359	IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPhelIeTyrPheIleLeuLeu	378
Db	1275	ATCATGTACTACGTGATGGATGCTCACTCTCTTACAACTTCATCTACTCTCATCTGCTT	1334
Qy	379	IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe	398
Db	1335	ATCATAGTGGCTCTCTTTCATGATCAACCTGTGCTCTGTGTATAGGACCCAGTTC	1394
Qy	399	SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer	418
Db	1395	TCGGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCGGCGAGCGCTACCTGTCC	1454
Qy	419	AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys	438
Db	1455	---TCCAGCACGGTGGCCAGCTACCGAGCCCTGGGACCTGCTACGAGGAGATCTTCCAG	1511
Qy	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaAla	458
Db	1512	TATGCTCGCACATCTCTGGCAAGGCCAAGGCC-----CGCGCCCTG	1553
Qy	459	GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGlnThrGlnPro	478
Db	1554	GGCCTCTACCGAGGCCCTGCAGAGCGCGGCCCGCCCTGGGC-----	1595

Qy	479	SerSerSerCysSerArgSerHisArgLeuSerValHisHisLeuValHisHisHis	498
Db	1595	-----	1595
Qy	499	HisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer	518
Db	1595	-----	1595
Qy	519	ProGluLeuGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer	538
Db	1596	-----	1596
Qy	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis	558
Db	1602	GCCTCCGCC-----CCCGCCAAACTGGGCC-----CAC	1631
Qy	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu	578
Db	1632	GCCAAG-----GAGCCCCGGCACTACCAGCTGTGCCGCAACATGCCCTTGGAT	1682
Qy	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro	598
Db	1683	GCGACGCCCCACACCTCG-----GTGCAGCCCATC	1712
Qy	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr	618
Db	1713	CCGCGCCACGCTG-----	1724
Qy	619	LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr	638
Db	1724	-----	1724
Qy	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658
Db	1724	-----	1724
Qy	659	SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg-----	672
Db	1725	-----GCTTCCGATCCCGCAGCTCCCTTGTGCAGCATGAGCAGCGCCGCGGCC	1778
Qy	673	AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla	692
Db	1779	TCGGGCGCTGGCAGCACCAG-----TCGGCCAGAGAGGCTCGGCTCCGGAGCTCCGCT	1835
Qy	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712
Db	1836	GTGTGGCGAG-----CACGAGGGCGATGGGACGGGCCCGGAGCAGCAGGACGAGCC	1889
Qy	713	GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-----	726
Db	1890	TCCTCAGAACTGGGAAGGAGGAGGAGGAGGAGCAGCGCGATGGCGGTCTGGCTG	1949
Qy	727	-----AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr	744
Db	1950	TGCGGGGATGTGTGGCGGGAGAGCGCAGGCCAAGCTCGCGGCATCTGTGACACAAGTAC	2009
Qy	745	PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr	764
Db	2010	TTCAACGGGGCATCATGATGGCCATCTTGTCACACCGTCAGCATGGGCATCGAGCAC	2069
Qy	765	HisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer	784
Db	2070	CACGAGCAGCGGAGGAGCTGACCAACATCCTGGAGATCTGCAATGTGGTCTTCACGAGC	2129
Qy	785	LeuPheAlaLeuGluMetLeuLysLeuValTyrGlyProPheGlyTyrIleLys	804
Db	2130	ATGTTTGCCTCGAGATGATCTCTGAAGAGCTGGCTGCAATTTGGGCTCTTCGACTACCTCGCT	2189
Qy	805	AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGly	824
Db	2190	AACCCCTACAAACATCTTCGACACATCATGTCTATCATCAGCATCTCGGAGATCTGGGG	2249
Qy	825	GlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu	844

Db 2250 CAGCGGACGGTGGGCTGCTGGTCTGGGACCTTCGGCTGCTGGCGTCTGAACATG 2309
Qy ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
Db 2310 GTGGCTTCATGCTGCTGGCTGGCGGCGAGCTCGTGGTGTCTCATGAAGACCATGGACAAC 2369
Qy 865 ValAlaThrPheCysMetLeuLeuMetLeuPheLeuPheLeuPheLeuPheLeuGlyMet 884
Db 2370 GTGGCCACTTCGATCTGCTCATGCTCTTCATCTTCATCTTCAGCATCTTGGGATG 2429
Qy 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGCTGCAAGTTGAGCTCGCGACGACACTGGAGACACGGTGGCCGACAGG 2489
Qy 904 LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
Db 2490 AAGAACTTCGACTCCCTGCTGGGCCATCGTCACTGTGTTCAGATCCTCACCGAGGAG 2549
Qy 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr 943
Db 2550 GACTGGAACTGCTTCTACAAATGGCATGGCTCCACTTCTCCCTGGGCTCCCTCTAC 2609
Qy 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963
Db 2610 TTGTGCGCCCTCATGACCTTCGGGCACTATGTGCTCTCAACCTGCTGGTGGCCATCTCG 2669
Qy 964 ValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
Db 2670 GTGGAGGCTTCACAGCGGAG----- 2690
Qy 984 CysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTGACGCCAATCGCTCTACTCGAGCAG 2720
Qy 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACCCAGACTATCCAAATAGAGAGTTGATTAAGCTCCAGGAAGGCTCGACAGCAGC 2780
Qy 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAGATCCCAAGCTCTGCCCAATCCCATCCCATCCCAATGGGCAC----- 2825
Qy 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
Db 2826 -----CTGGACCCC-----AGTCTCCCACTGGGT 2849
Qy 1054 ThrSerThrGlyLeuGlyAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGCACTAGGTCTGTGGGCTCGGGAGCTCGCCGACCTGCCCCGACTCTCACTCGACCGGAC 2909
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGGTGGCCCTGGGCTCCGAAAGAGCAGTGTCTATAGGAGGATGAGC 2969
Qy 1081 HisGluMetLysSerProProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATGACCAAGCGCTCCCTGCTCCAGCTCCCGAGCTCTACTACGGGCCATGGGCGCGCAGC 3029
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 GCGGCTGGGCCAGCGCTCGCTCCAGCTGGAAAC-----AGCCTCAAG 3071
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGlu---GlyGlnGluSer 1139
Db 3072 CACAAGCCCGCTCGCGGAGCATGAGTCCCTGTCTCTCGGAGCGCGGCGCGCGGCC 3131
Qy 1140 GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGCTGTCGAGGTTGCCCGGACGAGGGGCGCGCGGCGCGCCCTGCACACCCCA 3191
Qy 1158 His-----ArgHisArgGly 1162

Db 3192 CACGCCCAACACATTATCATCGGGCCCCATCTGGCGACCGCCACCGCCACCGCCGCGG 3251
Qy 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACGTGTCTCCCTCGACAACAGGAGCTCGTGGTACCTGGCCAGCTGGTGGCCGCGGTGGGC 3311
Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCCACCCCGGGCGGCTGGAGGGCGGAGCCCGGCCCGCCCGGCATGAGGACTGCAT 3371
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220
Db 3372 GGCAGGAT-GCCCAAGCATCGC---CAAAGACGTCTTCAACCAAGATGGCGGACCGCGGGA 3427
Qy 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 3428 TCGCGGGAGGATGAGGAGAAATCGACTACACCTGTGCTTCGCGTCCGCAAGATGAT 3487
Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260
Db 3488 CGACGTCTATAAGCCCGACTGGTGGAGGTCGCGAGACTGGTCTGTCTACCTCTTCTC 3547
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAGAACAGGTTCCGGTCTGTGTGACAGACCATATTGCCACAAACTCTTCGACTA 3607
Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3608 CGTCTGCTGGCTTCATCTTCTCAACTGCATCACCATCGCCCTGGAGCGGCTTCAGAT 3667
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 3668 CGAGCGCGGACGACCCGAAACGATCTTCTCACCGTGTCCAACTACATCTTTCACGCCCAT 3727
Qy 1320 lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
Db 3728 CTTCTGGGCGAGATGACATTGAAGTAGTCTCGTGGGCTGTACTTCGGCGAGCAGGC 3787
Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 3788 GTACCTAGCGACGACGTGGAACGCTGCTGGTGGCTTCTGTCTTCTGCTGCATCATCGA 3847
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValle 1380
Db 3848 CATGTGTGTCTCCCTGGCCTCAGCGGGGAGCAAGATCTTGGGGTCTCCCGAGTCTT 3907
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGGCTCTGGCGCACCCCTACGCCCTCGTGTGCATCAGCGCGGCGCGCGGCTCAAGCT 3967
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGGTGAGACATCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTGCATCTGTGTG 4027
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4028 TGCCTCTTTCATCATCTTTGGCATCTCTGGAGTGCAGCTCTTCAAGGCAAGTCTACCA 4087
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGGCTGGAGACCCCGCAACATCACCAACCGCTCGGACTGCATGGCGCGCAACTA 4147
Qy 1460 rArgTrpValArgHisLysTyrAsnPheAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGTGGGTTCATCACAATACAACTTCGAAACCTGGGCCAGGCTCTGATGTCTCCTCTT 4207
Qy 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGl 1500
Db 4208 TGTCTCGCATCCAAAGATGTTGGTGAAACATCATGTACATGATGAGCTGGATGCTTGC 4267
Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520
Db 4268 TGTGGACGAGCCTGTGTGACCAACCAACACCCCTGGATGTGTGTGTACTTTCATCTCCTT 4327

1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
1540 eHisLysCysArgGlnHisGlnGluGluGluAlaAArgArgArgGluGluLysArgLe 1560
4328 CTGCTCATCGTCAGCTCTTTGTGCTCAACATGTTTGGTGTCTGTTGGAGAACTT 4387
1540 eHisLysCysArgGlnHisGlnGluGluGluAlaAArgArgArgGluGluLysArgLe 1560
4388 CCACAGTGGCGGAGAGGCTGAAGAGGACCGCGCGGTGAGGAGAAAGCGGCT 4447
1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580
4448 GCGGCGCTGAGAAAGAGCGCGGAAGCGCCAGCGGCTGCGCTTACATGACCACTATTG 4507
1580 rArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleTh 1600
4508 TCACACCGCGGTGCTCATCCACTCCATGTCACACGACCACTACCTGGACATCTTCATCAC 4567
1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI 1620
4568 CTTTCATCATCTGCTCAACGTTGTCACCATGTCCTGGAGCACTACCAATCAGCCACGTC 4627
1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640
4628 CTTGGAGACAGCCCTCAAGTACTGCAACTATATGTTTCCACTGTCTTTGTGCTGGAGGC 4687
1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLe 1660
4688 TGTGCTGAGCTGTGGCATTTGCTCAGCGCTTCTTCAAGGACCGATGGACCACTGCT 4747
1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluLysLeuValAs 1680
4748 GGACCTGGCCATTGTGCTACTGTGTCAGTCATGGGCATCACCTGGAGGAGATCGAGATCAA 4807
1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
4808 TGGCGGCTGCCATCAATCCACCATCATCCGATCATGAGGTTCTTGGGCATTTGCCCG 4867
1700 qValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720
4868 AGTCTGAGCTGTGAAGATGGCCACAGGATCGGGCCCTGCTGGACAGGTGGTGCA 4927
1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl 1740
4928 AGCTTTGCCCGAGTGGCAACCTGGGCTCTCTTATGCTGCTCTTCTTCTATCTATGC 4987
1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760
4988 TGCTCTGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACAGCAGAGAACCCGTGCGAGGG 5047
1760 YLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780
5048 CATGAGCGGATGCCACCTTCGAGAACTTCGGCATGGCCCTTCTCATCTTCTCCAGGT 5107
1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspGl 1799
5108 CTCACCGGTGACAACTGGAACGGATCATGAAGACACACGCTGCGGGACTGCACCCACGA 5167
1799 nGluSerThrCysTyrAsnThrVal-----lLeSerProIleTyrPheValSerPheVa 1817
5168 CGAGCGGAGCTGCTGAGACGCTGCAATTTGTGTGCGCGCTGTACTTCGTGAGCTTCGT 5227
1817 lLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGl 1837
5228 GCTCACCGCGGAGTTCTGTCATCAACGTGGTGGTGGTGTGCTGCTCATGAAGACCACTGGA 5287
1837 uGluSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluLeuGluMe 1857
5288 CGACAGCAACAGGAGGCGCAGGAGGACCGCAGATGGATGCCGAGCTCGAGCTGGAGAT 5347
1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGl 1876
5348 GGCCCATGGCTGGGCGCTGGCCCGAGGCTGCTACCGGCTCCCGGCGGCC---CCTGG 5404

1876 yValGluGlyProAspSerProAsp----- 1884
5405 C---CGAGGGCCGGAGGGCGGGCGGGCGGCGACACCGAGGGCGGCTTGTGCCGCG 5461
1885 -----SerProLysProGlyAlaLeu----- 1891
5462 CTGCTACTCGCTGCCAGGACTCTCTTGGAGGGGAGCTGACCATCATCGACAACCTGTC 5521
1892 -----HisProAlaAlaHisAla----- 1897
5522 GGGCTCATCTTCCACCACTACTCTCTCGCTGCGGGTGCAGGAAGTGTACCACGACAA 5581
1898 ----- 1901
5582 GCAAGAGGTGCAGCTGGCTGAGACGGAGGCTTCTCCCTGAACTCAGACAGGCTCTCGTC 5641
1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
5642 CATCTCTGCTGGTGACACCTGAGTCTCGAGGACCCACAGCCTGCCACCTGGCGCGCAA 5701
1913 ---HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929
5702 GGACAGCAAGGGTGAGCTGGACCCACCTGAGCCCATCGTGTGGAGACCTGGCGCAATG 5761
1930 -----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHi 1945
5762 CTTCTCCCTTGTCTCTACGGCGCTCTCGCGGATCCAGAGAACTTCTGTGTGAGAT 5821
1945 sGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSe 1965
5822 GGAGGAGATCCCATTCACCCCTGTC-----CGTCTCTGG-----CTGAACATGACAG 5869
1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr 1985
5870 CAGTCAAGCACCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCTCTGCCCATGCC 5929
1985 oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999
5930 AGCGAGTCTTCCACCTGCACTGTCTGCGCAGCCAGAAAGGCCACAGAAAGGCACCTGG 5989
1999 rTrpGlyThrIleProLysLeuProProGly-----ArgSerProLe 2014
5990 CACTGGAACCTCTCCCAAGATTGGCTGCGAGGGTCTCTGGGCATCTCTGGCGTCAACAAG 6049
2014 uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGl 2034
6050 GGTCAACTGTACCTCTCTCGGAGGGCCACCGGAGCGACACGTCGCTGGAC----- 6101
2034 YLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeuAlaAr 2054
6102 -----GCCAGCCCGCAGCAGCTCCGCGGCGAG 6127
2054 gAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSerHisSe 2074
6128 CCTGCACACCACTCGAGGACAGCTGACCTCAGGAGACAGCCCGCGGCTGCC----- 6182
2074 rLysIleSerLysHisMetThrProAlaProCysProGlyProGluProAsnTrpGl 2094
6183 -----CTGGGGCGCGCGGCTCTCCAGACCCCGCGGCGGCTGTC 6226
2094 YLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe 2114
6227 C-----CCCGCGCTCGCGCGCTGAGCTG----- 6254
2114 rGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLy 2134
6255 -----CGCGCGCGGCGCTCTTCAG 6274
2134 sCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGl 2154
6275 CCTCGGGGGCTCGGGCG-----CATCA 6298
2154 nArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyTh 2174

```
Db 6299 GCGAGCCACAGCAGCGGGGCTCC---ACCAGCCCGGGCTGCACCCACACGACTCCAT 6355
Qy 2174 rAspProSerAsn-----LeuGlyGlnProLeuGlyGlnProGlySerArgPr 2191
Db 6356 GGACCCCTCGAGAGGAGCGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 6415
Qy 2191 oLysAlaLysLeuSerProProSerIleThr-----IleAspProProGluSerG1 2208
Db 6416 CTCGGAGACCTCAGACGCTCTCGCTCACCCTCCCTCTTCTTGGCCCGCGCC----- 6467
Qy 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6468 -----CCGCGCGCAGCCCGCGGCTCAGCCCGCGCGCGCGCGCGCGCGCGCGAG 6517
Qy 2228 pSer-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSe 2244
Db 6518 CAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 6577
Qy 2244 rProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264
Db 6578 CCCCTCGTGGCGCGCGGAC-----CGCAGCAAGACCCCGCGCGCGCGCGCGCG 6619
Qy 2264 uAspPro 2266
Db 6620 GGCACCG 6626

RESULT 9
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5484.00 Matches: 1237
Percent Similarity: 59.9% Conservative: 211
Best Local Similarity: 51.2% Mismatches: 507
Query Match: 46.1% Indels: 462
Db: 3 Gaps: 56

US-09-611-257A-37 (1-2266) x US-09-404-650-3 (1-6855)
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 264 CAGCCCGGACCCCGAGGCCCCCATCTCCCGCGCAGCGCGCTGGAGGACCTCTGGATGGA 323
Qy 51 -----LeuProTyProAlaLeuAlaProValAlaProValAlaPhePheTyLeuSerGln 66
Db 324 GCTGATCTCATGTGCCACACCCAGACCTGGCGCTATTGCGCTTCTTCTGCTGCGACAG 383
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 384 ACCACCGCCCGCGGAGCTGTGTCAAGATGGTGTCAACCCCGTGTGAAATGTGTC 443
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
```

```
Db 444 AGCATGCTGGTGATCTCTGCTGAACCTGGCATGTGACAGCTGGCATGTGACAGCGTGCAGCAC 503
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGACTGCCTGTCCGACCGCTGCAAGATCTCGAGGTCTTTGATGATCTTCATCTTTATC 563
Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 564 TTTCTTTCATGAGATGGTGCTCAAGATGGTGCCCTGGGGAATTTTGGCAAGAGTGC 623
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTCGGGGACACATGGAACCGCTGGAATTTCTTCATCGTCATGGCAGGATGGTCGAG 683
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGGACCTTCAGAACATCAACCTGTCAACCATCCGACCTCCGACCGTGGCGTCTTGAGG 743
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
Db 744 CCCCTCAAGAGCATCAACCGCGTCCAGATGATCGGATCTCTGGTGAACCTGCTCTTGAC 803
Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuCysPhePheValPhePheIlePheGly 226
Db 804 ACCTGCCCCATGCTGGGGAATGCTGCTGCTCTGCTCTTTGCTCTTCTTCATCTTTGGC 863
Qy 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 864 ATCATAGTGTGACAGCTCTGGCGGGCTGCTGGGTAAACCGCTCTCTCTGGAGAGAAC 923
Qy 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db 924 TTCACCATACAGGGGATGGCGCTTGCCTCCATACCTACACGCGGAGGAGGATGATGAG 983
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 984 ATGCCCTTCATCTGCTCCCTGTCGGGGCACAATGGGATAATGGGCTGCCATGAGATCCCC 1043
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1044 CCGCTCAAGGAGCAG-----GGCGGTGAGTGTGCTGCTCCAGGACGACGCTCTAC 1094
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
Db 1095 GACTTTGGGCGGGCGCGCAGGACCTCAATCCAGCGGCTCTGTGTCACTGGNACCGT 1154
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 1155 TACTACAATGTGTCGCGCAGCGGCGGCCAACCCCAAGGGTGCATCACTTTTGAC 1214
Qy 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
Db 1215 AACATCGGTATGCTGGATGTCTTCAGGTGATCACTCTGGAAGGCTGGGTGGAG 1274
Qy 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db 1275 ATCATGTACTACGTGATGGATGCTCACTCTTCTACAACCTTCATCTACTCTCTCTGCTT 1334
Qy 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
Db 1335 ATCATAGTGGGCTCTTCTTCATGATCAACCTGCTGCTGCTGTGTCATAGCAGCCAGTTC 1394
Qy 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1395 TCGGAGACCAAGCAACGGGAGCACCGCTGATGTGGAGGACGCGGACGCTACCTGTGCC 1454
Qy 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys 438
Db 1455 ---TCCAGCAGGTGGCCAGCTAGCCGAGCTGGCGAGCTGCTAGGAGGATCTTCCAG 1511
Qy 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
```

Db 1512 TATGTCGCCACATCTCGCGCAAGCCCAAGCGC-----CGCGCCCTG 1553
Qy 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
Db 1554 GGCCTCTACAGGCCCTGCGAGAGCGCGCGCCAGCGCCCTGGGC----- 1595
Qy 479 SerSerSerCysSerArgSerHisArgLeuSerValHisHisLeuValHisHis 498
Db 1595 ----- 1595
Qy 499 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518
Db 1595 ----- 1595
Qy 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
Db 1596 -----CCGAG 1601
Qy 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis 558
Db 1602 GCCCGGCC-----CCGCCAAACCTGGGCC-----CAC 1631
Qy 559 AlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerProSerGlu 578
Db 1632 GCCAAG-----GAGCCCGCGCACTACCCAGCTGTGCCGCAACATAGCCCTGGAT 1682
Qy 579 AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro 598
Db 1683 GCGAGCGCCCAACCCCTG-----GTGACGCCCATC 1712
Qy 599 ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProThr 618
Db 1713 CCCGCCAGCTG----- 1724
Qy 619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr 638
Db 1724 ----- 1724
Qy 639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658
Db 1724 ----- 1724
Qy 659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1725 -----GCTTCGATCCCGCCAGCTGCCCTGTGTCAGCATGAGGCGCGCGCGCC 1778
Qy 673 AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla 692
Db 1779 TCGGGCCTGGGCAGCAGCCGAC---TCGGGCCAGGAGGGCTCGGGCTCGGGAGCTCCGCT 1835
Qy 693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712
Db 1836 GGTGGCGAG-----GACGAGCGCGATGGGACCGGGCCCGGACGAGCGAGCGGAGCC 1889
Qy 713 GlnArgSerLeuGlyProAspAlaGlnProSerSerValLeu----- 726
Db 1890 TCCTCAGAACTGGGGAAGGAGGAGGAGGAGGAGCGCGGATGGCGCGCTGCGCTG 1949
Qy 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744
Db 1950 TCGCGGGATGTGGCGGAGACGCGACCAAGCTGGCGGCATCTGTGGACAGCAAGTAC 2009
Qy 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
Db 2010 TTCAACCGGGGCATCATGATGCCATCTCTGTCAACACCGTCAGCATGGGCATCGAGCAC 2069
Qy 765 HisGluGlnProGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
Db 2070 CACGAGACGCGGAGGAGCTACCCACATCTCTGGAGATCTGCATGTGGTCTTACCCAGC 2129
Qy 785 LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTGCCCTGGAGATGATCTCTGAAGCTGGCTGCTGCTTGGCTCTTTCGACTACTCGCT 2189

Qy 805 AsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValcyl 824
Db 2190 AACCCCTACACATCTTCGACAGCATCATTTGTTCATCATCAGCATCTGGAGATCGTGGG 2249
Qy 825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
Db 2250 CAGCGGACGGTGGCTGTGCTGCTCGGACCTTCGCGCTTCGCGCTGCTGCTGCTGCTG 2309
Qy 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
Db 2310 GTGCGCTTCATGCTGCCCTGCGCGCCAGCTCGTGTGCTCATGACCATCGACAC 2369
Qy 865 ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet 884
Db 2370 GTGGCCACCTTCTGCATGCTGCTCATGCTCTTCATCTTCATCTTCAGCATCTTGGGATG 2429
Qy 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGCTGCAAGTTTCAGCCTCCGACGCGACACTGGAGACAGGGTCCCGACAGG 2489
Qy 904 LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
Db 2490 AAGAACCTTCAGCTCCCTGCTGTGGGCCATCGTCACTGTGTCAGATCCTCACCAGGAG 2549
Qy 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr 943
Db 2550 GACTGGACGCTGCTCTACATGGATGGCTCCACTCTCCCTGGCGCTCCTCTAC 2609
Qy 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963
Db 2610 TTTGTGCGCTCATGACTTCGCGCAACTATGTGCTCTTCAACCTGCTGGTGGCCATCCTG 2669
Qy 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
Db 2670 GTGAGGGCTTCCAGGCGGAG----- 2690
Qy 984 CysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTCAGCCCAATCGCTCTCTACTCGGACGAG 2720
Qy 1004 AspPheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACCAGAGCTCATCAACATAGAGAGTTTATAGCTCCAGGAAGGCTGGACAGCAGC 2780
Qy 1014 GlyAspArgLysCysLysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGCGAC----- 2825
Qy 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
Db 2826 -----CTGACCC-----AGTCTCCACTGGGT 2849
Qy 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgThr----- 1069
Db 2850 GGGCACCTAGTCTCTGCTGGGCTGCGGAGCTGCCCGGACTCTCACTGACGCGGAC 2909
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGTGGCCCTGGGCTCCGAAAGAGAGTGTCTGCTCTAGGAGGATGAGC 2969
Qy 1081 HisGluMetLysSerProProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATGACGAGCGCTCCCTGTCTCCAGCTCCGGAGCTCTTACTACGGGCCATGGGCGGACG 3029
Qy 1101 SerSerTrpThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 GCGGCTGGGCGACCGCTGCTCCAGCTGGAGC-----AGCCTCAAG 3071
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139
Db 3072 CACAAGCGCGCTCGGCGGAGCATGAGTCCCTGCTCTTCGCGAGCGCGCGGCGGCC 3131

Qy 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluLeuSerAsnIleValPheThrSer 784
Db 2070 CACGAGCAGCGGAGGAGTGACCAACATCTCGGAGATCTGCAATGTGGTCTTCCACGAGC 2129
Qy 785 LeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTGCTTGGAGATGATCTGAAGCTGGCTGCATTTGGGCTCTTCGACTACTCGCT 2189
Qy 805 AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTyrGluIleValGly 824
Db 2190 AACCCCTACACATCTTCGACGATCATTTGTCATCATCAGCATCTGGAGATCGTGGG 2249
Qy 825 GlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
Db 2250 CAGCGGAGCGGTGGCTGTGGTCTCGGACCTTCGGCTGCTCGCGGTGCTGAACATG 2309
Qy 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
Db 2310 GTGGCTTTCATGCTGCTGCGGCGGAGCTCGTGTGTGCTCATGAAGACCATGGCAAC 2369
Qy 865 ValAlaThrPheCysMetLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet 884
Db 2370 GTGGCCACCTTCTGCATGCTGCTCATGCTTTCATCTTCATCTTCAGCATCTTGGGATG 2429
Qy 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGTGCAGTTCAGCTCCGACGACACTGGAGACACGGTCCGACAGG 2489
Qy 904 LysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
Db 2490 AAGAACTTCGACTCCCTGCTGGGCCATGCTACTGTGTTCAGATCCTCACCCAGGAG 2549
Qy 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTyrAlaAlaLeuTyr 943
Db 2550 GACTGGAAACGCTGCTCTCAATGGCATGGCTCCACTTCTCCCTGGGCTCCCTCTAC 2609
Qy 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963
Db 2610 TTTGTGCGCTCATGACTTCGGCACTATGTGCTCTCAACTGCTGTGGTGGCCATCTG 2669
Qy 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
Db 2670 GTGGAGGCTTCCAGGCGGAG-- 2690
Qy 984 CysIleGlnLeuProValAspSerGlnGlyClyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTGACGCCAATCGCTCTACTCTCGGACGAG 2720
Qy 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACCAGAGCTATCCACATAGAGAGTTTGATTAAGCTCCAGGAAGCGCTGGACGAGCAGC 2780
Qy 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAGATCCCAAGCTCGCCCAATCCCAATGACCCCAATGGGCAC----- 2825
Qy 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053
Db 2826 -----CTGGACCCC-----AGTCTCCCACTGGGT 2849
Qy 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGCACCTAGTCTCTGTGGGGCTCGGGGACCTGCCCCCGACCTCTCACTCGACCCGGAC 2909
Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGGGGCCCTGGGCTCCCGAAAGAGAGTGTCATGTCTCTAGGAGGATGAGC 2969
Qy 1081 HisGluMetLysSerProProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATGACGAGCGCTCCCTTCAGCTCCCGGAGCTCTACTACGGGCCCATGGGGCCGAGC 3029

Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 CGGCGCTGGCCAGCGCTGCTCGCTCAGCTGGAAC-----AGCCTCAAG 3071
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139
Db 3072 CACAAGCGCGCTGGCGGAGCATAGTCCCTGCTCTCGGAGCGCGCGCGCGCGCC 3131
Qy 1140 GlnAspGluGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGCTGTGCGAGGTTCGCGCGGAGGCGCGCGCGCGCGCGCACCCCTGCACACCCCA 3191
Qy 1158 His-----ArgHisArgGly 1162
Db 3192 CAGCCCCACCACTTCATCAGCGGCCCATCTGCGGCACCGCCACCGCCACCGCGCG 3251
Qy 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACCTGTCTCTCGACCAACAGGAGCTCGGTGGACCTGCCGAGCTGTGCGCGCGGTGGGC 3311
Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCACCCCGCGCGCTGGAGGCGGCGAGCGCGCGCGCGCGCGCATAGGACTGCAAT 3371
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspProProLeu-As 1220
Db 3372 GGCAGGAT-GCCGAGCATCGC---CAAAGACGCTTCCACCAAGATGGCGCGCGGGA 3427
Qy 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTyrIle 1240
Db 3428 TCGCGGAGGAGTGGAGGAAATCGACTACACCTGTCTTCCGCTGCTCGCGCAAGATGAT 3487
Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTyrSerAlaTyrIlePhePr 1260
Db 3488 CGAGCTCTATAAGCCGACTGGTGGAGGTCGCGAAGACTGCTCTCTACCTCTCTC 3547
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCGAGAACAGGTTCCGGGTCTGTGTAGACCATATTGCCCAAACTCTTCGACTA 3607
Qy 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3608 CGTGTCTCGCTTCTCTTCTCAACTGCATCACCCTCGCTGGCGGCGCTCAGAT 3667
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 3668 CGAGCGCGGACGACCGAAGCATCTTTCTCACCGTGTCAACTACATCTTCACGGCCAT 3727
Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAl 1340
Db 3728 CTTGTGGCGGAGATGACATTGAAGGTAGTCTCGCTGGCTGTACTTCGGCGAGCAGC 3787
Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLeuSerValIleAs 1360
Db 3788 GTACTACGAGCAGCTGGAACGTCGTGTGGTGTCTGTCTGTCTGTCTCATCATCGA 3847
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
Db 3848 CATCGTGTGTCTCGCTCGCTCAGCGGGGAGCCCAAGATCTTGGGGGTCTTCCAGATCTT 3907
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGGCTCTCGCACCTACGCCCTCGCTGCTCATCAGCGCGCGCGCGCGCGCTGAAGCT 3967
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGTGGAGACATCATCTCTCTCCCTCAAGCCCATCGCAACATCGTGTCTCATCTGCTG 4027
Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4028 TGCCTCTTTCATCATCTTTGGCATCTTGGGAGTGCAGCTCTTCAAGGCAAGTCTTACCA 4087
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460

[illegible]

```
Qy 2081 rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProGluThrAr 2101
|||
Db 6227 GCCGCCGCGCTGCTCCAGGACCCCGCGCGCGCTGTCC-----CCCGCGCTCG 6277
|||
Qy 2101 qSerSerLeuLeuAspThrGluLeuSerTrpIleSerClyAspLeuLeuProGlu 2121
|||
Db 6278 CCGCGCGCTGAGCTG----- 6293
|||
Qy 2121 yGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaG1 2141
|||
Db 6294 -----CCGCGCGCGGCTCTTTCAGCTGCGGGGCTGCGGGCG-- 6332
|||
Qy 2141 nSerCysGlnArgProThrSerTrpLeuAspGluGlnArgHisSerIleAlaVa 2161
|||
Db 6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358
|||
Qy 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
|||
Db 6359 CTCC---ACCAGCCCGGCTGCACCCACGACTCCATGAGACCCCTCGAGCAGGAGG 6415
|||
Qy 2179 -LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPr 2198
|||
Db 6416 CCGCGGTGGCGGGCGGGCGGGCGGGCAGCAGCAGCAGCAGCAGCAGCAGCCT 6475
|||
Qy 2198 oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSe 2215
|||
Db 6476 CTGCTCACCTCCCTCTTCTGCGCGCGCGCC-----CCGCGCGCGCAGC 6517
|||
Qy 2215 rProGlyLeuCysLeuArgArgAlaProSerSerAspSer-----LysAs 2231
|||
Db 6518 CCGCGGCTCAGCGCCCGCGCGGAGATTGAGCAGCAGCAGCAGCAGCAGCAGCAGC 6577
|||
Qy 2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa 2251
|||
Db 6578 CCCCCACGCGCGCGCTGGCCACGCGCTGGCGGAGCCCTCGTGGCGCGCGGAC-- 6635
|||
Qy 2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
|||
Db 6636 -----CGCAGCAGGACCCCGCGCGCGCGCAGC 6665
|||
```

RESULT 11

```
US-10-425-800-3
; Sequence 3, Application US/10425800
; Patent No. 6893842
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-10-425-800-3
```

Alignment Scores:

Pred. No.:	0	Length:	6855
Score:	5484.00	Matches:	1237
Percent Similarity:	59.5%	Conservative:	211
Best Local Similarity:	51.2%	Mismatches:	507
Query Match:	46.1%	Indels:	462
DB:	3	Gaps:	56

```
US-09-611-257A-37 (1-2266) x US-10-425-800-3 (1-6855)
Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
|||
Db 264 CAGCCCGGACCCCGGAGCCCATCTCCCGCCAGGCGCTGGAGGACCTCTGGATGGA 323
|||
Qy 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66
|||
Db 324 GCTGATCCTCATGTCCACACACCCAGACCTGGCGCTATTGCTTCTTCTGCTCGACAG 383
|||
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
|||
Db 384 ACCACCAACCCCGGAACTGGTGATCAAGATGGTGCAACCCGCTTTGAATGTGTC 443
|||
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
|||
Db 444 AGCATGCTGGTGATCTCTGCTGNACTGGTGACACTTGGCATGTACACGCGTGGCAGC 503
|||
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
|||
Db 504 ATGACTGCTGTCCGACCGCTGCAAGATCTGCAGGTCTTTGATGACTTCATCTTTATC 563
|||
Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys 146
|||
Db 564 TTCTTTGCCATGGAGATGGTGCTCAAGATGGTGCCCTGGGGATTTTGGCAAGATGC 623
|||
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGlu 166
|||
Db 624 TACCTCGGGACACATGGAACCGCTGGATTTCTTCATGTCATGCGCAGGATGGTCGAG 683
|||
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
|||
Db 684 TACTCCCTGACCTTCAGAAACATCAACCTGTGACCCATCGCACCGTGGCGTCTCTGAGG 743
|||
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
|||
Db 744 CCCCTCAAGCCATCAACCGCTGCCAGTATGCCGATCTCTGGTGAACCTGCTCTCTGAC 803
|||
Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPheIlePheGly 226
|||
Db 804 ACATGCCCATGTCTGGGGAATGCTCTGCTGCTCTGCTCTTTGCTCTTCTCTCTTGGC 863
|||
Qy 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
|||
Db 864 ATCATAGTGTGACAGCTCTCGCGCGGCTGCTGCTGTAACCGCTCTTCTCTGAGAGAAC 923
|||
Qy 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
|||
Db 924 TTCACCATACAAGGGGATGTGGCTTGGCCCATCTACTACCGCCGCGAGGAGGATGATGAG 983
|||
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
|||
Db 984 ATGCCCTTCATCTGCTCCCTGTCGGGCGCAATGGGATAATGGCTGCGCATGAGATCCCC 1043
|||
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
|||
Db 1044 CCGCTCAAGGAGCAG-----GGCGGTGAGTGTGCTGCCAAGGACGACGCTCTAC 1094
|||
Qy 301 AspTyrGluAlaTyrAsnSerSerSerSerSerThr-----CysValAsnTrpAsnGln 318
|||
Db 1095 GACTTTGGGGCGGGCGCCAGGACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGT 1154
|||
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
|||
Db 1155 TACTACAATGTGTCCGCGGCGGCGGCGGCAACCCCGCAGGGGTGCATCACTTTGAC 1214
|||
Qy 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
|||
Db 1215 AACATCGGTTATGCTTGATTTGATCTTCCAGGTGATCACTCTGGAAGGCTGGTGGAG 1274
|||
Qy 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
|||
```


Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCATGCTGGTGGCCCTCCGAAAGACGAGTGTCTAGGAGGATGAGC 2969
Qy 1081 HisGluMetLysSerProSerAlaArgSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATACACGAGCGCTCCCTGCTCCAGCTCCGGAGCTCTACTACGGGCCATGGGCGCGAGC 3029
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 CGGCGCTGGGCCAGCGCTCCAGCTGGAC-----AGCCTCAAG 3071
Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGlu---GlyGlnGluSer 1139
Db 3072 CACAAGCGCGCTCGCGGAGCATGAGTCCCTGCTCTCGCGAGCGCGCGCGCGGCC 3131
Qy 1140 GlnAspGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGCTCTGCGAGGTTGCGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGGCCA 3191
Qy 1158 His-----ArgHisArgGly 1162
Db 3192 CACGCCACACCATTCATACGGGCCCATCTGGCGCACCGCCACCGCCACCGCGG 3251
Qy 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACGTGTCCCTCGACACAGGAGCTCGGTGACCTGGCGAGCTGGTCCCGCGGTGGGC 3311
Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCACACCGCGCGCGCTGGAGGGCGGACGGCCCGCGCGCATGAGGACTGCAAT 3371
Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaArgProAspAspProProLeu-As 1220
Db 3372 GGCAGGAT-GCCCGAGTCGC---CAAAGACGCTCTTCCACAGATGGCGGACCGCGGGA 3427
Qy 1220 pGlyAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpI 1240
Db 3428 TCGCGGGGAGGATGAGGAGAAATCGACTACACCCCTGTGCTTCGCGCTCCGCAAGATGAT 3487
Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260
Db 3488 CGACGCTCTATAAGCCCGACGTGGTGGAGGTCCGGGAGAGCTGTCTCTACCTCTCTC 3547
Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAGAACAGGTTCCGGGTCCTGTGTGACACCATATTGCCCCAACAACTCTTCGACTA 3607
Qy 1280 sValValLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI 1300
Db 3608 CGTGTCTTGGCTTCATCTTCTCACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3667
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 3668 CGAGCGCGGACGACACCGCATCTTCTCACCGTGTCCAACATACATCTTCACGGCCAT 3727
Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
Db 3728 CTTGTGGGCGAGATGACATGAAGGTAGTCTCGTGGGCTGTACTTCGGCGAGCGGC 3787
Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 3788 GTACTACGACGACGTGGAACGTGCTGGATGGCTTCTTGTCTCTGCTGCTCATCATCGA 3847
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
Db 3848 CATCGTGTGTCTCTGGCCTCAGCGGGGAGCCAGACATCTTGGGGGTCTCTCCAGTCTT 3907
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGGCTCTCGGCACCCCTACGCCCTCGGTGTCTATCAGCGCGCGCGCGCGCGTGAAGCT 3967
Qy 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420

Db 3968 GGTGGTGGAGACATCATCTCCTCCTCAAGCCCATCGCAACATCGTGTCTCATCTGCTG 4027
Qy 1420 sAlaPhePheIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4028 TGCCTTCTTTCATCATCTTTGGCATCTCTGGGAGTGCAGCTCTTCAAGGCGAAGTTCTACCA 4087
Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGGCGTGGACACCCCGCAACATCACCAACCGCTCGAGCTGCATGGCGCCCACTA 4147
Qy 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGCTGGGTCCATCACAAATACAACTTCGACAACTCGAGCAGGCTCTGATGTCCCTCTT 4207
Qy 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValG 1500
Db 4208 TGTCTGGCATCAAGATGTTGGGTGAACATCATGTACAATGATGATGATGCTGTTC 4267
Qy 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520
Db 4268 TGTGGACACGAGCTGTGACCAACCAACCCCTGATGCTGTCTTCTTCTTCTTCTT 4327
Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
Db 4328 CTTGCTCATCGTCAGCTTCTTGTCTCAACATGTTGTGGTGTCTGTGTGTGGAGAACTT 4387
Qy 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCACAAAGTGGCGGAGCAGCAGGAGGCTGAAGAGGACGCGGCGGTGAGGAGAACGGCT 4447
Qy 1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTrpSerAspTyrSe 1580
Db 4448 GCGGCGCTGGAGAGAAGCGCGGAGGCGCCAGCGCTGCCCTACTATGCCACCTATTG 4507
Qy 1580 rArgPheArgLeuLeuValHisLeuCysThrSerHisTyrIleuAspLeuPheIleTh 1600
Db 4508 TCACACCGCGCTGTCTATCCACTCCATGTGCACCGACCACTTACCCTGGACATCTTTCATCAC 4567
Qy 1600 rGlyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnI 1620
Db 4568 CTTTCATCATCTGCTCAACGTGTGCACATGTCCCTGGAGCACTTACAAATCAGCCACGTC 4627
Qy 1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640
Db 4628 CTTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCCACCACTCTCTTGTGTGGAGGC 4687
Qy 1640 rValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLe 1660
Db 4688 TGTGCTGAAGCTGGTGGCATTTGCTGTAGGCGCTTCTTCAAGGACCGATGGAACACAGCT 4747
Qy 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
Db 4748 GGAACCTGGCCATTTGTCTACTGTCTGTCAGTCATGGGCATCACCTTGGAGAGATCGAGATCAA 4807
Qy 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TGGGCGCTGCCCATCATCCACCATCATCCGATCATGAGGTTCTGGCGATTTGCCCG 4867
Qy 1700 gValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720
Db 4868 AGTGTGAAGCTGTTGAAGATGCCACAGGAATCGCGGCCCTGTCTGGACACGGTGGTGCA 4927
Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPhePheIlePheAl 1740
Db 4928 AGCTTTGCCCGGAGTGGCAACCTGGCCCTCTTTCATGCTGTCTTCTTCTTCTATGTC 4987
Qy 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760
Db 4988 TGTCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGTCTGCAACGACGAGAACCCGCTCGGAGG 5047
Qy 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780

Db 5048 CATGAGCGGCATGCCACCTTCGAGAACTTCGGCATGGCTTCCTCACACTCTTCACAGT 5107
Qy 1780 lserThrGlyAspAenTrpAenGlylleMetLysAspThrLeuArgAspCys----AspG1 1799
Db 5108 CTCACCGGTGACAACTGGAACCGGATCATGAAGGACACGCTGCGGAGTGCACCCACGA 5167
Qy 1799 ngluserThrCysThrAenThrVal-----lleserProIleThrPheValserPheVa 1817
Db 5168 CGAGCGAGCTGCTGCGACGCTGAGTGTGTGCGCGCTGACTTCGTGAGACTTCGT 5227
Qy 1817 lLeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuG1 1837
Db 5228 GCTCACCGCGAGTTCGTGCTCATCAACGTGTGTGTGCTGTGCTCATGAAGACCTCGA 5287
Qy 1837 uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMe 1857
Db 5288 CGACAGCAACAAGAGGCGGAGGAGGAGCGCGAGATGGATCCGAGCTCGAGCTGGAGAT 5347
Qy 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG1 1876
Db 5348 GGGCCATGGCTGGGCGCTGGCGGAGGCTGCTACCGGCTCCCGGGCGCC-----CTGG 5404
Qy 1876 yValGluGlyProAsp----- 1881
Db 5405 C---CGAGGCGCGGAGGCGGCGGCGGCGGCGACACCGAGGCGGCTTGTGCGGCG 5461
Qy 1882 -----SerPro----- 1893
Db 5462 CTGCTACTCGCTGCCAGGAGAACTGTGCTGGACAGCGCTCTCTTTAATCATCAAGGA 5521
Qy 1894 -----AspSerProLysProGlyAlaLeuHis----- 1892
Db 5522 CTCCTTGAGGGGAGTGCATCATCGACAACCTGTGGGCTCCATCTTCCACCTA 5581
Qy 1895 -----ProAlaala----- 1895
Db 5592 CTCCTCGCTCGCGCTGCAAGAGTGCACACGACAAGCAAGAGTGCAGCTGGTGA 5641
Qy 1896 -----HisAlaArgSerAlaSer-----HisPh 1903
Db 5642 GACGAGGCGCTTCTCCCTGAACTCAGACAGGTCTCTCGTCCATCTCTGCTGGTGACGACCT 5701
Qy 1903 eSerLeuGluHisProThrMetGlnPro-----HisProThrGluLeuPr 1918
Db 5702 GAGTCTCAGAGACCCCAAGCGCTGCCACCTGGCGGCGCAAGACAGAGGTGAGCTGGA 5761
Qy 1918 oGlyProAspLeuThrValArgLysSerGly-----ValSerArgTh 1933
Db 5762 CCCACTGAGCCCATCGTGTGGGAGACCTGGGGAATGCTTCTTCCCTTGTCTCTAC 5821
Qy 1933 rHisSerLeuProAsn-----AspSerTyrMetCysArgHisGlySerThrAlaGluGlyPr 1952
Db 5822 GCGCGTCTCGCGGATCCAGAGAACTCTCTGTGTGAGATGGAGGAGATCCCATTCACCC 5881
Qy 1952 oLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi 1972
Db 5892 TGTC-----CGTCTCTG-----CTGAACATGACAGCAGTCAAGCACCCCAAGTCC 5929
Qy 1972 sSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHis----- 1990
Db 5930 CTTCCTCCCGGATGCTCCAGCGCTCTCTGCGCATGCGAGCGAGTTCCTCCACCTGCG 5989
Qy 1991 -----LeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe 2006
Db 5990 AGTGTCTGCCAGCCAGAAAGGCCCAAGAGGCGACTGGCACTGGAACTCCCAAGAT 6049
Qy 2006 uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 6050 TCGCGTGGAGGCTCTCTGGGATCTCTCGGGTACCAAGGGTCAACTGTACCTCTCTCG 6109
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 6110 GCAGGCCACCGGAGCGACACGTCTGCTGGAC----- 6140

Qy 2041 uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyG1 2061
Db 6141 -----GCCAGCCCCAGCATCTCGGGGCGAGCTGCAGACCACTCGTCGAGGA 6187
Qy 2061 nSerSerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMetTh 2081
Db 6188 CAGCTGACCTGAGCGACAGACCCCGCGCTGCC-----CTGGG 6226
Qy 2081 rProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProGluThrAr 2101
Db 6227 GCGCGCGCGCTGCTCAGGACCCCGCGGCGCTGTCC-----CCGCGCGCTCG 6277
Qy 2101 gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProG1 2121
Db 6278 CCGCGCGCTGAGCTG----- 6293
Qy 2121 yGlyGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaG1 2141
Db 6294 -----CGCGCGCGGGCTCTTTCAGCTGCGGGGCTGCGGGCG-- 6332
Qy 2141 nSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgHisSerIleAlaVa 2161
Db 6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358
Qy 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
Db 6359 CTCC---ACGAGCCCGGCTGACCCACCAAGCTCATCGACCCCTCGGACGAGGGG 6415
Qy 2179 -LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPr 2198
Db 6416 CCGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6475
Qy 2198 oSerIleThr-----lleAspProProGluSerGlnGlyProArgThrProProSe 2215
Db 6476 CTCCTCATCTCCCTCTTCTGCGCGCGCC-----CCGCGCGCGCAGC 6517
Qy 2215 rProGlylleCysLeuArgArgAlaProSerSerAspSer-----LysAs 2231
Db 6518 CCGCGGCTCAGCG 6577
Qy 2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa 2251
Db 6578 CCG 6635
Qy 2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6636 -----CGCAGCAAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6665

RESULT 12

US-09-404-650-12
; Sequence 12, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: McGivern, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12

Alignment Scores:
Pred. No.: 2,61e-316 Length: 6503
Score: 5418.50 Matches: 1212
Percent Similarity: 60.5% Conservative: 209

Best Local Similarity: 51.6% Mismatches: 446
Query Match: 45.5% Indels: 484
DB: 3 Gaps: 53

US-09-611-257A-37 (1-2266) x US-09-404-650-12 (1-6503)

Qy 27 GlyAlaGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46
Db 320 GGAATCACTGAGCAGCGGGCCCGAGTCCCTCCATCCCTCCAGGCTCGAGGAG 379
Qy 47 GluAlaGluGly-----LeuProTyrProAlaLeuAlaProValValPhePhe 62
Db 380 CCATTGGAAGAACCAACCTGAGCTCCACATCCAGACCTGGCTCTGTTGCTTTCTTC 439
Qy 63 TyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyr 82
Db 440 TGCCTGCGCCAGACCAGGAGCCACGGAACCTGGTGCATCAAGATGGTTTGAACCCGTGG 499
Qy 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 500 TTCAGTGTGTGAGCATGCTGTTATTCTGCTGAACCTGTGACCTGGCATGTACCAG 559
Qy 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
Db 560 CCATGTGATGACATGAGTGTCTGTCGACCGTTCGAAATCCTCGAGGTCTTCGATGAC 619
Qy 123 PheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyIlePhe 142
Db 620 TTCACTTTCATCTCTTTGCCATGGAGATGGTGTAAAGTGGTGGCCCTGGGCAATTTT 679
Qy 143 GlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAla 162
Db 680 GGCAAGAAGTCTACCTCGGAGACACATGGAACCGCTGGATTTCTTCAATGTTCATGGCA 739
Qy 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
Db 740 GGGATGGTGTAGTACTCTCTGGACCTACAGAACATCAACCTGTGAGCCATCCGACCTGTG 799
Qy 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
Db 800 CGTGTCTGAGCCCTCAAGACCATCAACCGTGTACCCAGCATCGGATCCTGGTGAAC 859
Qy 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPheValPhe 222
Db 860 CTGCTGTCTGACACGCTGCCCATGCTGGGAACGTGCTCTGCTCTGTTCTTCTGCTTC 919
Qy 223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuArgAsnArgCysPhe 242
Db 920 TTCACTCTCGGCATCATGGCGTGCAGCTCTGGGAGCGCTGTACGGAAACCGCTGCTTC 979
Qy 243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
Db 980 CTGGAAGAGAACTTCACCATACAGGGATGTGGCCCTGGCCCTTATTACCAACACAGAG 1039
Qy 263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
Db 1040 GAGGATCAGCAGATGCCCTTTATCTCTCCCTGACTGGGACAATGGCATCATGGGCTGC 1099
Qy 283 ArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1100 CACGAGATCCCCCACTGAAGAGGAGCAG-----GGCCGGGAATGCTGCTTCCAAA 1150
Qy 301 -----AspTyrGluAlaTyrAsnSerSerAsnThrThr-----CysVal 314
Db 1151 GATGATGTATGACTTCGGGGGGGGCGCCAGGACCTCAACGGCAGCGGTCTGTGGGTC 1210
Qy 315 AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAla 334
Db 1211 AACTGGAACCGCTACTACAACGTCTGCGCAGCGGCAACGCCCTCAACAGGGCGCC 1270
Qy 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354
Db 1271 ATCAACTTTGCAACATTTGGCTATGCCGGGATTTGTGATTTTCCAGGTGATCACTCTGGAA 1330

Qy 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374
Db 1331 GGCTGGGTGGAGATCATGTACTATGTGATGACGACATCTCTTCTACAACTTCATCTAC 1390
Qy 375 PheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIle 394
Db 1391 TTCACTTCTGTCATCATAGTGGGCTCTCTTCTCATGATCAACTTGTGCTCTGTGTATA 1450
Qy 395 AlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414
Db 1451 GCACCCAGTTCTCTGAGACCAAGCAGGAGCACCCTGCTGATGCTGGACCAAGCCAG 1510
Qy 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434
Db 1511 CGCTACCTGTCC---TCCAGCAGCGTGGCCAGTTACGCTGAGCCGGTGTATGCTATGAG 1567
Qy 435 GluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnVal 454
Db 1568 GAGATCTTCCAATATGTCTGTACATCTTCGCAAGCCCAAGCCCGCTGCCCTAGGCCCTC 1627
Qy 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474
Db 1628 TACCAGGCCCTGCAGAACCCG----- 1648
Qy 475 GluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisLeu 494
Db 1648 ----- 1648
Qy 495 ValHisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAla 514
Db 1648 ----- 1648
Qy 515 ProArgAlaSerProGluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeu 534
Db 1649 -----CGCCAGGCCATGGC----- 1663
Qy 535 ProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHis 554
Db 1664 -----CCGGGGACACACAGCC-----CCTGCCAAGCTGGGCC----- 1696
Qy 555 SerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArg 574
Db 1697 -----CATGCCAAG-----GAGCCAGCCACTGCAAGCTGTGCCACGACAC 1738
Qy 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594
Db 1739 AGCCCTCTGAC-----CCACTCCCCAC 1762
Qy 595 ThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSer 614
Db 1763 ACCTGGTGCAGCCC----- 1777
Qy 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634
Db 1777 ----- 1777
Qy 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys 654
Db 1778 -----ATCTCTGCCATT 1789
Qy 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1790 CTGGCCCTCTGAC-----CCAGCAGCTGCCCTCACTGCCAGCAGGAGCA 1834
Qy 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSer 688
Db 1835 GGCAGGGCGCCCTCTGCCCTGGCAGCAGCTGAC---TCAGCCAGGAAGCGCTCAGGTCT 1891
Qy 689 AspSerGluAlaValTyrGluPheThrGlnAspAla---GlnHisSerAsp-LeuArgAs 707
Db 1892 GGTGGCTCTGCAGAGGCGGGAAGCCCAATGGGATGGACTCCAGAGCAGTGGAGTGGGTC 1951

Db 3937 CAAGATTCTGGGGTCTCTCGGGTCTCTCGGCTCTCTCGGTACCTTACGTCTTTGAGGGT 3996
Qy 1391 lIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysPr 1411
Db 3997 TATCAGCGGGCCCTCGGCTGAAGCTGGTGTAGAGACGCTCATCTCTCTCCCTCAAGCC 4056
Qy 1411 oIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVa 1431
Db 4057 CATTTGGGAACATCGCTCATCTGCTGCTGCTTCTTCATCATCTTCGGCATCTCTGGGGGT 4116
Qy 1431 lGlnLeuPheLysGlyLysPhePheValCysGlnGlyValuAspThrArgAsnIleThrAs 1451
Db 4117 GCAGCTTTTCAAGGCAAGTTCTACCATTTGTTGGAGTGGACCCCGAAACATCACCA 4176
Qy 1451 nLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsnPheAspAs 1471
Db 4177 CCGATCTGACTGCTGGCGGCAACTACCGCTGGGTGCATCACAAATACAACTTTGACAA 4236
Qy 1471 nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIl 1491
Db 4237 CCTGGCCAGGCAATTGATGCTCTCTTGTCTGGCTTCCAAAGGACGCTGGGTGAACAT 4296
Qy 1491 eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr 1511
Db 4297 CATGTATATGATAGATTAGATGCTGTTGCTGTGGACGAGCCAGTGCAGAACCAACCC 4356
Qy 1511 oTrpMetLeuLeuTyrPheIleSerPheLeuIleValAlaPhePheValLeuAsnMe 1531
Db 4357 CTGGATGCTACTGTTACTTTCCTGCTGCTCATCTGTCAGCTTCTTTGTGCTCAACAT 4416
Qy 1531 tPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGlu 1551
Db 4417 GTTTGTGGGCTGCTCGTGAGAACTTCCAAAGTGGCGGAGCCAGCAGGAGGCTGAGGA 4476
Qy 1551 uAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgLysAlaGlu 1571
Db 4477 GGCCCGAGGGCTGAGAGAAACGGCTCGCGCGCTGGAAAGAGCGCCGTAAAGGCTCA 4536
Qy 1571 nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLeuCysTh 1591
Db 4537 GAGGCTGCCCTACTATGCTACTACTGTCCACAAAGGCTGCTCATCCACTCCATGTGCAC 4596
Qy 1591 rSerHisTyrLeuAspPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1611
Db 4597 CAGCCACTACTCGACATCTTCATTACTTCATCATCTGCTCAATGTTGTCAACCATGTC 4656
Qy 1611 aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysLysCysAsnTyrIl 1631
Db 4657 CCTGGAGCACTACAACACAGCCTACATCCCTAGACACAGCCCTTAAGTACTGCAACTACAT 4716
Qy 1631 ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr 1651
Db 4717 GTTCACCACTGCTTTGTGTGGAGGCTGCTGCTGAAGCTGTGTGGCATTTGCGCTGAGGCG 4776
Qy 1651 gPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGl 1671
Db 4777 TTTCTTCAAGGACCGATGGAACACAGCTGGACCTGGCCATTGCTGCTGCTCGCTCATGGG 4836
Qy 1671 YIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr 1691
Db 4837 CATCACCTGGAGGAGATCGAGATCAATGCGGCCCTTCCCATCAACCCCAACATCATCCG 4896
Qy 1691 gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMe 1711
Db 4897 TATCATGCGTTCCTGCGATGCGCGGGTGTGAAGCTATTGAAGATGGCCACAGGAAT 4956
Qy 1711 tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe 1731
Db 4957 GCGGGCCCTGTGGACACAGTGGTACAGGCTCTGCCCCAGGTGGGCAACCTGGGCCCTGCT 5016
Qy 1731 uPheMetLeuLeuPhePheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGl 1751
Db 5017 CTTTCATGCTGCTCTTCTCATCTATGCTGCTGCGGAGTGGAGCTCTTCGGAAGCTGGT 5076

Qy 1751 uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGl 1771
Db 5077 CTGCAATGACAGAAACCGGTGTGAGGCGATGAGCGGCGACCCACCTTTGAAACTTCGG 5136
Qy 1771 yMetAlaPheIleuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy 1791
Db 5137 CATGGCCTTCTCAGCTCTTCCAGGTCTCCACAGGCGATAACTGGAATGAAATTATGAA 5196
Qy 1791 sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il 1808
Db 5197 GGACACCTCGGAGACTGTACCCATGATGAGCGCACGCTGCTTAAGCAGCCTGCAGTTGT 5256
Qy 1808 eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa 1828
Db 5257 GTCACCGCTCTACTTGTGAGCTTCGTGCTCAGAGCTCAGTTCGTGCTCATCAACGCTGT 5316
Qy 1828 lIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGl 1848
Db 5317 GGTGGCGCTGCTGATGAAACATCTGGATGACAGCAACAGGAGGCCAGGAGATGCAGA 5376
Qy 1848 uLeuGluAlaGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr 1867
Db 5377 GATGATGCTGAGATCAGCTGGAGTGGCCATGGCTGCGCTCGGCCCTGCCCT----- 5428
Qy 1867 oLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLy 1887
Db 5429 -----GGCCCTGT 5436
Qy 1887 sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi 1907
Db 5437 CCCTGGT----- 5443
Qy 1907 sProThrMetGlnProHisProThrGluLeuLeuProGlyProAspLeuLeuThrVal----- 1925
Db 5444 -CCCTGCCCTGCCCCCTGCCCCCTGCTGCTGGCCCGGAGGCTGCCCATAGTTACACC 5502
Qy 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941
Db 5503 TGGGGCTCGGGCGAGGATCGGGAGGCGAGGCTGGTGGAGGC--GACACCGAGAGTCA 5559
Qy 1941 rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuPr 1961
Db 5560 CCTGTGCGG----- 5569
Qy 1961 oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIl 1981
Db 5569 ----- 5569
Qy 1981 eLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGl 2001
Db 5570 -----CACTGCTATTCTCCAGCCCGAGGAGACCTGTGG-- 5602
Qy 2001 yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 5603 -----CTGGACAG 5610
Qy 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 5611 CGTCTCTTTAATCATCAAGGACTCCTTGGAG-----GGGGAGCTGACCAT 5655
Qy 2041 uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTyrSerPheTrpGly 2060
Db 5656 CATTGACAACCTGCTCGGTCCGCTTCCACCATCGCTCACCTGACGCGCTGGGCAA 5715
Qy 2061 GlnSerSerThrGlnAlaGlnHisSerArgSer-----HisSerLysIleSer 2077
Db 5716 GTGTCCCATGACAAGCAAGACAGACAGGTCTTCATCCATCCTGCTGGGGGATGACGTAGT 5775
Qy 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 5776 -----CTTGAGGACCCCAACGCGCTGCCA-----CAGGGCCCC 5808

Db 1391 TTCAATTCGTCTCATAGTGGGCTCTCTTCTCATGATCAACTGTGTGCTGTCATA 1450
Qy 395 AlathrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414
Db 1451 GCAACCCAGTTCTCTGAGACCAACAGCGGAGCACCGGCTGATGCTGGAGCAACGCCAG 1510
Qy 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434
Db 1511 CGCTACCTGTCC---TCCAGCACGGTGGCCAGTTACGCTGAGCCCGGTGATTGTATGAG 1567
Qy 435 GluLeuLeuLysTyrLeuValTyrIleuArgLysAlaAlaArgArgLeuAlaGlnVal 454
Db 1568 GAGATCTCCAAATGCTGTGTCATCTTCGAAAGCCAGCCGCTGCGCTTAGGCCCTC 1627
Qy 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474
Db 1628 TACCAGGCCCTGCAGAACCGG----- 1648
Qy 475 GluThrGlnProSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeu 494
Db 1648 ----- 1648
Qy 495 ValHisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAla 514
Db 1648 ----- 1648
Qy 515 ProArgAlaSerProGluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeu 534
Db 1649 -----GCCAGGCCATGGCC----- 1663
Qy 535 ProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHis 554
Db 1664 -----CGGGGACACAGCC-----CCTGCCAAGCCTGGGCC----- 1696
Qy 555 SerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArg 574
Db 1697 -----CATGCCAAG-----GAGCCAGCCACTGCAAGCTGTGCCACAGAC 1738
Qy 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594
Db 1739 AGCCCTCTGGAC-----CCACTCCCCAC 1762
Qy 595 ThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSer 614
Db 1763 AACTGGTGACGCC----- 1777
Qy 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634
Db 1777 ----- 1777
Qy 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys 654
Db 1778 -----ATCTCTGCCATT 1789
Qy 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1790 CTGGCCCTGAC-----CCAGCAGCTGCTCCCTCACTGCCAGCACGAGGCA 1834
Qy 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSer 688
Db 1835 GGCAGCGGCCCTCTGGCTGGCGAGCACTGAC---TCAGGCCAGGAAGGCTCAGTTCT 1891
Qy 689 AspSerGluAlaValTyrGluPheThrGlnAspAla---GlnHisSerAsp-LeuArgAs 707
Db 1892 GGTGGCTCTGAGAGCGCCAGACCCAAATGGGATGGACTCCAGAGCAGTGAGGATGGGGTC 1951
Qy 707 pProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe 724
Db 1952 TCCTCGACCTGGGGAAGAGGAGGAGGACAGAGGAGCGGG-----CAGCCGACTG 2002
Qy 724 rValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTy 744
Db 2003 TGTGGG-GATGTGTGGCGGAGACACGAAAAAGCTGGCGGGCATCGTGGAGCAGCAAGTA 2061

Qy 744 rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTy 764
Db 2062 CTTCAACAGAGGTATCATGATGGCTATCTCTGGTGAAACACAGTCAGCATGGGCATCGAGCA 2121
Qy 764 rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe 784
Db 2122 CCAGAACACGCCGAGGAGCTGACCAACATCTCTGGAGATCTGCATATGGTCTTCACAG 2181
Qy 784 rLeuPheAlaLeuGluMetLeuLysLeuValValTyrGlyProPheGlyTyrIleLy 804
Db 2182 TATGTTTGCCCTGGAGATGATCTGAAACTGGCGCCTTTGGGCTCTTCGACTACCTGCG 2241
Qy 804 sAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGl 824
Db 2242 GAACCCCTTACAACATCTTTGACAGCATCATCGTCATCATCAGCATCTGGGAAATCGTGG 2301
Qy 824 yGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLe 844
Db 2302 GCAGCGGAGCGGTGGCTGTCTGTGTCGCGACCTTCGGTGTGTCGGGTGCTGAAGCT 2361
Qy 844 uValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAs 864
Db 2362 GGTGGCTTTCATGCCGCGCTGCGGCGCAGCTCGTGTCTCATGAAGACCATGGACAA 2421
Qy 864 nValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMe 884
Db 2422 CGTGGCCACCTTCATGCTGCTCTCATCTTCATCTTCATCTTCAGCATCTCTGGGAT 2481
Qy 884 tHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspAr 903
Db 2482 GCATATCTTTGGTGCATAATTCAGCCTCCGACGACGACCGGACACCGTTCCTGACAG 2541
Qy 903 gLysAsnPheAspSerLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGl 923
Db 2542 GAAGAACTTCGATTCCTTACTGTGGGCGCATCGTCACAGTGTTCAGATCTCTCACTCAGGA 2601
Qy 923 uAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTy 943
Db 2602 GGACTGGAACGTTGTCTCTGTACAAATGGCATGGCTCCACACCCCTGGGCTCCCTCTA 2661
Qy 943 rPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuAlaIleLe 963
Db 2662 TTTTGTGGCTCATGACCTTTGGCAACTACGTTCTCTCAATCTCTGGTGGCTATCTCT 2721
Qy 963 uValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe 983
Db 2722 GGTAGAGGGTTTCAGGCTGAG----- 2743
Qy 983 rCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPr 1003
Db 2744 -----GGTGTGCTAATCGTCTCTCTCTGTATGA 2772
Qy 1003 oAspPhePheSerProSer-----LeuAspGlyAs 1013
Db 2773 GGACAGAGCTCATCCAAATTTGGAGGAGTTTGACAAAGCTCCAGAGGCGCTGGGACACAG 2832
Qy 1013 pGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLy 1033
Db 2833 TAGAGATCTCAAGCTCTGCCCAATACCATGACACCAATGGACAC----- 2878
Qy 1033 sSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSe 1053
Db 2879 -----CTGAGACCT-----AGCCTCCCT----- 2896
Qy 1053 rThrSerThrGlyLeuGlyGluAlaLeuGlyProAla----- 1065
Db 2897 -----CTGGGTGGCATCTGGTCTCTGCTGTGTACCATGGGTACTGCCCCCG 2943
Qy 1066 -----SerArgArgThrSerSerSe 1072
Db 2944 CCTCTACTGAGCCAGACCCGGTACTGTGGGCCCTAGACTCTCGAAAAAGCAGGTGTCTAT 3003

Qy 1072 rGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSe 1092
Db 3004 GTCCCTGGGAGG-----ATGAGCTATGATCAGGGATCCTTGTCCAGCTCCCCGAGCTC 3057
Qy 1092 rProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAnSe 1112
Db 3058 CTACTACGGGCGCTGGGGCCGAGTGGGACCTGGGCTAGCGCCGCTCCAGCTGGAAC-- 3115
Qy 1112 rLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLe 1132
Db 3116 -----AGCCTGAAACACAAACCGCCCTCAGCTGAGCATGATGCTTACT 3159
Qy 1132 uSerGlyGluGlnGlnSerGlnAspGluGlu---GluSerSerGluGluGlu----- 1149
Db 3160 GTCTGGGAGGAGTGGAGTACTGCTGGCTCAGGCGCTGTGAAGCGCCCGGGAGGAGCGGCC 3219
Qy 1150 ----ArgAlaSerProAlaGlySerAspHis----- 1158
Db 3220 AACTCGCACCGACCCCTCGATGCTCCACACCGCGCACCGACCATGACCCACCT 3279
Qy 1159 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAs 1173
Db 3280 GGCACACCGTCACCGACACCAACCGCGGACTCTGTCCCTTGATACAGGGACTCTGTGTA 3339
Qy 1173 pLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG1 1191
Db 3340 CTGGGAGAGTGTGGCCGCTGGTGGTGGCCACTCAGCGGCGCTGGAGGGGGGGGG 3399
Qy 1191 ySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAl 1211
Db 3400 TCAGSCCCTGGGCACGAGGAGTCAATGGCAGAAATGCCCAACATAGCAAGGATGTCTT 3459
Qy 1211 aLeuArgProAspAspPropLeuAspGlyAspAlaAspAspGluGlyAsnLeuSe 1231
Db 3460 CACCAAGATGATGATGACCCCGCGACCCCGCGGGAGGAC---GAGGAGGATCGCATATAC 3516
Qy 1231 rLysGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluAr 1251
Db 3517 CTGTGTTTCGGGTCCGCAAGATGATTGATGTGTACAAAGCGGAGCTGGTCGGAAGTCCG 3576
Qy 1251 gAspSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeuLeuCysHisAr 1271
Db 3577 CGAGGACTGGTGGCTACCTCTCTCCCGAGAAACAAGTTCGGATCTGTGTGCAGAC 3636
Qy 1271 gIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI1 1291
Db 3637 CATCATTTGCTCACAAGCTTTTGTGACTAGCTGGTCTGTGGCCTTTATCTCTCCCACTGTAT 3696
Qy 1291 eThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuTh 1311
Db 3697 CACCATTTGCTCTGGAGAGACCCAGATTGAAGCTGGTAGCACTGAGCCGATCTTCTCTCAC 3756
Qy 1311 rLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAl 1331
Db 3757 GGTGTCTAACTACATCTTTCACAGCCATCTTGTGGCGGAGATGACACTGAAGGTGTTTC 3816
Qy 1331 aLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuArgSerSerTrpAsnValLeuAspG1 1351
Db 3817 TCTGGGCTGTACTTTGTGTGAGCAGCGCTACTGCTGTAGCAGCTGGAATGACTGGATGG 3876
Qy 1351 yLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyTh 1371
Db 3877 TTTCTGTGCTTGTGTCTCATCATCATCATCGTAGTGTCCGTGGGCTCTGCTGGGGAGC 3936
Qy 1371 rLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgVa 1391
Db 3937 CAAGATTCTGGGGCTCTCGGGCTCTCGGGCTCTCGGGCTACCTTACCTCTTTCAGGGT 3996
Qy 1391 lIleSerArgAlaGlnGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysPr 1411
Db 3997 TATACGCGGGGCTCTGGGCTGAAAGCTGTGTGTAGAGACGCTCATCTCTCTCCCTCAAGCC 4056
Qy 1411 oIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVa 1431

Db 4057 CATTTGGGAACATCGTCTCTCATCTGCTGCTTCTTTCATCATCTTCGGCATCTCTGGGGGT 4116
Qy 1431 lGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAs 1451
Db 4117 GCAGCTTTTCAAAGCGCAAGTTCTACCATTTGTTGGAGTGGACACCCGAAACATCACCAG 4176
Qy 1451 nLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTrpAsnPheAspAs 1471
Db 4177 CCGATCTGACTGCTGGCGGCAACTACCGCTGGTGGTCATCACAAATACAACTTTGACAA 4236
Qy 1471 nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAsp11 1491
Db 4237 CTTGGGCGAGCATTTGATGCTCTTTGCTTGGCTTCCAAGGACGCTGGTGAACAT 4296
Qy 1491 eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr 1511
Db 4297 CATGTATAATGGAATTAGATTGCTTGTGTGGACAGCAGCAGTGAAGAACCAACCC 4356
Qy 1511 oTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe 1531
Db 4357 CTGATGCTACTGTACTTTCATTTCTGCTCTCTCATCTGCTAGCTTCTTTGTCTCAACAT 4416
Qy 1531 tPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG1 1551
Db 4417 GTTTGTGGCGTGTCTGTGGAGAACTTCCACAAGTGGCGGACGACGAGGAGGCTGAGGA 4476
Qy 1551 uAlaArgArgGlnGluLysArgLeuArgArgLeuGluLysLysArgArgLysAlaG1 1571
Db 4477 GGCAGGAGGCGTGGAGAGAAACGGCTCGCGGCTGTGAAAAGAGCGCCGCTAAGGCTCA 4536
Qy 1571 nCysLysProTrpTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCysTh 1591
Db 4537 GAGCTCGCTTACTTGTACTTACTGTCCCAAGGCTGTCTCATCTCCACTCCATGTGCAC 4596
Qy 1591 rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1611
Db 4597 CAGCCACTACCTGACATCTTCACTTTCATCTCATCTGCTCAATGTTGTGCCATGTC 4656
Qy 1611 aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTrp11 1631
Db 4657 CTTGGAGCACTTACAAACAGCCCTACATCTAGAGAGAGCCCTTAAGTACTCCAACTATAC 4716
Qy 1631 ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr 1651
Db 4717 GTTCAACACTGTCTTTGTCTGGAGGTGTGCTGAGCTGTGTGGCATTTGGCTGAGGCG 4776
Qy 1651 gPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG1 1671
Db 4777 TTTCTTCAAGGACGATGGAAACAGCTGGACCTGGCCATTGCTGTGCTGTCCGTCCATGGG 4836
Qy 1671 yIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr 1691
Db 4837 CATCACATGAGGAGATCGAGATCAATGCGCGCTTCCCATCAACCCCACTCATCCG 4896
Qy 1691 gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyWe 1711
Db 4897 TATCATGCGTGTCTGCGTATCGCCGGGTGTTGAGCTATTGAGATGGCCACAGGAAT 4956
Qy 1711 tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe 1731
Db 4957 CGGGCCCTGCTGGACACAGTGGTACAGGCTCTGCCCGAGTGGGCAACCTTGGGCTGCT 5016
Qy 1731 uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG1 1751
Db 5017 CTTCATGCTGTCTTCTTCATCTATGTGCTCTGGAGTGGAGCTCTTCGGAAAGCTGGT 5076
Qy 1751 uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG1 1771
Db 5077 CTGAATGACAGAACCCGCTGTGAGGATGAGCGGACCGCCACCTTTGAAACCTTCGG 5136
Qy 1771 yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetL1 1791

5137	Db	CATGGCCTTCCTCAAGCTCTTCACAGGTCCTCCACAGGCGATAACATGGGAATGGAATTATGAA	5199
1791	Qy	sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----II	1808
5197	Db	GGACACCTCGGAGACTGTACCCATGATGAGCGCACGTGCCTAAGCAGCCTGCAGTTGT	5256
1808	Qy	eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa	1828
5257	Db	GTCAACCGCTCTACTTGTGTGAGCTTCGTGCTCACAAGCTCAGTTCTGTGCTCATCAACGTGGT	5316
1828	Qy	LIleAlaValLeuMetIysHisLeuGluGluSerAsnIysGluAlaLysGluGluAlaGI	1848
5317	Db	GGTGGCCGTGCTGATGAACATCTGGAGATGAGCAACAAGAGAGCCAGGAGGATGCAGA	5376
1848	Qy	uLeuGluAlaGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr	1867
5377	Db	GATGGATGCTGAGATCAGCTGGAGATGGCCCTCGGCCCTCGGCCCTCGCCCT	5428
1867	Qy	oLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLy	1887
5429	Db	-----GGCCCTCG	5436
1887	Qy	sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi	1907
5437	Db	CCCTGGT-----	5443
1907	Qy	sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal----	1925
5444	Db	-CCCTGCCCTGCCCTCGCCCTCGCTGGCCCGAGGCTGCCACTAGTTCACC	5502
1926	Qy	-----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy	1941
5503	Db	TGGGGCTCCGGGGCGAGACTCGGAGGGCGAGGTGCTGGAGGC--GACACCGAGAGTCA	5559
1941	Qy	rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuPr	1961
5560	Db	CCTGTGCCG-----	5569
1961	Qy	oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyriI	1981
5569	Db	-----	5569
1981	Qy	eLeuGlnLeuProLysAspAlaProHisLeuGlnProHisSerAlaProThrTrpGI	2001
5570	Db	-----CACTGCTATTCTCCAGCCCGAGGACCCCTGTGG--	5602
2001	Qy	yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr	2021
5603	Db	-----CTGGACAG	5610
2021	Qy	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe	2041
5611	Db	CGTCTCTTTAATCATCAAGGACTCCTTGGAG-----GGGAGCTGACCAT	5655
2041	Qy	uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTyrSerPheTrpGly	2060
5656	Db	CATTGACAACTGTCTGGTCCGCTCTCCACCACCTACGCCTCACCTGACGGCTGTGCAA	5715
2061	Qy	GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer	2077
5716	Db	GTGTCCACCATCAAGAAGACAGACAGAGTCTTCATCCATCTCTGTGGGGATGACCTAGT	5775
2078	Qy	LyHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro	2097
5776	Db	-----CTTGAGGACCCACCGCTGCCCA-----CAGGGCCCC	5808
2098	Qy	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117
5809	Db	AAGAGAGACAG-----GGTGACTA	5829
2118	Qy	LeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyr---	2136
5830	Db	GAGCCTCG-----GACCCATGCAGGCTGAGACCTGGATGAATGCTTTGG	5877

Qy	2137	-----Serval-----	2138
Db	5878	CCCTTTGCCAAGGAGGACGCTGCTGTGCGAGATGGGGC	5879
Qy	2139	--GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgArgHi	2157
Db	5938	CATTCCATTCAACCTGCTGCAG-----TCTGGCTCAACACGAGAGACGCCA	5985
Qy	2157	SerIleAlaValSerCysLeuAspSerGlySerGlnPro-----	2170
Db	5986	AGCACCCACAGACCCCTTCTCCCGGATGCTCCAGCCCTCTCCTGTAGATGCTGCTGA	6045
Qy	2171	-----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGl	2188
Db	6046	GTTCTTCCACCCCTGCTGTCTGCCAGCCAGAGGGCGCAGAACCGGGCATGAGTGCAGG	6105
Qy	2188	YSerArgProLysIleLysLeuSerProProSerIleThrIleAspProGluSerGl	2208
Db	6106	AACCTGCCCAAGATTGCACCTTCAG-----GGTCTCTG	6138
Qy	2208	nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs	2228
Db	6139	GGCATCGCTCAGTCACCGAGTGTCACTGCACCCCTCTTCGGCCAGGCTACTGTGAGTGA	6198
Qy	2228	pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy	2248
Db	6199	CACGTCC-----TTGGATGCCAGTCTCTAGCAGTCAGCGGCAGCGCTACAGACCACACT	6252
Qy	2248	sLysAspValLeuSerLeuSer	2255
Db	6253	GGAAGACAGTCTGACTCTGAGT	6274

RESULT 14

US-10-425-800-12

; Sequence 12, Application US/10425800

; Patent No. 6893842

; GENERAL INFORMATION:

; APPLICANT: McGivern, Paul S.

; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;

; TITLE OF INVENTION: AND USES

; FILE REFERENCE: R0043B-REG sequence listing

; CURRENT APPLICATION NUMBER: US/10/425,800

; CURRENT FILING DATE: 2003-04-29

; PRIOR APPLICATION NUMBER: US/09/404,650

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 12

; LENGTH: 6503

; TYPE: DNA

; ORGANISM: Rattus sp.

US-10-425-800-12

Alignment Scores:			
Pred. No.:	2,61e-316	Length:	6503
Score:	5418.50	Matches:	1212
Percent Similarity:	60.5%	Conservative:	209
Best Local Similarity:	51.6%	Mismatches:	446
Query Match:	45.5%	Indels:	484
DB:	3	Gaps:	53

US-09-611-257A-37 (1-2266) x US-10-425-800-12 (1-6503)

Db 2122 CCAGAACAGCCCGAGGAGCTGACCAACATCTCGAGATCTGCAATGTGGTCTTCCACGAG 2181
Qy 784 rLeuPheAlaLeuGluMetLeuLeuValTyrGlyProPheGlyTyrIleLy 804
Db 2182 TATGTTGGCTTGGAGATGATCTGAAACTGGCCGCTTGGGCTCTTCGACTACCTGGC 2241
Qy 804 sAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrpGluIleValGI 824
Db 2242 GAACCCCTTACAACATCTTTGACAGCATCATCGTCATCATCAGCATCTGGGAAATCGTGGG 2301
Qy 824 yGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuIleLyLe 844
Db 2302 GCAGCGGACCGGTGGCTCTGTCTGCTGCGCACCTTCCGGTGTCTGGGGTGTCTGAAAGCT 2361
Qy 844 uValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetIleYsThrMetAspAs 864
Db 2362 GGTGGCTTCATGCGCGGCTGCGGCGCCAGCTCGTGGTGTCTCATGAAGACCATGGACAA 2421
Qy 864 nValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMe 884
Db 2422 CGTGGCCACCTTCTGCATGTACTCATCTGTTCATCTTCATCTTCAGCATCTTGGGAT 2481
Qy 884 tHisLeuPheGlyCysIleYsPheAlaSerGluArgAsp---GlyAspThrLeuProAspAr 903
Db 2482 GCATATCTTTGGCTGCAAAATTCAGCCTCCGACGACACCGGAGACACCGTTCCTGACAG 2541
Qy 903 gLyAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGI 923
Db 2542 GAAGAACTTCGATTCCTTACTTGTGGCCATCGTCACAGTGTTCAGATCTTCATCTCAGGA 2601
Qy 923 uAspTrpAsnIleYsValLeuTyrAsnGlyMetAlaSerThrSerTrpAlaIaLeuTy 943
Db 2602 GGACTGGAACCTGTCTCTGTAACAATGGCATGGCTCCACACCCCTCGGGCTCCCTCTA 2661
Qy 943 rPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuAlaIleLe 963
Db 2662 TTTTGTGGCTTCATGACCTTTGGCACTACGTTCTCTTCAATCTCCTGGTGGCTATCCT 2721
Qy 963 uValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe 983
Db 2722 GGTAGAGGTTTCAGGCTGAG----- 2743
Qy 983 rCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnIleYsSerGluSerGluPr 1003
Db 2744 -----GGTGATGCTAATCTGTTCTCTCTCTGATGA 2772
Qy 1003 oAspPhePheSerProSer-----LeuAspGlyAs 1013
Db 2773 GGACCAGAGCTCATCCCAATTTGGAGAGTTTGACAAGCTCCAGAGGCGCTGGACAACAG 2832
Qy 1013 pGlyAspArgIleYsCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLy 1033
Db 2833 TAGAGATCTCAAGCTCTGCCAATACCATCCATGACCCCAATGGACAC----- 2878
Qy 1033 sSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSe 1053
Db 2879 -----CTGGACCT-----AGCCTCCCT----- 2896
Qy 1053 rThrSerThrGlyLeuGlyGluAlaLeuGlyProAla----- 1065
Db 2897 -----CTGGGTGGCATCTGGGCTCTGGTCTGATGAGTGGGTACTGGCCCCCGC 2943
Qy 1066 -----SerArgArgThrSerSerSe 1072
Db 2944 CCTCTACTGCAGCAGACCGGTAAGTCTGGTGGCCCTAGACTCTCGAAGAACGATGTGCAT 3003
Qy 1072 rGlySerAlaGluProGlyAlaAlaHisGluMetIleYsSerProProSerAlaArgSerSe 1092
Db 3004 GTCCCTGGGACG-----ATGAGTATGATCAGGATCCTTGTCCAGCTCCCGGAGCTC 3057
Qy 1092 rProHisSerProTrpSerAlaAlaSerTrpThrSerArgArgSerSerArgAnSe 1112
Db 3058 CTACTACGGGCTTGGGCGCAGTGGGACCTGGGCTAGCGCGGCTCCAGCTCGGAAC-- 3115

Qy 1112 rLeuGlyArgAlaProSerLeuIleYsArgSerProSerGlyGluArgArgSerLeuLe 1132
Db 3116 -----AGCCTGAAACAACAAGCCGCTCTCAGCTGAGCATGAGTCTCTACT 3159
Qy 1132 uSerGlyGluGlyGlnGluSerGlnAspGluGlu---GluSerSerGluGluGlu----- 1149
Db 3160 GTCTGGGAGGCTGGAGTGTCTCGTCAGGGCCTGTGAAGCGCCCGGGAGGAGCGCC 3219
Qy 1150 ---ArgAlaSerProAlaGlySerAspHis----- 1158
Db 3220 AACTCGACCCGACCCCTGCATGCTCCACCGCCGACCCAGCCACCATGACCCCACT 3279
Qy 1159 -----ArgHisArgGlySerLeuGluArgGluAlaIleYsSerPheAs 1173
Db 3280 GGCACACCGCTCACCGACACACCGCCGAGCTCTGTCCCTGTATACCAGGACTCTGTTGA 3339
Qy 1173 pLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgGI 1191
Db 3340 CTTGGGAGAGCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3399
Qy 1191 ySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAl 1211
Db 3400 TCAGGCCCCCTGGGACGAGGACTGCAATGGCAGAAATGCCCAACATAGCCCAAGGATGCTT 3459
Qy 1211 aLeuArgProAspAspProProLeuAspGlyAspAlaAspAspGluGlyAsnLeuSe 1231
Db 3460 CACCAAGATGATGACCCGCGGACCGCGGGGAGGAC---GAGGAGGAGATCGACTATAC 3516
Qy 1231 rLysGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluAr 1251
Db 3517 CTTGTGTTCCGGTTCGGCAGATGATTGATGTGTACAAGCCGGAAGTGGTGGGAGTCCG 3576
Qy 1251 qAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeuCysHisAr 1271
Db 3577 CGAGGACTGGTGGTCTACCTCTTCTCCCGAACAAGTTCGGATCTCTGTGTGCAGAC 3636
Qy 1271 gIleIleThrHisIleYsMetPheAspHisValValLeuValIleIlePheLeuAsnCysI 1291
Db 3637 CATCATTTGCTCACAAGCTTTTGTACTACGTGGTCTTGCCCTTATCTTCTCACTGAT 3696
Qy 1291 eThrIleAlaMetGluArgProIleYsIleAspProHisSerAlaGluArgIlePheLeuTh 1311
Db 3697 CACCATTTGCTTGAGAGAGCCCAAGATGAAGCTGGTAGCAGTACAGGCGATCTTCTCCAC 3756
Qy 1311 rLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValIleYsValAl 1331
Db 3757 GGTGTCTAACTTACATCTTTCAGGCCATCTTCGTGGCGAGATGACACTGAAGGTGGTTTC 3816
Qy 1331 aLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGI 1351
Db 3817 TCTGGGCTGTACTTTGGTGAGCAGCGGTACTCTGGTAGCAGCTGGAATGTACTGGATGG 3876
Qy 1351 yLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyTh 1371
Db 3877 TTTCTGCTGTTGTGTCCATCATCATGATATCGTAGTGTCCGTGGCCTCTGTGGGGAGC 3936
Qy 1371 rLysIleLeuGlyMetLeuArgValLeuArgLeuArgThrLeuArgProLeuArgVa 1391
Db 3937 CAAGATTCTGGGGTCTCTCGGGTCTCTCGGCTCTCTCGTACCTTACGCTCTCTTGAGGGT 3996
Qy 1391 lIleSerArgAlaGlnGlyLeuIleYsLeuValValGluThrLeuMetSerSerLeuIleYsPr 1411
Db 3997 TATCAGCGGGCCCTGGGCTGAAGCTGGTGGTAGAGCGCTCATCTCTCTCCCTCAAGCC 4056
Qy 1411 oIleGlyAsnIleValValIleCysAlaPhePheIleIlePheGlyIleLeuGlyVa 1431
Db 4057 CATTGGGAACATCGCT 4116
Qy 1431 lGlnLeuPheIleYsPhePheValCysGlnGlyGluAspThrArgAsnIleThrAs 1451
Db 4117 GCAGCTTTTCAAAGGCAAGTTCTACCATTTGTTGGGAGTGGACACCCCGAAACATCACC 4176

1451 nLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsnPheAspAs 1471
1477 CCGATCTGACTGCTGGCGGCAACTACCGTGGGTGCATCACAATACAACTTTGACAA 4236
1471 nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIl 1491
4237 CCTGGCCAGGCAATGATGTCCTCTTTGCTTGGCCTCCAAGGACGGCTGGGTGAACAT 4296
1491 eMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIleMetAsnHisAsnPr 1511
4297 CATGTATATAGATAGATGCTGTGTGGACAGCAGCAGGACGACCAACCAACCC 4356
1511 oTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe 1531
4357 CTGGATGCTACTGATCTTCACTTCTGCTCTCATCTGCTGCTTCTTTGTGCTCAACAT 4416
1531 tPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG1 1551
4417 GTTTGTGGCGTGGTGGTGGAACTTCCAAAGTCCCGCAGCACCAGGAGGCTGAGGA 4476
1551 uAlaArgArgGluGluLysArgLeuArgGluLysLysArgArgLysAlaG1 1571
4477 GCGCGAGGCGTGAGGAGAAACGGCTCGCGCCCTGGAAGAGAGCCGCTAAAGGCTCA 4536
1571 nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysTh 1591
4537 GAGGCTGCCCTACTATGCTACTACTGCTCCCAAGGCTGCTCATCTCCATCTCATGTGCAC 4596
1591 rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1611
4597 CAGCCACTACCTGGACATCTTCACTTACCTTCACTCATCTGCTCAATGTGTCAACCATGTC 4656
1611 aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl 1631
4657 CCTGAGCAGCTACAAACAGGCTACATCCCTAGAGACAGCCCTTAAGTACTGCAACTACAT 4716
1631 ePheThrValIlePheValLeuLeuSerValPheLysLeuValAlaPheGlyPheArgAr 1651
4717 GTTACCACTGCTTTGTGCTGGAGCTGTGCTGAAGCTGTGGCATTTGGCTTGGCTCAGGCG 4776
1651 gPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG1 1671
4777 TTTCTTCAAGGACCGATGAAACAGCTGGACCTGGCCATTTGCTGCTGCTCGTCAATGGG 4836
1671 yIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleLeAr 1691
4837 CATCATCTGGAGGAGATCGAGATCAATGCCGCCCTTCCCATCAACCCACCATCATCCG 4896
1691 gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyWe 1711
4897 TATCATGGGTGTTCTGCGTATCGCCCGGGTGTGAAGCTATTGAAGATGGCCACAGGAAT 4956
1711 tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe 1731
4957 GCGGCCCTGCTGGACACAGTGGTACAGGCTCTGCCCCAGGTGGCAACCTTGGGCTGCT 5016
1731 uPheMetLeuLeuPheIlePheAlaLeuGlyValGluLeuPheGlyAspLeuG1 1751
5017 CTTCATGCTGCTCTTCTTCACTATGCTGCTCTGGAGTGGAGCTCTTCGGAAGCTGGT 5076
1751 uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheG1 1771
5077 CTGCAATGACGAGAACCCGTGTGAGGCAATGAGCCGCGCAGCCACTTTGAAACCTTCGG 5136
1771 yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTyrAsnGlyIleMetLys 1791
5137 CATGCCCTTCTCAGCTCTTCCAGTCTTCCACAGCGCAATACTGGAATGGAATATGAA 5196
1791 sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il 1808
5197 GGACACCTTCCGAGACTGTACCCATGATGAGCGCAGCTGCTTAAGCAGCGCTCAGCTTGT 5256
1808 eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa 1828

Db 5257 GTCAACGCTCTACTTTGTGAGCTTCGTCTCACAGCTCAGTTCGTGCTCATCAACGCTGT 5316
Qy 1828 lIlAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAlaG1 1848
Db 5317 GGTGGCCGTGTGATGAACATCTGATGACAGCAACAAGGAGGCCAGGAGGATGCA 5376
Qy 1848 uLeuGluAlaGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr 1867
Db 5377 GATGATGCTGATGATCGAGCTGGAGATGGCCATGGCTCGGCCCTGCCCT----- 5428
Qy 1867 oLeuGlySerProPheLeuTyrProGlyValGluGlyProAspSerProAspSerProLy 1887
Db 5429 -----GGCCCTCG 5436
Qy 1887 sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi 1907
Db 5437 CCCTTGGT----- 5443
Qy 1907 sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal----- 1925
Db 5444 -CCCTGCCCTTGGCCCTTGGCTGGCCCGGAGGCTGCCACTAGTTTACC 5502
Qy 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941
Db 5503 TGGGGCTCCGGGGCGAGGATCGGGAGGGCAGGTGCTGGAGGC---GACACCGAGAGTCA 5559
Qy 1941 rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuPr 1961
Db 5560 CCTGTGCCG----- 5569
Qy 1961 oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIl 1981
Db 5569 ----- 5569
Qy 1981 eLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGl 2001
Db 5570 -----CACTGCTATTCTCCAGCCAGGAGACCTCTGG-- 5602
Qy 2001 yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 5603 -----CTGCAG 5610
Qy 2021 gLlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 5611 CGTCTCTTAAATCATCAAGGACTCTTGGAG-----GGGAGCTGACCAT 5655
Qy 2041 uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTyrSerPheTrpGly 2060
Db 5656 CATTGACAACTGCTGGTCCGTCTTCCACCATACGCTCACCTGACGCTGCTGGCAA 5715
Qy 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer 2077
Db 5716 GTGTCAACATGACAAAGACAGACAGGCTTTCATCCATCTCTGCTGGGGATGATCAGT 5775
Qy 2078 LysHisMetThrProAlaProCysProGlyProGluProAsnTyrGlyLysGlyPro 2097
Db 5776 -----CTTGAGGACCCACCGCTGCCA-----CAGGGCCCC 5808
Qy 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 5809 AAGGAGACCAAG-----GGTGAACATA 5829
Qy 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysCysTyr--- 2136
Db 5830 GAGCCCTCCG-----GAGCCCATGAGGCTGGAGACCTGGATGCTTTTGG 5877
Qy 2137 -----SerVal----- 2138
Db 5878 CCCTTGGCAAGCGACGCTGCTCCAGGCCAGAGACCTGCTGTCGAGATGGGGC 5937
Qy 2139 ---GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgArgHi 2157

```
Db 5938 CATTCCATTCAACCTGTCCAG-----TCCTGGGTCAAAACAGAGACAGCCA 5985
Qy 2157 sSerileAlaValSerCysLeuAspSerGlySerGlnPro----- 2170
Db 5986 AGCACCCAGAGCCCTTTCTCCCGGATGGCTCCAGCCCTCTCCTGTAGATGCCTGTGA 6045
Qy 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProG1 2188
Db 6046 GTTCTTCCACCCTGTGTGTCTGCCAGCCAGAGGGGCGAGAACCGGCAGTGAGTGCAGG 6105
Qy 2188 ySerArgProLysLysLeuSerProProSerileThrIleAspProProGluSerG1 2208
Db 6106 AACCTGCCAAGATTGCACCTCAG-----GGGTCTCTG 6138
Qy 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6139 GGCATCGTGGTCAACGAGTGTCACACTGCACCTCTTGGCCAGGCTACTGTGAGTGA 6198
Qy 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248
Db 6199 CACGTCC-----TTGGATGCCAGTCTTAGCAGCTCAGCGGCGAGCTACAGACCACACT 6252
Qy 2248 sLysAspValLeuSerLeuSer 2255
Db 6253 GGAAGACAGTCTGACTCTGAGT 6274

RESULT 15
US-09-949-016-15601
; Sequence 15601. Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15601

Alignment Scores:
Pred. No.: 3,41e-123 Length: 70308
Score: 2237.00 Matches: 730
Percent Similarity: 21.9% Conservative: 25
Best Local Similarity: 21.2% Mismatches: 64
Query Match: 18.8% Indels: 2626
DB: 3 Gaps: 19

US-09-611-257A-37 (1-2266) x US-09-949-016-15601 (1-70308)
Qy 2 AspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArg----- 17
Db 9554 GATGAGAA-----GCTGGGTCCAGAGAGGGTGAGATGACCAAGGTGGGACTCCCT 9604
Qy 18 SerPheMetArgLeuAsnAspLeuSerGlyAlaGlyGlyArg-----ProGlyProGly 35
Db 9605 TCTCTGATGAGAGTCTGGGGCTG---GGGGTGTGTCTGCGTGTATGTATGTCAGGGGCCCTGGC 9661
Qy 36 SerAla-----GluLysAspProGly----- 42
Db 9662 ACCACACCTGTTAGCTTCAGATGAGCCAGAGAGGTAAACGAGGAGGAGGTGTAGGGCG 9721
```

```
Qy 43 SerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePhe 62
Db 9722 GGGTCGGGGGGCCGCGCTCAGCTCAGCTTGGCCAGCTGTTTCC----- 9766
Qy 63 TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82
Db 9767 -----TTGACTGCCAGTACCTGG 9784
Qy 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 9785 TTTGAGCGCATCAGATGTTGTCATCTTCACTGCGTGACCTGGCATGTTCCGG 9844
Qy 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeu----- 117
Db 9845 CCATCGAGGACATCGCTGTGACTCCCGCGCTGCCGATCCTGCAGGTGAGTGTGTGT 9904
Qy 117 ----- 117
Db 9905 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGGGTGTGGCCCTCTTAATCTTAATAC 9964
Qy 117 ----- 117
Db 9965 CCTTACTCTCTGCAAGAGGCGCTGACCCAACTGGTGGGACTAGGTGGGACTAGAGG 10024
Qy 118 -----GlnAlaPheAsp 121
Db 10025 GTATTCCCTCACCCACGCTCAGTTTCAGCCACCTCTTGTCCCCACATCAGCGCTTTGAT 10084
Qy 122 AspPheIlePheAlaPhePheAlaValGluMetValValValMetValAlaLeuGlyIle 141
Db 10085 GACTTCATCTTTTGCTCTTTTGGCGTGAGATGGTGGTGAAGATGGTGGCTTTGGGCATC 10144
Qy 142 PheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIle 161
Db 10145 TTTGGGAAAAAGTGTACTCTGGAGACACTTGGAAACCGCTTGACTTTTCATCGTCATC 10204
Qy 161 ----- 161
Db 10205 GCAGGTGAGGACCTGGGCTGGGGTGGGAGAGCAATGGATCAGATCGGCTCCCTCCCGG 10264
Qy 161 ----- 161
Db 10265 GGCCAGGGTTCTGGGCTGTGACCTCTCAGCTCCAGCCAGGTTACAGCACCATTTTCTCC 10324
Qy 161 ----- 161
Db 10325 CTGGCTATCTCTGAGGGTCTGAGGCTGCCCTGCTCTAGCACTGACCTATATCTAA 10384
Qy 161 ----- 161
Db 10385 ATTCGAAGGCCCTATTCTCTAATTCTGCCCTTCTCTGATGGCAATCTGCTCTTGTCTC 10444
Qy 161 ----- 161
Db 10445 GGGGTAGCCTTGGCCCCCAGACAGAGAGCCGATCTTCAGGGTCCCTTGGTGAAGAGAA 10504
Qy 161 ----- 161
Db 10505 GAAGGAGTCAGAGTCATCTGCTGCCCTAAAGCAGGATTCCTCATTGACCTCTTGTGA 10564
Qy 162 -----AlaGlyMetLeu 165
Db 10565 CCCCACTGTGGCTCAGACTCAAGGGGCTCCCTTTGGGCCCTCCCTGCAGGATG-CTG 10623
Qy 166 GluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeu 185
Db 10624 GAGTACTCGCTGGACCTGCAGAACGCTTCTCAGCTGTCTCAGGACAGTCCGTGTGTCTG 10683
Qy 186 ArgProLeuArgAlaIleAsnArgValProSer----- 196
Db 10684 CGACCGCTCAGGGCCATTAAACCGGGTGCCTCAGTGTGACCCCTCAGCCCTCAGCCCTG 10743
Qy 196 ----- 196
```


Qy	248	rLeu-----	249	380	-----	380
Db	12964	CCTGTGAGTGGTGACAGGGTCCAGGAGGACCTGGGAGTGGTTATGGGGCTGGGCACCC	13023	14043	GTGAGTGACTCCTCAGATCCCGTGGGATCGGCGATCCTGGGACACCTGTGGGGCAG	14102
Qy	249	-----	249	380	-----	380
Db	13024	CCCCAAGTTCCTCACTTCCGGTTGCTACTGACATATCTGTTCTAACATCTGAGACATATC	13083	14103	TCAGAGAGGGGATAGTTTGCTCTGTCTGAAGTTTTTAGCTCTCAGGACAAGTCTCTGTAG	14162
Qy	249	-----	249	380	-----	380
Db	13084	TGGTCTCAAACTTGGCTACCCATTTGGAACCACTGGGGAGTTTAAAAAGTACTGATGC	13143	14163	AGAGGGCATCCATCATATAGTAGGAGGCACACAGATGCAGAGTCAGAGGAAATCCAAG	14222
Qy	249	-----	249	380	-----	380
Db	13144	CTGGGTGCCACCTCCAGAGATTCTGATTTCATTGCTCTGGGGCTCAGCTTGATGTAAGG	13203	14223	GTCAAGCGGGACTTAACCTGCTATTGGGACCTTGGGCAAGTCATCTCCATGAGGCCTCC	14282
Qy	249	-----	249	380	-----	380
Db	13204	ATTTTTCAACCCCTCCAGTGATCCTAACTTGCAGTGAAATTTGAAAATCACTATTCCAG	13263	14283	AGCACTGCTCTGGGCCCTCTGTTCTTCATGGGTAAAATGAATGGTTCTCAACCTGAGATG	14342
Qy	249	-----	249	380	-----	380
Db	13264	GATGTGACCTTCCAACATCCTGAGTCTGGAGTTTCCCACTCAGGCGCTCATGCTCCTGGT	13323	14343	ATACCACCTCTCCAGAGGGCAITTTGGAATGGGAAAGGGTGATTCTGGTTTTCGATTTT	14402
Qy	249	-----	249	380	-----	380
Db	13324	GCCCAAAATCCCTGCGCTGCCAGTCCCTTCCCAATCTCTGGTCTCGCCCTGCTCACCC	13383	14403	TTTAATAGCTTTATTGAGACATAACTCACATATCATTTCAATTCATCCCTTTGAATGAATC	14462
Qy	249	-----	249	380	-----	380
Db	13384	TATATGCTCGAGCACTCGTGCCATCTCTCCCTTCTGGGCCCTCTCCCTGGAGAGCCCA	13443	14463	CAGTGGTTTTTAAAGCATGTTTACAGAGTCTCTGTTTTTTTGTAAAGACAAGGGAGTGCA	14522
Qy	250	-----	256	380	-----	380
Db	13444	CTCCCCAGTCTACCCCTGTTCCCTTCCCACTCGAGCCCTCGAGCGTGGACCTGGA	13503	14523	ATTGGCAATTTGTACTGGGGAGGGAGAGAACTAAACATCTCGAAATCTTGGCAAT	14582
Qy	256	uAtGTYrTYrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgG1	276	380	-----	380
Db	13504	CGGCTATTACAGACAGAGAACGAGGATGAGAGCCCTTCACTCTGCTCCAGCACCAGGA	13563	14583	AAAGAAATTATTCTACCCAAAATTCGTATCAGTGATCAATTTGGTGTTAATGCTGCCTGAT	14642
Qy	276	uAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyPr	296	380	-----	380
Db	13564	GAACGGCATGGTCTCTCAGAAAGCGTCCCAAGCGTCCGCGGGGACGGGGCGGTGGCC	13623	14643	CTCTTATCTCGCCAGTTCAGAAATGCCAGACTTTAAGAAGGGCAGAGACGGAGGCAAA	14702
Qy	296	oProCysGlyLeuAspTYrGluAlaTYrAsnSerSerSerAsnThrThrCysValAsnTr	316	380	-----	380
Db	13624	ACCTTGGCGTCTGGACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCAACTG	13683	14703	AGCAGCAATATTTAATAGTTTTTAATCACTACCATTCATAGTTAATACTTCATCGCCACC	14762
Qy	316	pAsnGlnTYrTYrThrAsnCysSerAlaGlyGluHisAsnProPheIlySlyAlaIleAs	336	380	-----	380
Db	13684	GAACAGTACTACACCAACTGCTCAGCGGGGAGGACAAACCCCTTCAAGGGCGGCATCAA	13743	14763	ACTTTGAGCTAAATATTATTATTGAGCACTTACTATGCGCAGCCCTGATCTAAGCACTTTC	14822
Qy	336	nPheAspAsnIleGlyTYrAlaTrpIleAlaIlePheGln	349	380	-----	380
Db	13744	CTTTGACAACTTGGCTATGCTGATCGCATCTTCCAGTGGGGCAGCCTGGGCCCCG	13803	14823	AATGTGTGTGTCATTTAATCTCACCCTGATCTCTCCATTTTACAGATGAGGAAACTG	14882
Qy	349	-----	349	380	-----	380
Db	13804	GGAGTCTCCCAAGAACACAGCCCCAGACACAGCCAGGATCGGAGTGGTCTCTCAG	13863	14883	ACATTTCTCATTTATCTGACCCCTACCAGAGCTTTGCCTATGCTGTGTATTAACTCCA	14942
Qy	349	-----	349	380	-----	380
Db	13864	GTTGGGTGGGGTCAAGGCTCTGAGAGAGACTGAAGGAGGATTTGGTGGGCCCATAG	13923	14943	AGAGTGGGGCATCACTGCTGACGTATGCTGTAAACATCTGCTGCCTGTTTAACTCTCTGTCG	15002
Qy	350	-----	361	380	-----	380
Db	13924	TCAGCCTGCCCTCTGCACCCCTAGGTATCATCAGCTGAGGGCTGGGTGACATCATGT	13983	15003	TCCCTCTGTGAGTCCCGGAGGAGGATTTGGTCCCCATCTCTTAAATGAGAAATTCAGCG	15062
Qy	361	yrPheValMetAspAlaHisSerPheTYrAsnPheIleTYrPheIleLeuLeullelle-	380	380	-----	380
Db	13984	ACTTTGTATGATGCTATCTCTTACAAATTTTCATCTACTTCACTCTCTCTCATCAT-C	14042	15063	CCCCAGAGGTGGGTCACTGGGCCAAGATCACACAGAAAGTAAGCGGCTGGGCTGAGAA	15122
				380	-----	380

Db	15123	TTCACTCCAGGCTAAACGACTCCACATTCACGCTTCTCTCCATGTCACCAAGAGGCCAAC	15182	Db	16203	AGAGCTTGGTTCCAGTCTTAGCCTTGCTCTGAATTAGCTGAGTGATCTTGGGCAAAATGTT	16262
Qy	380	-----	380	Qy	380	-----	380
Db	15183	GACAGCCACAGACAGAGGACAGACATTTGAGAGAAAGAGATTAAGAAAGATTAAGATCTA	15242	Db	16263	TGACCTCTGTGGACCTGAGTTTCTTACCTGTCTGATGGAGATTACAATAGCATCACCTC	16322
Qy	380	-----	380	Qy	380	-----	380
Db	15243	CTCAGGACCTAGGACTAGCTCCAGAGAGAGATGAAGACAAAATAAGGCAGCTCCTTTGTGA	15302	Db	16323	CTGAGGCTGTCTTAAAAATAAATAGATATGCTTGGAAAAATAACTGAGCGTGGCGCTT	16382
Qy	380	-----	380	Qy	380	-----	380
Db	15303	GAGACAGAGGTAGGCCCTGAGAAAGACGAAGTCCCAAGGCCACCTCATTTCTGCCTGCG	15362	Db	16383	GGCTCATAGGAATGCCTCCGTATGTGTGGCTGCATTTGTGATTCATTTTCTCAGGAC	16442
Qy	380	-----	380	Qy	381	-----ValGlySerPhePheMetIleAsnLeuCysL	391
Db	15363	TAACTTCCCTGGTCCGAAGAGTGGCGAGGCTTTGGGCGAAGCCTGACTGGAGGCCCTGT	15422	Db	16443	ATTTCTCTTCTCTGCCACCCCTACAGGTGGGCTCTCTTCTATGATCAACCTGTGCC	16502
Qy	380	-----	380	Qy	391	euValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetArgG	411
Db	15423	TCCCATCCCTGGCCACCACTCAAGGGGTGAGGCCAGTGCTTCAGGGGAAGTGGGGTCTTC	15482	Db	16503	TGGTGGTGATTGCCACGCACTTCTCAGACACCAAGCAGCGGAAAGCCAGCTGATCGGG	16562
Qy	380	-----	380	Qy	411	luGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlyS	431
Db	15483	TCACCATGTGCCCCCCCCACCCCTCCCTTCCCTCTGGGCTTGGGAGAGGGGAAG	15542	Db	16563	AGCAGCGTGTGGGTTCTCTGTCCAAGCCAGCACCTGGCTAGCTTCTCTGAGCCCGCA	16622
Qy	380	-----	380	Qy	431	erCysTyrGluGluLeuLeuLysTyrIleuValTyrIleLeuArgLysAlaAlaArgL	451
Db	15543	GAAGCAGACAGGGAGATAAGGGGCTAGTTTCCACCTCCACACACACCCCTGAAAAATC	15602	Db	16623	GCTCTATGAGGAGCTGCTCAAGTACCTGGTGTATACCTTCTGTAAGCAGACCCCGCAGGC	16682
Qy	380	-----	380	Qy	451	euAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProL	471
Db	15603	TTTCTTAACAGCTCTCTGGAATCACACTAGTGAAGCTAAATTATCATATTAAGGACAC	15662	Db	16683	TGGCTCAGGTTCTCTCGGAGCAGCTGTGCGGGTGGCTGCTCAGCAGCCAGCACCCC	16742
Qy	380	-----	380	Qy	471	euGlyGlyGlnGluThrGlnProSerSerCysSerArgSerHisArgArgLeuSerV	491
Db	15663	GATCTAGAAAAAATAATCTGTTTGTCCACCAATAATTCATTCTCTTCTTTGGGATT	15722	Db	16743	TCGGGGGCCAGGAGACCCAGCCAGCAGCAGCTGCTCTCGCTCCACCGCGCTATCCG	16802
Qy	380	-----	380	Qy	491	alHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis	511
Db	15723	GTTGTCCAAGCAATGGCTGTTCCAGAGTTCTGGGAAACTGAGGCGTGGAGATGGGGACT	15782	Db	16803	TCCACCACTTGGTGACACACCACCACCACCACCACCACCACCACCACCACCACCACCACC	16862
Qy	380	-----	380	Qy	511	hrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgA	531
Db	15783	GGGTAGTGTGAGCAAGTCAGGTGGCAGCCTGACTAGTCTGTAGGGTCAAGGGTTCAGCC	15842	Db	16863	CGCTCAGGGCCCCCGGCGCAGCCCGGAGATCCAGGACAGGATGCCAATGGTCCCGCC	16922
Qy	380	-----	380	Qy	531	rgLeuMetLeuProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaG	551
Db	15843	CCTCCACATCTGAGGGAGGGGGCACAGGAAATGGGGACAGACAAAGGCCAATGGTCC	15902	Db	16923	GGCTCATGCTGCCACCACTCCGACGCTGCTCTCGGGGGCCCCCTCGTGGCGCAG	16982
Qy	380	-----	380	Qy	551	luSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlap	571
Db	15903	CTGTTTTCAGATGAGGATPATGAGTCCCATGGCTAAGGGTCTCTGGCCCCAAAGTCACACA	15962	Db	16983	AGTCTGTGCACAGCTTACCATGCCACTTACAGCCAGTCCGCTCGCTGCCAGGGCC	17042
Qy	380	-----	380	Qy	571	roProProArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrP	591
Db	15963	CCTAGAATTGGGCTAGAACGAGGAGTCTTGTAATGATGTTTTTGTCAAGATCTCAAGG	16022	Db	17043	CCCTCCACAGTCCCATCTCAGGCATCCGCGCAGACTGTGGCGAGCGGAAGGTGTATC	17102
Qy	380	-----	380	Qy	591	roThrValHisThrSerProProGluThrLeuLysGluLysAlaLeuValGluValA	611
Db	16023	CTCAATAAATTTGAAAACCCCATGTCCTCCCTAATATTGGTTTCATTTCCACAGCATTCGCT	16082	Db	17103	CCACCGTGCAACACAGGCCCTCCACCGGAGACGCTGAAGGAGAAGGCACTAGTAGAGTGG	17162
Qy	380	-----	380	Qy	611	laAlaSerSerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerS	631
Db	16083	ACTCCTAATGGAAATTGCGGAAGGGGTGCTCGTCTCTGCAGGTGTGCGTGTATTAGGGAC	16142	Db	17163	CTGCCAGTCTGGGGCCCCCAACCTCCACACCTCAACATCCACCCCGGGCCCTACAGCT	17222
Qy	380	-----	380	Qy	631	erMetHisLysLeuLeuGluThrGlnSerThr-----	641
Db	16143	AGGGNAATTGAGAGATTGCAGGATAACACCATGTTCAATAGCAATATCTTGGAAATTTCA	16202	Db	17223	CCATGCACAAGCTGCTGGAGACACAGAGTACAGGTGAGAACTCTTGGGTGGAGCATGTGG	17282
Qy	380	-----	380	Qy	641	-----	641
				Db	17283	GTGCCCTCTGCTGGGGAAGTGGGTGGCGTCCAGAGGGGACTAGGGGGTCTTGGAGTCAGAG	17342

Qy 641 ----- 641
Db 17343 GGACGAGGCTTATATCTCATGCTGCTCTCATGGCTTAGGCACCTTCAACCAAGTCACA 17402
Qy 641 ----- 641
Db 17403 TCCCTGCTATGAGCTCGAATTTTCTCATCTGCTAAAGTGAACCTATAATTCCTACATTG 17462
Qy 641 ----- 641
Db 17463 TAATAGCAGTAACATATCATGTAATAAGCACCTGCTTCGTGCTTTGCAATGATCTCTAG 17522
Qy 641 ----- 641
Db 17523 CAACGTGGCACACAGCAATGGCTGTGTGCTGTGCATGCTTTGCGGGCAAAATTCAT 17582
Qy 641 ----- 641
Db 17583 TGGATCCTCTCTACCCATTAAAGTGATAGGCTTTCTTAGCATCCCATTTGTGTGATGAGA 17642
Qy 641 ----- 641
Db 17643 ACCAGGAGCTTGAGGGGATTCATGACTTGCCCAAGCCTTTGCTATTGGTGAGGGGCGG 17702
Qy 641 ----- 641
Db 17703 ACTCGGGCCCGCACTCGGACTCCTTGTGTGAGGCTCAGAGAGGAATGGTGTGTGAC 17762
Qy 641 ----- 641
Db 17763 TGTGCCAGCTTCATGCCCACTGGCTAAACCTGAGTCTCATTTGCTCCGCACAGGGAGA 17822
Qy 641 ----- 641
Db 17823 CCCAGTTCAGGAGCTGCTGTGTGATGGGTGACACTCCAGTGTGCGGGGAGTGAG 17882
Qy 641 ----- 641
Db 17883 ACATAGGAGCTCGGGCTCTCCCAGCAGACAGGTTCACTGTAGTGTGACGCCACGGC 17942
Qy 641 ----- 641
Db 17943 CTGTGTTTCAGGAAGGATGTGCACGTGGGAGCAGCGGGATATTCTGTGGGATGTTACG 18002
Qy 641 ----- 641
Db 18003 TGGGAATGTGGGCTGGGACCAGAGGTGCTATCACAGAACCAGAGCGAAAGTTCTAT 18062
Qy 641 ----- 641
Db 18063 GCCAGCTCCTCCACTACCTGCCAGGACGTGGGCCAGTGCATGCACCCACCGTTTATA 18122
Qy 641 ----- 641
Db 18123 TTTCTCTCTGTAAAGCAAGCTGGGCCCAATAATTACTCTCAGTGGGTGCTTACTGA 18182
Qy 641 ----- 641
Db 18183 CTCCCTCCTGTGTGCAGATGCAGTCAAGGGAGAAATGTCGTGAGAGCCACCTGGGGCC 18242
Qy 641 ----- 641
Db 18243 AGGCCCTGAGCGGGGGCTTCACATCCATGCTTTACTGTGCTACTCTCTGAGGTTCTCAT 18302
Qy 641 ----- 641
Db 18303 ATTCTGTGATCAAGCTGAATTTAAAGGACATTGATGCTTTGGGCTAGGTCCTCGAGTG 18362
Qy 641 ----- 641
Db 18363 TGTGGCACGAGTGATCTAGTATGCGTGTATGCGTCTATGCTCCATGAAGGGGTCACGTG 18422

Qy 641 ----- 641
Db 18423 TGTGTGTGCGTGTGTGCATGCACGTGTCTGGGTTCATATGATATGATGTGTGCATGT 18482
Qy 641 ----- 641
Db 18483 GCTTGATGTGTAGGTGCATGTGCGATGTGAAGCTCTTTCTTGGTGTGTGTGCATGTG 18542
Qy 641 ----- 641
Db 18543 TGCATATGCTGGCATATGTGCCGTGTGTGAATGTGTTGTGCACACATGTGTGGTATG 18602
Qy 641 ----- 641
Db 18603 TGCATGTATGTGCCCATATGTGGTGTCTCCAAATAGTATACATGTGTACACGAGTGTG 18662
Qy 641 ----- 641
Db 18663 GCATCTGGACACGTGTGCAGGTGCACGTGTCTGGTGTGGTGTGTGTCAAGTGCACGT 18722
Qy 641 ----- 641
Db 18723 GTGTGGCGGTCTTTAAGGATCCCATGGAAAGTCTGCTCAGAACAGTGTGTGATGTAGTC 18782
Qy 641 ----- 641
Db 18783 CTGCTTTCTGGGAAGGGAGGGGAGCGAGGCTCCTTGTCTGAAGGCACCTAGGATATAGG 18842
Qy 641 ----- 641
Db 18843 AGCTGTCCAGGACCTCAGAGGACATCCAGGCCACCTCTCTGAGGCCCCAGGACACTCAGCA 18902
Qy 641 ----- 641
Db 18903 GTGACTGTCAATGAATGTCTATTTCACATTAGGGCATCTTGTGGGTCAAGACTGCCCACT 18962
Qy 641 ----- 641
Db 18963 TGCCTGACATTTCAGCACCCCTGGCCCACTAAGTGCCTAGCACCCCATCACTGTAAACAAC 19022
Qy 641 ----- 641
Db 19023 CCAGACTCCCTGACTCATTTTACACATACTCACAGGCAGGTTAGCCCCAGGTACGAGAC 19082
Qy 642 ----- GlyAlaCysGlnSerSerCysIysIle 650
Db 19083 TCTGGAGCCTCTACCTCTACTCTCTGTTTCCAGGTGCTGCCAAAGCTCTTGCAAGATC 19142
Qy 651 SerSerProCysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCys 670
Db 19143 TCCAGCCTTGTCTTGAAGCAGACAGTGGAGCCTGTGGTCCAGACAGCTGCCCTACTGT 19202
Qy 671 AlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSer 690
Db 19203 GCCCGGCCGGGCGAGGGAGGTGGAGCTGCCACCGTGAATTCCTGACTCAGACAGC 19262
Qy 691 GluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSer 710
Db 19263 GAGCAGTTTATGATGTCACACAGGATGCCAGACAGCGACCTCCGGGACCCCAACAGC 19322
Qy 711 ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArg 730
Db 19323 CGGGCGGCAACGGAGCTTGGGCCCAGATGCAGAGCCAGCTCTGTGCTGGCCTTCTGGAGG 19382
Qy 731 LeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMet 750
Db 19383 CTATCTGTGACACCTTCCGAAAGATTGTGCACAGCAAGTACTTTGGCCGGGGAATCATG 19442
Qy 751 IleAlaIleLeuValAsnThrLeuSerMetClyIleGluTyrHisGluGlnProGluGlu 770
Db 19443 ATCCCACTCTGGTCAACACACTCAGCATGGGATCGAATACCAACAGCAGGTAGGAGAG 19502
Qy 771 LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet 790

```

Db      19503 TGGGAGAGGCA-----|||
Qy      791 LeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe 810
Db      19536 CGCCTGGGGCTG-----GGGCTTCTACCTCCCTCCGACCCCTCTCTCTGAGCTC 19586
Qy      811 AspGlyValIleValIleSer-ValTrpGluIleValGlyGlnGlnGlyGlyLe 830
Db      19587 AGCTTCTCTCCATGCTAGCCACCTGGCAGGTAGGAGGGAGGTGGGTGATGGA-- 19644
Qy      830 uSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe----- 847
Db      19645 ----GCAATGCATGGGGATTCTCTAGAGGGAGTGCTTAAAGTCTCTGAGTATGGAGGTCTG 19700
Qy      848 -----LeuPro-----AlaLeuGlnArgGlnLeuValVa 857
Db      19701 CCTCAGGTAGGCCACAGGGTATGTTCTACCCAGGAAGGCTGCTCAGAGGAGGCTGGCTTT 19760
Qy      857 I 857
Db      19761 G 19761

```

Search completed: July 10, 2006, 07:29:43
Job time : 1276.26 secs